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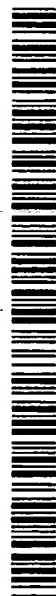
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(54) Title: NOVEL HUMAN GENES AND GENE EXPRESSION PRODUCTS

(57) Abstract: The invention provides novel polynucleotides. The invention further provides novel members of protein families, and polynucleotides that are differentially expressed in cancer cells relative to normal cells, and in metastatic cancer cells relative to normal cells or non-metastatic cancer cells.



WO 01/02568 A2

NOVEL HUMAN GENES AND GENE EXPRESSION PRODUCTS

FIELD OF THE INVENTION

The present invention relates to novel polynucleotides of human origin and the encoded gene products.

5 BACKGROUND OF THE INVENTION

Identification of novel polynucleotides, particularly those that encode an expressed gene product, is important in the advancement of drug discovery, diagnostic technologies, and the understanding of the progression and nature of complex diseases such as cancer. Identification of genes expressed in different cell types isolated from
10 sources that differ in disease state or stage, developmental stage, exposure to various environmental factors, the tissue of origin, the species from which the tissue was isolated, and the like is key to identifying the genetic factors that are responsible for the phenotypes associated with these various differences.

This invention provides novel human polynucleotides, the polypeptides
15 encoded by these polynucleotides, and the genes and proteins corresponding to these novel polynucleotides.

SUMMARY OF THE INVENTION

This invention relates to novel human polynucleotides and variants thereof, their encoded polypeptides and variants thereof, to genes corresponding to these
20 polynucleotides and to proteins expressed by the genes. The invention also relates to diagnostics and therapeutics comprising such novel human polynucleotides, their corresponding genes or gene products, including probes, antisense nucleotides, and antibodies. The polynucleotides of the invention correspond to a polynucleotide comprising the sequence information of at least one of SEQ ID NOs: 1-3351.

25 Various aspects and embodiments of the invention will be readily apparent to the ordinarily skilled artisan upon reading the description provided herein.

DETAILED DESCRIPTION OF THE INVENTION

The invention relates to polynucleotides comprising the disclosed nucleotide sequences, to full length cDNA, mRNA genomic sequences, and genes

corresponding to these sequences and degenerate variants thereof, and to polypeptides encoded by the polynucleotides of the invention and polypeptide variants.

Polypeptide variants differ from wild type protein in having one or more amino acid substitutions that either enhance, add, or diminish a biological activity of the wild type protein.

Six of the polypeptides disclosed herein encode new members of the MKK kinase family; the coding region is found within the nucleotide region in parentheses: SEQ ID NO:29 (nucleotides 295-421); SEQ ID NO:31 (298-397); SEQ ID NO:196 (37-322); SEQ ID NO:3175 (nucleotides 14-164); SEQ ID NO:3190 (229-390); and SEQ ID NO:3281 (15-182). Twenty-four of the polypeptides encode new members of the family of transcription factor proteins having a basic region plus leucine zipper: SEQ ID NO:410 (42-191); SEQ ID NO:552 (116-288); SEQ ID NO:768 (116-288); SEQ ID NO:822 (108-262); SEQ ID NO:836 (158-353); SEQ ID NO:1288 (73-234); SEQ ID NO:1365 (69-257); SEQ ID NO:1540 (289-471); SEQ ID NO:1549 (200-391); SEQ ID NO:1556 (163-354); SEQ ID NO:1557 (207-398); SEQ ID NO:1563 (107-298); SEQ ID NO:1622 (180-365); SEQ ID NO:1630 (100-291); SEQ ID NO:1704 (184-372); SEQ ID NO:1808 (36-161); SEQ ID NO:1454 (49-209); SEQ ID NO:2363 (48-211); SEQ ID NO:2424 (43-194); SEQ ID NO:3147 (190-369); SEQ ID NO:3152 (129-320); SEQ ID NO:3158 (167-334); and SEQ ID NO:3208 (34-256).

SEQ ID NOs:186 (175-395); 2591 (60-165); 3307 (43-321); and 3339 (94-342) encode polypeptides having an SH2 domain, and SEQ ID NOs:234 (23-121), 1832 (18-173), and 1835 (57-206) encode polypeptides having an SH3 domain. Nine polypeptides encode new members of the family of proteins having Ank repeat regions: SEQ ID NO:187 (358-432); SEQ ID NO:1268 (238-315); SEQ ID NO:1804 (301-378); SEQ ID NO:1819 (278-355); SEQ ID NO:1839 (224-307); SEQ ID NO:1830 (184-267); SEQ ID NO:2562 (18-101); SEQ ID NO:3015 (131-214); and SEQ ID NO:3267 (97-180).

The following eleven polynucleotides encode polypeptides having a C2H2 type zinc finger: SEQ ID NOs:308 (110-172); 807 (339-392); 1324 (294-356); 1503 (154-216); 1527 (156-212); 1674 (196-258); 1779 (64-126); 1801 (295-351); 3081 (190-252); 3193 (293-355); and 3306 (161-223). Eight polynucleotides encode polypeptides of the family of ATPases: SEQ ID NOs:431 (71-428); 639 (157-561); 2135 (2-401); 2684 (9-461); 2859 (100-320); 3178 (45-386); 3197 (281-343) and 3266 (8-139). Polypeptides having a fibronectin type III domain are encoded by SEQ ID NO:746 (209-427) and 1192 (186-416). Polypeptides having an EF-hand domain are encoded by SEQ ID NO:820 (341-

406); 1755 (281-367) and 3285(16-102). Six polypeptides of the protein kinase family are encoded by SEQ ID NOs:1157 (41-444); 1478 (54-437), 1496 (241-520); 2286 (12-182); 2969 (5-387); and 3190 (118-390).

LIM domain-containing polypeptides are encoded by SEQ ID NO:1269 (79-240); 1309 (248-404); 1360 (222-377); and 1386 (243-398). Two polypeptides of the family having a C2 domain (protein kinase C-like) are encoded by SEQ ID NO:1325 (1-234) and 2282(183-353). Polypeptides having a WD domain, G-beta repeat motif are encoded by SEQ ID NOs:1336 (66-164); 1380 (42-140); 1711 (263-361); 1762 (236-334); 1909 (160-258); 2218 (127-225); 3047 (191-292); 3108 (275-367) and 3292 (208-300).

10 SEQ ID NO:1410 (222-350) encodes a member of the trypsin family. SEQ ID NOs:1417 (8-354); 2281 (20-387) and 2310 (20-371) encode members of the protein tyrosine phosphatase family. SEQ ID NOs:1464 (4-180) and 1514 (2-252) encode members of the family having an RNA recognition motif (also known as RRM, RBD, or RNP domain). SEQ ID NOs:1496 (241-520) and 3297(7-153) encode helicases having a
15 conserved C-terminal domain. SEQ ID NO:1538 (9-635) encodes a member of the wnt family of developmental signaling proteins.

Three polynucleotides encode polypeptides having a homeobox domain: SEQ ID NOs:1676 (9-86); 1820 (123-299); and 1821 (127-303). A novel thioredoxin is encoded by SEQ ID NO:1677 (316-369). Two novel members of the ras family are
20 encoded by SEQ ID NO:1688(109-410) and 3258(138-394). A novel polypeptide having a phosphatidylinositol-specific phospholipase C Y-domain is encoded by SEQ ID NO:1707 (92-439). A novel serine carboxypeptidase is encoded by SEQ ID NO:1744 (238-433). A novel polypeptide having N-terminal homology in the Ets domain is encoded by SEQ ID NO:1811 (184-315). A novel polypeptide having a bromodomain is encoded by SEQ ID
25 NO:1814 (127-294). A novel polypeptide having a double-stranded RNA binding motif is encoded by SEQ ID NO:1818 (9-146). A novel polypeptide having a G-protein alpha subunit is encoded by SEQ ID NO:1846 (12-398).

SEQ ID NOs:1911 (35-151) and 1980 (60-197) encode polypeptides having a C3HC4 type zinc finger domain (RING finger). SEQ ID NO:2065 (253-306)
30 encodes a polypeptide having a CCHC zinc finger domain. SEQ ID NO:2216 (90-179) encodes a polypeptide having a WW/rsp5/WWP domain. SEQ ID NO:2428 (25-350) encodes a polypeptide member of the dual specificity phosphatase family, having a catalytic domain.

SEQ ID NOs:2577 (0-311); 3183 (14-215); and 3195 (0-215) encode
35 members of the 4 transmembrane segment integral membrane protein family. SEQ ID

NOs:2826 (116-400) and 2871 (198-392) encode polypeptides of the DEAD and DEAH box helicase family. SEQ ID NO:2944 (18-281) encodes a polypeptide having a calpain large subunit, domain III.

5 SEQ ID NO:3274 (11-187) encodes a eukaryotic transcription factor with a fork head domain. SEQ ID NO:3345 (65-271) encodes a polypeptide having a PDZ domain, and SEQ ID NO:3351 (124-270) encodes a polypeptide in the family of phorbol esters/glycerol binding proteins.

Described below are polynucleotide compositions encompassed by the invention, methods for obtaining cDNA or genomic DNA encoding a full-length gene
10 product, expression of these polynucleotides and genes, identification of structural motifs of the polynucleotides and genes, identification of the function of a gene product encoded by a gene corresponding to a polynucleotide of the invention, use of the provided polynucleotides as probes and in mapping and in tissue profiling, use of the corresponding polypeptides and other gene products to raise antibodies, and use of the polynucleotides
15 and their encoded gene products for therapeutic and diagnostic purposes.

Polynucleotide Compositions

The scope of the invention with respect to polynucleotide compositions includes, but is not necessarily limited to, polynucleotides having a sequence set forth in any one of SEQ ID NOs:1-3351; polynucleotides obtained from the biological materials
20 described herein or other biological sources (particularly human sources) by hybridization under stringent conditions (particularly conditions of high stringency); genes corresponding to the provided polynucleotides; variants of the provided polynucleotides and their corresponding genes, particularly those variants that retain a biological activity of the encoded gene product (*e.g.*, a biological activity ascribed to a
25 gene product corresponding to the provided polynucleotides as a result of the assignment of the gene product to a protein family(ies) and/or identification of a functional domain present in the gene product). Other nucleic acid compositions contemplated by and within the scope of the present invention will be readily apparent to one of ordinary skill in the art when provided with the disclosure here.
30 "Polynucleotide" and "nucleic acid" as used herein with reference to nucleic acids of the composition is not intended to be limiting as to the length or structure of the nucleic acid unless specifically indicated.

The invention features polynucleotides that are expressed in human tissue, specifically human colon, breast, and/or lung tissue. Novel nucleic acid

compositions of the invention comprise a sequence set forth in any one of SEQ ID NOs:1-3351 or an identifying sequence thereof. An "identifying sequence" is a contiguous sequence of residues at least about 10 nt to about 20 nt in length, usually at least about 50 nt to about 100 nt in length, that uniquely identifies a polynucleotide sequence, *e.g.*, exhibits less than 90%, usually less than about 80% to about 85% sequence identity to any contiguous nucleotide sequence of more than about 20 nt. Thus, the subject novel nucleic acid compositions include full length cDNAs or mRNAs that encompass an identifying sequence of contiguous nucleotides from any one of SEQ ID NOs:1-3351.

10 The polynucleotides of the invention also include polynucleotides having sequence similarity or sequence identity. Nucleic acids having sequence similarity are detected by hybridization under low stringency conditions, for example, at 50°C and 10XSSC (0.9 M saline/0.09 M sodium citrate) and remain bound when subjected to washing at 55°C in 1XSSC. Sequence identity can be determined by hybridization
15 under stringent conditions, for example, at 50°C or higher and 0.1XSSC (9 mM saline/0.9 mM sodium citrate). Hybridization methods and conditions are well known in the art, see, *e.g.*, U.S. Patent No. 5,707,829. Nucleic acids that are substantially identical to the provided polynucleotide sequences, *e.g.*, allelic variants, genetically altered versions of the gene, *etc.*, bind to the provided polynucleotide sequences (SEQ
20 ID NOs:1-3351) under stringent hybridization conditions. By using probes, particularly labeled probes of DNA sequences, one can isolate homologous or related genes. The source of homologous genes can be any species, *e.g.*, primate species, particularly human; rodents, such as rats and mice; canines, felines, bovines, ovines, equines, yeast, nematodes, *etc.*

25 Preferably, hybridization is performed using at least 15 contiguous nucleotides (nt) of at least one of SEQ ID NOs:1-3351. That is, when at least 15 contiguous nt of one of the disclosed SEQ ID NOs. is used as a probe, the probe will preferentially hybridize with a nucleic acid comprising the complementary sequence, allowing the identification and retrieval of the nucleic acids that uniquely hybridize to
30 the selected probe. Probes from more than one SEQ ID NO. can hybridize with the same nucleic acid if the cDNA from which they were derived corresponds to one mRNA. Probes of more than 15 nt can be used, *e.g.*, probes of from about 18 nt to about 100 nt, but 15 nt represents sufficient sequence for unique identification.

35 The polynucleotides of the invention also include naturally occurring variants of the nucleotide sequences (*e.g.*, degenerate variants, allelic variants).

5 Variants of the polynucleotides of the invention are identified by hybridization of putative variants with nucleotide sequences disclosed herein, preferably by hybridization under stringent conditions. For example, by using appropriate wash conditions, variants of the polynucleotides of the invention can be identified where the allelic variant exhibits at most about 25-30% base pair (bp) mismatches relative to the selected polynucleotide probe. In general, allelic variants contain 15-25% bp mismatches, and can contain as little as even 5-15%, or 2-5%, or 1-2% bp mismatches, as well as a single bp mismatch.

10 The invention also encompasses homologs corresponding to the polynucleotides of SEQ ID NOs:1-3351, where the source of homologous genes can be any mammalian species, *e.g.*, primate species, particularly human; rodents, such as rats; canines, felines, bovines, ovines, equines, yeast, nematodes, *etc.* Between mammalian species, *e.g.*, human and mouse, homologs generally have substantial sequence similarity, *e.g.*, at least 75% sequence identity, usually at least 90%, more usually at least 95% between nucleotide sequences. Sequence similarity is calculated based on a reference sequence, which may be a subset of a larger sequence, such as a conserved motif, coding region, flanking region, *etc.* A reference sequence will usually be at least about 18 contiguous nt long, more usually at least about 30 nt long, and may extend to the complete sequence that is being compared. Algorithms for sequence analysis are known in the art, such as BLAST, described in Altschul et al., *J. Mol. Biol.* (1990) 215:403-10.

25 In general, variants of the invention have a sequence identity greater than at least about 65%, preferably at least about 75%, more preferably at least about 85%, and can be greater than at least about 90%, 91%, 92%, 93%, 94%, 95%, or 96%, most preferably 97%, 98% or 99%. For the purposes of this invention, a preferred method of calculating percent identity is the Smith-Waterman algorithm, using the following. Global DNA sequence identity must be greater than 65% as determined by the Smith-Waterman homology search algorithm as implemented in MPSRCH program (Oxford Molecular) using an affine gap search with the following search parameters: gap open penalty, 12; and gap extension penalty, 1.

30 The subject nucleic acids can be cDNAs or genomic DNAs, as well as fragments thereof, particularly fragments that encode a biologically active gene product and/or are useful in the methods disclosed herein (*e.g.*, in diagnosis, as a unique identifier of a differentially expressed gene of interest, *etc.*). The term "cDNA" as used herein is intended to include all nucleic acids that share the arrangement of sequence

elements found in native mature mRNA species, where sequence elements are exons and 3' and 5' non-coding regions. Normally mRNA species have contiguous exons, with the intervening introns, when present, being removed by nuclear RNA splicing, to create a continuous open reading frame encoding a polypeptide of the invention.

5 A genomic sequence of interest comprises the nucleic acid present between the initiation codon and the stop codon, as defined in the listed sequences, including all of the introns that are normally present in a native chromosome. It can further include the 3' and 5' untranslated regions found in the mature mRNA. It can further include specific transcriptional and translational regulatory sequences, such as
10 promoters, enhancers, *etc.*, including about 1 kb, but possibly more, of flanking genomic DNA at either the 5' and 3' end of the transcribed region. The genomic DNA can be isolated as a fragment of 100 kbp or smaller; and substantially free of flanking chromosomal sequence. The genomic DNA flanking the coding region, either 3' and 5', or internal regulatory sequences as sometimes found in introns, contains sequences
15 required for proper tissue, stage-specific, or disease-state specific expression.

The nucleic acid compositions of the subject invention can encode all or a part of the subject polypeptides. Double or single stranded fragments can be obtained from the DNA sequence by chemically synthesizing oligonucleotides in accordance with conventional methods, by restriction enzyme digestion, by PCR amplification, *etc.*
20 Isolated polynucleotides and polynucleotide fragments of the invention comprise at least about 10, about 15, about 20, about 35, about 50, about 100, about 150 to about 200, about 250 to about 300, or about 350 contiguous nt selected from the polynucleotide sequences as shown in SEQ ID NOs:1-3351. The fragments also include those of lengths intermediate to the specifically mentioned lengths, such as 35,
25 36, 37, 38, 39, *etc.*; 150, 151, 152, 153, 154, *etc.* For the most part, fragments will be of at least 15 nt, usually at least 18 nt or 25 nt, and up to at least about 50 contiguous nt in length or more. In a preferred embodiment, the polynucleotide molecules comprise a contiguous sequence of at least 12 nt selected from the group consisting of the polynucleotides shown in SEQ ID NOs:1-3351.

30 Probes specific to the polynucleotides of the invention can be generated using the polynucleotide sequences disclosed in SEQ ID NOs:1-3351. The probes are preferably at least about a 12, 15, 16, 18, 20, 22, 24, or 25 nt fragment of a corresponding contiguous sequence of SEQ ID NOs:1-3351, and can be less than 2, 1, 0.5, 0.1, or 0.05 kb in length. The probes can be synthesized chemically or can be
35 generated from longer polynucleotides using restriction enzymes. The probes can be

labeled, for example, with a radioactive, biotinylated, or fluorescent tag. Preferably, probes are designed based upon an identifying sequence of a polynucleotide of one of SEQ ID NOs:1-3351. More preferably, probes are designed based on a contiguous sequence of one of the subject polynucleotides that remain unmasked following
5 application of a masking program for masking low complexity (*e.g.*, XBLAST) to the sequence., *i.e.*, one would select an unmasked region, as indicated by the polynucleotides outside the poly-n stretches of the masked sequence produced by the masking program.

The polynucleotides of the subject invention are isolated and obtained in
10 substantial purity, generally as other than an intact chromosome. Usually, the polynucleotides, either as DNA or RNA, will be obtained substantially free of other naturally-occurring nucleic acid sequences, generally being at least about 50%, usually at least about 90% pure and are typically "recombinant", *e.g.*, flanked by one or more nucleotides with which it is not normally associated on a naturally occurring
15 chromosome.

The polynucleotides of the invention can be provided as a linear molecule or within a circular molecule, and can be provided within autonomously replicating molecules (vectors) or within molecules without replication sequences. Expression of the polynucleotides can be regulated by their own or by other regulatory
20 sequences known in the art. The polynucleotides of the invention can be introduced into suitable host cells using a variety of techniques available in the art, such as transferrin polycation-mediated DNA transfer, transfection with naked or encapsulated nucleic acids, liposome-mediated DNA transfer, intracellular transportation of DNA-coated latex beads, protoplast fusion, viral infection, electroporation, gene gun, calcium
25 phosphate-mediated transfection, and the like.

The subject nucleic acid compositions can be used to, for example, produce polypeptides, as probes for the detection of mRNA of the invention in biological samples (*e.g.*, extracts of human cells) to generate additional copies of the polynucleotides, to generate ribozymes or antisense oligonucleotides, and as single
30 stranded DNA probes or as triple-strand forming oligonucleotides. The probes described herein can be used to, for example, determine the presence or absence of the polynucleotide sequences as shown in SEQ ID NOs:1-3351 or variants thereof in a sample. These and other uses are described in more detail below.

Use of Polynucleotides to Obtain Full-Length cDNA, Gene, and Promoter Region

Full-length cDNA molecules comprising the disclosed polynucleotides are obtained as follows. A polynucleotide having a sequence of one of SEQ ID NOs:1-3351, or a portion thereof comprising at least 12, 15, 18, or 20 nt, is used as a hybridization probe to detect hybridizing members of a cDNA library using probe design methods, cloning methods, and clone selection techniques such as those described in U.S. Patent No. 5,654,173. Libraries of cDNA are made from selected tissues, such as normal or tumor tissue, or from tissues of a mammal treated with, for example, a pharmaceutical agent. Preferably, the tissue is the same as the tissue from which the polynucleotides of the invention were isolated, as both the polynucleotides described herein and the cDNA represent expressed genes. Most preferably, the cDNA library is made from the biological material described herein in the Examples. The choice of cell type for library construction can be made after the identity of the protein encoded by the gene corresponding to the polynucleotide of the invention is known. This will indicate which tissue and cell types are likely to express the related gene, and thus represent a suitable source for the mRNA for generating the cDNA. As described in the Examples, cDNA of the invention was isolated from specific cell or tissue types, and such cells and tissues are preferable for obtaining related nucleic acids.

Techniques for producing and probing nucleic acid sequence libraries are described, for example, in Sambrook et al., *Molecular Cloning: A Laboratory Manual, 2nd Ed.*, (1989) Cold Spring Harbor Press, Cold Spring Harbor, NY. The cDNA can be prepared by using primers based on sequence from SEQ ID NOs:1-3351. In one embodiment, the cDNA library can be made from only poly-adenylated mRNA. Thus, poly-T primers can be used to prepare cDNA from the mRNA.

Members of the library that are larger than the provided polynucleotides, and preferably that encompass the complete coding sequence of the native message, are obtained. In order to confirm that the entire cDNA has been obtained, RNA protection experiments are performed as follows. Hybridization of a full-length cDNA to an mRNA will protect the RNA from RNase degradation. If the cDNA is not full length, then the portions of the mRNA that are not hybridized will be subject to RNase degradation. This is assayed, as is known in the art, by changes in electrophoretic mobility on polyacrylamide gels, or by detection of released monoribonucleotides. Sambrook et al., *Molecular Cloning: A Laboratory Manual, 2nd Ed.*, (1989) Cold Spring Harbor Press, Cold Spring Harbor, NY. In order to obtain additional sequences

5' to the end of a partial cDNA, 5' RACE (*PCR Protocols: A Guide to Methods and Applications*, (1990) Academic Press, Inc.) can be performed.

Genomic DNA is isolated using the provided polynucleotides in a manner similar to the isolation of full-length cDNAs. Briefly, the provided
5 polynucleotides, or portions thereof, are used as probes to libraries of genomic DNA. Preferably, the library is obtained from the cell type that was used to generate the polynucleotides of the invention, but this is not essential. Most preferably, the genomic DNA is obtained from the biological material described herein in the Examples. Such libraries can be in vectors suitable for carrying large segments of a genome, such as P1
10 or YAC, as described in detail in Sambrook et al., 9.4-9.30. In addition, genomic sequences can be isolated from human BAC libraries, which are commercially available from Research Genetics, Inc., Huntsville, Alabama, USA, for example. In order to obtain additional 5' or 3' sequences, chromosome walking is performed, as described in Sambrook et al., such that adjacent and overlapping fragments of genomic DNA are
15 isolated. These are mapped and pieced together, as is known in the art, using restriction digestion enzymes and DNA ligase.

Using the polynucleotide sequences of the invention, corresponding full-length genes can be isolated using both classical and PCR methods to construct and probe cDNA libraries. Using either method, Northern blots, preferably, are performed
20 on a number of cell types to determine which cell lines express the gene of interest at the highest level. Classical methods of constructing cDNA libraries are taught in Sambrook et al., *supra*. With these methods, cDNA can be produced from mRNA and inserted into viral or expression vectors. Typically, libraries of mRNA comprising poly(A) tails can be produced with poly(T) primers. Similarly, cDNA libraries can be
25 produced using the instant sequences as primers.

PCR methods are used to amplify the members of a cDNA library that comprise the desired insert. In this case, the desired insert will contain sequence from the full length cDNA that corresponds to the instant polynucleotides. Such PCR methods include gene trapping and RACE methods as described in Gruber et al., WO
30 95/04745 and Gruber et al., U.S. Patent No. 5,500,356. Kits are commercially available to perform gene trapping experiments from, for example, Life Technologies, Gaithersburg, Maryland, USA. In preferred embodiments of RACE, a common primer is designed to anneal to an arbitrary adaptor sequence ligated to cDNA ends (Apte and Siebert, *Biotechniques* (1993) 15:890-893; Edwards et al., *Nuc. Acids Res.* (1991)
35 19:5227-5232). When a single gene-specific RACE primer is paired with the common

primer, preferential amplification of sequences between the single gene specific primer and the common primer occurs. Commercial cDNA pools modified for use in RACE are available.

5 The promoter region of a gene generally is located 5' to the initiation site for RNA polymerase II. Hundreds of promoter regions contain the "TATA" box, a sequence such as TATTA or TATAA, which is sensitive to mutations. The promoter region can be obtained by performing 5' RACE using a primer from the coding region of the gene. Alternatively, the cDNA can be used as a probe for the genomic sequence, and the region 5' to the coding region is identified by "walking up." If the gene is
10 highly expressed or differentially expressed, the promoter from the gene can be of use in a regulatory construct for a heterologous gene.

Once the full-length cDNA or gene is obtained, DNA encoding variants can be prepared by site-directed mutagenesis, described in detail in Sambrook et al., 15.3-15.63. The choice of codon or nucleotide to be replaced can be based on disclosure
15 herein on optional changes in amino acids to achieve altered protein structure and/or function.

As an alternative method to obtaining DNA or RNA from a biological material, nucleic acid comprising nucleotides having the sequence of one or more polynucleotides of the invention can be synthesized. Thus, the invention encompasses
20 nucleic acid molecules ranging in length from 15 nt (corresponding to at least 15 contiguous nt of one of SEQ ID NOs:1-3351) up to a maximum length suitable for one or more biological manipulations, including replication and expression, of the nucleic acid molecule. The invention includes but is not limited to (a) nucleic acid having the size of a full gene, and comprising at least one of SEQ ID NOs:1-3351; (b) the nucleic
25 acid of (a) also comprising at least one additional polynucleotide or gene, operably linked to permit expression of a fusion protein; (c) an expression vector comprising (a) or (b); (d) a plasmid comprising (a) or (b) ; and (e) a recombinant viral particle comprising (a) or (b). Once provided with the polynucleotides disclosed herein, construction or preparation of (a) - (e) are well within the skill in the art.

30 The sequence of a nucleic acid comprising at least 15 contiguous nt of at least any one of SEQ ID NOs:1-3351, preferably the entire sequence of at least any one of SEQ ID NOs:1-3351, is not limited and can be any sequence of A, T, G, and/or C (for DNA) and A, U, G, and/or C (for RNA) or modified bases thereof, including inosine and pseudouridine. The choice of sequence will depend on the desired function
35 and can be dictated by coding regions desired, the intron-like regions desired, and the

regulatory regions desired. Where the entire sequence of any one of SEQ ID NOs:1-3351 is within the nucleic acid, the nucleic acid obtained is referred to herein as a polynucleotide comprising the sequence of any one of SEQ ID NOs:1-3351.

Expression of Polypeptide Encoded by Full-Length cDNA or Full-Length Gene

5 The provided polynucleotides (e.g., a polynucleotide having a sequence of one of SEQ ID NOs:1-3351), the corresponding cDNA, or the full-length gene is used to express a partial or complete gene product. Constructs of polynucleotides having sequences of SEQ ID NOs:1-3351 can be generated synthetically. Alternatively, single-step assembly of a gene and entire plasmid from large numbers of
10 oligodeoxyribonucleotides is described by, e.g., Stemmer et al., *Gene (Amsterdam)* (1995) 164(1):49-53. In this method, assembly PCR (the synthesis of long DNA sequences from large numbers of oligodeoxyribonucleotides (oligos)) is described. The method is derived from DNA shuffling (Stemmer, *Nature* (1994) 370:389-391), and does not rely on DNA ligase, but instead relies on DNA polymerase to build
15 increasingly longer DNA fragments during the assembly process.

Appropriate polynucleotide constructs are purified using standard recombinant DNA techniques as described in, for example, Sambrook et al., *Molecular Cloning: A Laboratory Manual, 2nd Ed.*, (1989) Cold Spring Harbor Press, Cold Spring Harbor, NY, and under current regulations described in United States Dept. of HHS,
20 National Institute of Health (NIH) Guidelines for Recombinant DNA Research. The gene product encoded by a polynucleotide of the invention is expressed in any expression system, including, for example, bacterial, yeast, insect, amphibian and mammalian systems. Vectors, host cells and methods for obtaining expression in same are well known in the art. Suitable vectors and host cells are described in U.S. Patent
25 No. 5,654,173.

Polynucleotide molecules comprising a polynucleotide sequence provided herein are generally propagated by placing the molecule in a vector. Viral and non-viral vectors are used, including plasmids. The choice of plasmid will depend on the type of cell in which propagation is desired and the purpose of propagation. Certain
30 vectors are useful for amplifying and making large amounts of the desired DNA sequence. Other vectors are suitable for expression in cells in culture. Still other vectors are suitable for transfer and expression in cells in a whole animal or person. The choice of appropriate vector is well within the skill of the art. Many such vectors are

available commercially. Methods for preparation of vectors comprising a desired sequence are well known in the art.

The polynucleotides set forth in SEQ ID NOs:1-3351 or their corresponding full-length polynucleotides are linked to regulatory sequences as appropriate to obtain the desired expression properties. These can include promoters (attached either at the 5' end of the sense strand or at the 3' end of the antisense strand), enhancers, terminators, operators, repressors, and inducers. The promoters can be regulated or constitutive. In some situations it may be desirable to use conditionally active promoters, such as tissue-specific or developmental stage-specific promoters. These are linked to the desired nucleotide sequence using the techniques described above for linkage to vectors. Any techniques known in the art can be used.

When any appropriate host cells or organisms are used to replicate and/or express the polynucleotides or nucleic acids of the invention, the resulting replicated nucleic acid, RNA, expressed protein or polypeptide, is within the scope of the invention as a product of the host cell or organism. The product is recovered by any appropriate means known in the art.

Once the gene corresponding to a selected polynucleotide is identified, its expression can be regulated in the cell to which the gene is native. For example, an endogenous gene of a cell can be regulated by an exogenous regulatory sequence as disclosed in U.S. Patent No. 5,641,670.

Identification of Functional and Structural Motifs of Novel Genes

Translations of the nucleotide sequence of the provided polynucleotides, cDNAs or full genes can be aligned with individual known sequences. Similarity with individual sequences can be used to determine the activity of the polypeptides encoded by the polynucleotides of the invention. Also, sequences exhibiting similarity with more than one individual sequence can exhibit activities that are characteristic of either or both individual sequences.

The full length sequences and fragments of the polynucleotide sequences of the nearest neighbors can be used as probes and primers to identify and isolate the full length sequence corresponding to provided polynucleotides. The nearest neighbors can indicate a tissue or cell type to be used to construct a library for the full-length sequences corresponding to the provided polynucleotides.

Typically, a selected polynucleotide is translated in all six frames to determine the best alignment with the individual sequences. The sequences disclosed

herein in the Sequence Listing are in a 5' to 3' orientation and translation in three frames can be sufficient. These amino acid sequences are referred to, generally, as query sequences, which will be aligned with the individual sequences. Databases with individual sequences are described in "Computer Methods for Macromolecular
5 Sequence Analysis" *Methods in Enzymology* (1996) 266, Doolittle, Academic Press, Inc., a division of Harcourt Brace & Co., San Diego, California, USA. Databases include Genbank, EMBL, and DNA Database of Japan (DDBJ).

Query and individual sequences can be aligned using the methods and computer programs described above, and include BLAST, available over the world
10 wide web at <http://www.ncbi.nlm.nih.gov/BLAST>. Another alignment algorithm is Fasta, available in the Genetics Computing Group (GCG) package, Madison, Wisconsin, USA, a wholly owned subsidiary of Oxford Molecular Group, Inc. Other techniques for alignment are described in Doolittle, *supra*. Preferably, an alignment program that permits gaps in the sequence is utilized to align the sequences. The
15 Smith-Waterman is one type of algorithm that permits gaps in sequence alignments. See *Meth. Mol. Biol.* (1997) 70: 173-187. Also, the GAP program using the Needleman and Wunsch alignment method can be utilized to align sequences. An alternative search strategy uses MPSRCH software, which runs on a MASPAR computer. MPSRCH uses a Smith-Waterman algorithm to score sequences on a massively parallel computer.
20 This approach improves ability to identify sequences that are distantly related matches, and is especially tolerant of small gaps and nucleotide sequence errors. Amino acid sequences encoded by the provided polynucleotides can be used to search both protein and DNA databases.

High Similarity. In general, in alignment results considered to be of high
25 similarity, the percent of the alignment region length is typically at least about 55% of total length query sequence; more typically, at least about 58%; even more typically; at least about 60% of the total residue length of the query sequence. Usually, percent length of the alignment region can be as much as about 62%; more usually, as much as about 64%; even more usually, as much as about 66%. Further, for high similarity, the
30 region of alignment, typically, exhibits at least about 75% of sequence identity; more typically, at least about 78%; even more typically; at least about 80% sequence identity. Usually, percent sequence identity can be as much as about 82%; more usually, as much as about 84%; even more usually, as much as about 86%.

The p value is used in conjunction with these methods. If high similarity
35 is found, the query sequence is considered to have high similarity with a profile

sequence when the p value is less than or equal to about 10^{-2} ; more usually; less than or equal to about 10^{-3} ; even more usually; less than or equal to about 10^{-4} . More typically, the p value is no more than about 10^{-5} ; more typically; no more than or equal to about 10^{-10} ; even more typically; no more than or equal to about 10^{-15} for the query sequence
5 to be considered high similarity.

Similarity Determined by Sequence Identity Alone. Sequence identity alone can be used to determine similarity of a query sequence to an individual sequence and can indicate the activity of the sequence. Such an alignment, preferably, permits gaps to align sequences. Typically, the query sequence is related to the profile sequence
10 if the sequence identity over the entire query sequence is at least about 15%; more typically, at least about 20%; even more typically, at least about 25%; even more typically, at least about 50%. Sequence identity alone as a measure of similarity is most useful when the query sequence is usually, at least 80 residues in length; more usually, 90 residues; even more usually, at least 95 amino acid residues in length. More
15 typically, similarity can be concluded based on sequence identity alone when the query sequence is preferably 100 residues in length; more preferably, 120 residues in length; even more preferably, 150 amino acid residues in length.

Alignments with Profile and Multiple Aligned Sequences. Translations of the provided polynucleotides can be aligned with amino acid profiles that define
20 either protein families or common motifs. Also, translations of the provided polynucleotides can be aligned to multiple sequence alignments (MSA) comprising the polypeptide sequences of members of protein families or motifs. Similarity or identity with profile sequences or MSAs can be used to determine the activity of the gene products (*e.g.*, polypeptides) encoded by the provided polynucleotides or corresponding
25 cDNA or genes. For example, sequences that show an identity or similarity with a chemokine profile or MSA can exhibit chemokine activities.

Profiles can be designed manually by (1) creating an MSA, which is an alignment of the amino acid sequence of members that belong to the family and (2) constructing a statistical representation of the alignment. Such methods are described,
30 for example, in Birney et al., *Nucl. Acid Res.* (1996) 24(14): 2730-2739. MSAs of some protein families and motifs are publicly available. MSAs are described also in Sonnhammer et al., *Proteins* (1997) 28: 405-420. A brief description of MSAs is reported in Pascarella et al., *Prot. Eng.* (1996) 9(3):249-251. Techniques for building profiles from MSAs are described in Sonnhammer et al., *supra*; Birney et al., *supra*;

and "Computer Methods for Macromolecular Sequence Analysis," *Methods in Enzymology* (1996) 266, Doolittle, Academic Press, Inc., San Diego, California, USA.

Similarity between a query sequence and a protein family or motif can be determined by (a) comparing the query sequence against the profile and/or (b) aligning
5 the query sequence with the members of the family or motif. Typically, a program such as Searchwise is used to compare the query sequence to the statistical representation of the multiple alignment, also known as a profile (see Birney et al., *supra*). Other techniques to compare the sequence and profile are described in Sonnhammer et al., *supra* and Doolittle, *supra*.

10 Next, methods described by Feng et al., *J. Mol. Evol.* (1987) 25:351 and Higgins et al., *CABIOS* (1989) 5:151 can be used align the query sequence with the members of a family or motif, also known as a MSA. Sequence alignments can be generated using any of a variety of software tools. Examples include PileUp, which creates a multiple sequence alignment, and is described in Feng et al., *J. Mol. Evol.*
15 (1987) 25:351. Another method, GAP, uses the alignment method of Needleman et al., *J. Mol. Biol.* (1970) 48:443. GAP is best suited for global alignment of sequences. A third method, BestFit, functions by inserting gaps to maximize the number of matches using the local homology algorithm of Smith et al., *Adv. Appl. Math.* (1981) 2:482. In general, the following factors are used to determine if a similarity between a query
20 sequence and a profile or MSA exists: (1) number of conserved residues found in the query sequence, (2) percentage of conserved residues found in the query sequence, (3) number of frameshifts, and (4) spacing between conserved residues.

Some alignment programs that both translate and align sequences can make any number of frameshifts when translating the nucleotide sequence to produce
25 the best alignment. The fewer frameshifts needed to produce an alignment, the stronger the similarity or identity between the query and profile or MSAs. For example, a weak similarity resulting from no frameshifts can be a better indication of activity or structure of a query sequence, than a strong similarity resulting from two frameshifts. Preferably, three or fewer frameshifts are found in an alignment; more preferably two or fewer
30 frameshifts; even more preferably, one or fewer frameshifts; even more preferably, no frameshifts are found in an alignment of query and profile or MSAs.

Conserved residues are those amino acids found at a particular position in all or some of the family or motif members. Alternatively, a position is considered conserved if only a certain class of amino acids is found in a particular position in all or

some of the family members. For example, the N-terminal position can contain a positively charged amino acid, such as lysine, arginine, or histidine.

Typically, a residue of a polypeptide is conserved when a class of amino acids or a single amino acid is found at a particular position in at least about 40% of all class members; more typically, at least about 50%; even more typically, at least about 60% of the members. Usually, a residue is conserved when a class or single amino acid is found in at least about 70% of the members of a family or motif; more usually, at least about 80%; even more usually, at least about 90%; even more usually, at least about 95%.

10 A residue is considered conserved when three unrelated amino acids are found at a particular position in the some or all of the members; more usually, two unrelated amino acids. These residues are conserved when the unrelated amino acids are found at particular positions in at least about 40% of all class member; more typically, at least about 50%; even more typically, at least about 60% of the members.
15 Usually, a residue is conserved when a class or single amino acid is found in at least about 70% of the members of a family or motif; more usually, at least about 80%; even more usually, at least about 90%; even more usually, at least about 95%.

A query sequence has similarity to a profile or MSA when the query sequence comprises at least about 25% of the conserved residues of the profile or MSA; more usually, at least about 30%; even more usually, at least about 40%. Typically, the query sequence has a stronger similarity to a profile sequence or MSA when the query sequence comprises at least about 45% of the conserved residues of the profile or MSA; more typically, at least about 50%; even more typically, at least about 55%.

Identification of Secreted and Membrane-Bound Polypeptides

25 Both secreted and membrane-bound polypeptides of the present invention are of particular interest. For example, levels of secreted polypeptides can be assayed in body fluids that are convenient, such as blood, plasma, serum, and other body fluids such as urine, prostatic fluid and semen. Membrane-bound polypeptides are useful for constructing vaccine antigens or inducing an immune response. Such
30 antigens would comprise all or part of the extracellular region of the membrane-bound polypeptides. Because both secreted and membrane-bound polypeptides comprise a fragment of contiguous hydrophobic amino acids, hydrophobicity predicting algorithms can be used to identify such polypeptides.

A signal sequence is usually encoded by both secreted and membrane-bound polypeptide genes to direct a polypeptide to the surface of the cell. The signal sequence usually comprises a stretch of hydrophobic residues. Such signal sequences can fold into helical structures. Membrane-bound polypeptides typically comprise at least one transmembrane region that possesses a stretch of hydrophobic amino acids that can transverse the membrane. Some transmembrane regions also exhibit a helical structure. Hydrophobic fragments within a polypeptide can be identified by using computer algorithms. Such algorithms include Hopp & Woods, *Proc. Natl. Acad. Sci. USA* (1981) 78:3824-3828; Kyte & Doolittle, *J. Mol. Biol.* (1982) 157: 105-132; and RAOAR algorithm, Degli Esposti et al., *Eur. J. Biochem.* (1990) 190: 207-219.

Another method of identifying secreted and membrane-bound polypeptides is to translate the polynucleotides of the invention in all six frames and determine if at least 8 contiguous hydrophobic amino acids are present. Those translated polypeptides with at least 8; more typically, 10; even more typically, 12 contiguous hydrophobic amino acids are considered to be either a putative secreted or membrane bound polypeptide. Hydrophobic amino acids include alanine, glycine, histidine, isoleucine, leucine, lysine, methionine, phenylalanine, proline, threonine, tryptophan, tyrosine, and valine

Identification of the Function of an Expression Product of a Full-Length Gene

Ribozymes, antisense constructs, and dominant negative mutants can be used to determine function of the expression product of a gene corresponding to a polynucleotide provided herein. The phosphoramidite method of oligonucleotide synthesis can be used to construct antisense molecules and ribozymes. See Beaucage et al., *Tet. Lett.* (1981) 22:1859 and U.S. Patent No. 4,668,777. Automated devices for synthesis are available to create oligonucleotides using this chemistry. Examples of such devices include Biosearch 8600, Models 392 and 394 by Applied Biosystems, a division of Perkin-Elmer Corp., Foster City, California, USA; and Expedite by Perceptive Biosystems, Framingham, Massachusetts, USA. Synthetic RNA, phosphate analog oligonucleotides, and chemically derivatized oligonucleotides can also be produced, and can be covalently attached to other molecules. RNA oligonucleotides can be synthesized, for example, using RNA phosphoramidites. This method can be performed on an automated synthesizer, such as Applied Biosystems, Models 392 and 394, Foster City, California, USA.

Oligonucleotides of up to 200 nt can be synthesized, more typically, 100 nt, more typically 50 nt; even more typically 30 to 40 nt. These synthetic fragments can be annealed and ligated together to construct larger fragments. See, for example, Sambrook et al., *supra*. Trans-cleaving catalytic RNAs (ribozymes) are RNA molecules possessing endoribonuclease activity. Ribozymes are specifically designed for a particular target, and the target message must contain a specific nucleotide sequence. They are engineered to cleave any RNA species site-specifically in the background of cellular RNA. The cleavage event renders the mRNA unstable and prevents protein expression. Importantly, ribozymes can be used to inhibit expression of a gene of unknown function for the purpose of determining its function in an *in vitro* or *in vivo* context, by detecting the phenotypic effect.

Antisense nucleic acids are designed to specifically bind to RNA, resulting in the formation of RNA-DNA or RNA-RNA hybrids, with an arrest of DNA replication, reverse transcription or messenger RNA translation. Antisense polynucleotides based on a selected polynucleotide sequence can interfere with expression of the corresponding gene. Antisense polynucleotides are typically generated within the cell by expression from antisense constructs that contain the antisense strand as the transcribed strand. Antisense polynucleotides based on the disclosed polynucleotides will bind and/or interfere with the translation of mRNA comprising a sequence complementary to the antisense polynucleotide. The expression products of control cells and cells treated with the antisense construct are compared to detect the protein product of the gene corresponding to the polynucleotide upon which the antisense construct is based. The protein is isolated and identified using routine biochemical methods.

Given the extensive background literature and clinical experience in antisense therapy, one skilled in the art can use selected polynucleotides of the invention as additional potential therapeutics. The choice of polynucleotide can be narrowed by first testing them for binding to "hot spot" regions of the genome of cancerous cells. If a polynucleotide is identified as binding to a "hot spot," testing the polynucleotide as an antisense compound in the corresponding cancer cells is warranted.

Dominant negative mutations also are readily generated for corresponding proteins that are active as homomultimers. A mutant polypeptide will interact with wild-type polypeptides (made from the other allele) and form a non-functional multimer. Thus, a mutation is in a substrate-binding domain, a catalytic

domain, or a cellular localization domain. Preferably, the mutant polypeptide will be overproduced. Point mutations are made that have such an effect. In addition, fusion of different polypeptides of various lengths to the terminus of a protein can yield dominant negative mutants. General strategies are available for making dominant negative mutants (see, *e.g.*, Herskowitz, *Nature* (1987) 329:219). Such techniques can be used to create loss of function mutations, which are useful for determining protein function.

Polypeptides and Variants Thereof

The polypeptides of the invention include those encoded by the disclosed polynucleotides, as well as nucleic acids that, by virtue of the degeneracy of the genetic code, are not identical in sequence to the disclosed polynucleotides. Thus, the invention includes within its scope a polypeptide encoded by a polynucleotide having the sequence of any one of SEQ ID NOs:1-3351 or a variant thereof.

In general, the term "polypeptide" as used herein refers to both the full length polypeptide encoded by the recited polynucleotide, the polypeptide encoded by the gene represented by the recited polynucleotide, as well as portions or fragments thereof. "Polypeptides" also includes variants of the naturally occurring proteins, where such variants are homologous or substantially similar to the naturally occurring protein, and can be of an origin of the same or different species as the naturally occurring protein (*e.g.*, human, murine, or some other species that naturally expresses the recited polypeptide, usually a mammalian species). In general, variant polypeptides have a sequence that has at least about 80%, usually at least about 90%, and more usually at least about 98% sequence identity with a differentially expressed polypeptide of the invention, as measured by BLAST using the parameters described above. The variant polypeptides can be naturally or non-naturally glycosylated, *i.e.*, the polypeptide has a glycosylation pattern that differs from the glycosylation pattern found in the corresponding naturally occurring protein.

The invention also encompasses homologs of the disclosed polypeptides (or fragments thereof) where the homologs are isolated from other species, *i.e.*, other animal or plant species, where such homologs, usually mammalian species, *e.g.*, rodents, such as mice, rats; domestic animals, *e.g.*, horse, cow, dog, cat; and humans. By "homolog" is meant a polypeptide having at least about 35%, usually at least about 40% and more usually at least about 60% amino acid sequence identity to a particular differentially expressed protein as identified above, where sequence identity is determined using the BLAST algorithm, with the parameters described above.

In general, the polypeptides of the subject invention are provided in a non-naturally occurring environment, *e.g.*, are separated from their naturally occurring environment. In certain embodiments, the subject protein is present in a composition that is enriched for the protein as compared to a control. As such, purified polypeptide
5 is provided, where by purified is meant that the protein is present in a composition that is substantially free of non-differentially expressed polypeptides, where by substantially free is meant that less than 90%, usually less than 60% and more usually less than 50% of the composition is made up of non-differentially expressed polypeptides.

Also within the scope of the invention are variants; variants of
10 polypeptides include mutants, fragments, and fusions. Mutants can include amino acid substitutions, additions or deletions. The amino acid substitutions can be conservative amino acid substitutions or substitutions to eliminate non-essential amino acids, such as to alter a glycosylation site, a phosphorylation site or an acetylation site, or to minimize misfolding by substitution or deletion of one or more cysteine residues that are not
15 necessary for function. Conservative amino acid substitutions are those that preserve the general charge, hydrophobicity/ hydrophilicity, and/or steric bulk of the amino acid substituted. Variants can be designed so as to retain biological activity of a particular region of the protein (*e.g.*, a functional domain and/or, where the polypeptide is a member of a protein family, a region associated with a consensus sequence). Selection
20 of amino acid alterations for production of variants can be based upon the accessibility (interior vs. exterior) of the amino acid (see, *e.g.*, Go et al., *Int. J. Peptide Protein Res.* (1980) 15:211), the thermostability of the variant polypeptide (see, *e.g.*, Querol et al., *Prot. Eng.* (1996) 9:265), desired glycosylation sites (see, *e.g.*, Olsen and Thomsen, *J. Gen. Microbiol.* (1991) 137:579), desired disulfide bridges (see, *e.g.*, Clarke et al.,
25 *Biochemistry* (1993) 32:4322; and Wakarchuk et al., *Protein Eng.* (1994) 7:1379), desired metal binding sites (see, *e.g.*, Toma et al., *Biochemistry* (1991) 30:97, and Haezebrouck et al., *Protein Eng.* (1993) 6:643), and desired substitutions with in proline loops (see, *e.g.*, Masul et al., *Appl. Env. Microbiol.* (1994) 60:3579). Cysteine-depleted muteins can be produced as disclosed in U.S. Patent No. 4,959,314.

30 Variants also include fragments of the polypeptides disclosed herein, particularly biologically active fragments and/or fragments corresponding to functional domains. Fragments of interest will typically be at least about 10 aa to at least about 15 aa in length, usually at least about 50 aa in length, and can be as long as 300 aa in length or longer, but will usually not exceed about 1000 aa in length, where the fragment will
35 have a stretch of amino acids that is identical to a polypeptide encoded by a

polynucleotide having a sequence of any SEQ ID NOs:1-3351, or a homolog thereof. The protein variants described herein are encoded by polynucleotides that are within the scope of the invention. The genetic code can be used to select the appropriate codons to construct the corresponding variants.

5 Computer-Related Embodiments

In general, a library of polynucleotides is a collection of sequence information, which information is provided in either biochemical form (*e.g.*, as a collection of polynucleotide molecules), or in electronic form (*e.g.*, as a collection of polynucleotide sequences stored in a computer-readable form, as in a computer system and/or as part of a computer program). The sequence information of the polynucleotides can be used in a variety of ways, *e.g.*, as a resource for gene discovery, as a representation of sequences expressed in a selected cell type (*e.g.*, cell type markers), and/or as markers of a given disease or disease state. In general, a disease marker is a representation of a gene product that is present in all cells affected by disease either at an increased or decreased level relative to a normal cell (*e.g.*, a cell of the same or similar type that is not substantially affected by disease). For example, a polynucleotide sequence in a library can be a polynucleotide that represents an mRNA, polypeptide, or other gene product encoded by the polynucleotide, that is either overexpressed or underexpressed in a breast ductal cell affected by cancer relative to a normal (*i.e.*, substantially disease-free) breast cell.

The nucleotide sequence information of the library can be embodied in any suitable form, *e.g.*, electronic or biochemical forms. For example, a library of sequence information embodied in electronic form comprises an accessible computer data file (or, in biochemical form, a collection of nucleic acid molecules) that contains the representative nucleotide sequences of genes that are differentially expressed (*e.g.*, overexpressed or underexpressed) as between, for example, i) a cancerous cell and a normal cell; ii) a cancerous cell and a dysplastic cell; iii) a cancerous cell and a cell affected by a disease or condition other than cancer; iv) a metastatic cancerous cell and a normal cell and/or non-metastatic cancerous cell; v) a malignant cancerous cell and a non-malignant cancerous cell (or a normal cell) and/or vi) a dysplastic cell relative to a normal cell. Other combinations and comparisons of cells affected by various diseases or stages of disease will be readily apparent to the ordinarily skilled artisan. Biochemical embodiments of the library include a collection of nucleic acids that have

the sequences of the genes in the library, where the nucleic acids can correspond to the entire gene in the library or to a fragment thereof, as described in greater detail below.

The polynucleotide libraries of the subject invention generally comprise sequence information of a plurality of polynucleotide sequences, where at least one of the polynucleotides has a sequence of any of SEQ ID NOs:1-3351. By plurality is meant at least 2, usually at least 3 and can include up to all of SEQ ID NOs:1-3351. The length and number of polynucleotides in the library will vary with the nature of the library, *e.g.*, if the library is an oligonucleotide array, a cDNA array, a computer database of the sequence information, *etc.*

Where the library is an electronic library, the nucleic acid sequence information can be present in a variety of media. "Media" refers to a manufacture, other than an isolated nucleic acid molecule, that contains the sequence information of the present invention. Such a manufacture provides the genome sequence or a subset thereof in a form that can be examined by means not directly applicable to the sequence as it exists in a nucleic acid. For example, the nucleotide sequence of the present invention, *e.g.*, the nucleic acid sequences of any of the polynucleotides of SEQ ID NOs:1-3351, can be recorded on computer readable media, *e.g.*, any medium that can be read and accessed directly by a computer. Such media include, but are not limited to: magnetic storage media, such as a floppy disc, a hard disc storage medium, and a magnetic tape; optical storage media such as CD-ROM; electrical storage media such as RAM and ROM; and hybrids of these categories such as magnetic/optical storage media. One of skill in the art can readily appreciate how any of the presently known computer readable mediums can be used to create a manufacture comprising a recording of the present sequence information. "Recorded" refers to a process for storing information on computer readable medium, using any such methods as known in the art. Any convenient data storage structure can be chosen, based on the means used to access the stored information. A variety of data processor programs and formats can be used for storage, *e.g.*, word processing text file, database format, *etc.* In addition to the sequence information, electronic versions of the libraries of the invention can be provided in conjunction or connection with other computer-readable information and/or other types of computer-readable files (*e.g.*, searchable files, executable files, *etc.*, including, but not limited to, for example, search program software, *etc.*).

By providing the nucleotide sequence in computer readable form, the information can be accessed for a variety of purposes. Computer software to access sequence information is publicly available. For example, the BLAST (Altschul et al.,

supra.) and BLAZE (Brutlag et al. *Comp. Chem.* (1993) 17:203) search algorithms on a Sybase system can be used to identify open reading frames (ORFs) within the genome that contain homology to ORFs from other organisms.

As used herein, "a computer-based system" refers to the hardware means, software means, and data storage means used to analyze the nucleotide sequence information of the present invention. The minimum hardware of the computer-based systems of the present invention comprises a central processing unit (CPU), input means, output means, and data storage means. A skilled artisan can readily appreciate that any one of the currently available computer-based system are suitable for use in the present invention. The data storage means can comprise any manufacture comprising a recording of the present sequence information as described above, or a memory access means that can access such a manufacture.

"Search means" refers to one or more programs implemented on the computer-based system, to compare a target sequence or target structural motif, or expression levels of a polynucleotide in a sample, with the stored sequence information. Search means can be used to identify fragments or regions of the genome that match a particular target sequence or target motif. A variety of known algorithms are publicly known and commercially available, *e.g.*, MacPattern (EMBL), BLASTN and BLASTX (NCBI). A "target sequence" can be any polynucleotide or amino acid sequence of six or more contiguous nucleotides or two or more amino acids, preferably from about 10 to 100 amino acids or from about 30 to 300 nt. A variety of comparing means can be used to accomplish comparison of sequence information from a sample (*e.g.*, to analyze target sequences, target motifs, or relative expression levels) with the data storage means. A skilled artisan can readily recognize that any one of the publicly available homology search programs can be used as the search means for the computer based systems of the present invention to accomplish comparison of target sequences and motifs. Computer programs to analyze expression levels in a sample and in controls are also known in the art.

A "target structural motif," or "target motif," refers to any rationally selected sequence or combination of sequences in which the sequence(s) are chosen based on a three-dimensional configuration that is formed upon the folding of the target motif, or on consensus sequences of regulatory or active sites. There are a variety of target motifs known in the art. Protein target motifs include, but are not limited to, enzyme active sites and signal sequences. Nucleic acid target motifs include, but are

not limited to, hairpin structures, promoter sequences and other expression elements such as binding sites for transcription factors.

A variety of structural formats for the input and output means can be used to input and output the information in the computer-based systems of the present invention. One format for an output means ranks the relative expression levels of different polynucleotides. Such presentation provides a skilled artisan with a ranking of relative expression levels to determine a gene expression profile.

As discussed above, the "library" of the invention also encompasses biochemical libraries of the polynucleotides of SEQ ID NOs:1-3351, *e.g.*, collections of nucleic acids representing the provided polynucleotides. The biochemical libraries can take a variety of forms, *e.g.*, a solution of cDNAs, a pattern of probe nucleic acids stably associated with a surface of a solid support (*i.e.*, an array) and the like. Of particular interest are nucleic acid arrays in which one or more of SEQ ID NOs:1-3351 is represented on the array. By array is meant an article of manufacture that has at least a substrate with at least two distinct nucleic acid targets on one of its surfaces, where the number of distinct nucleic acids can be considerably higher, typically being at least 10 nt, usually at least 20 nt and often at least 25 nt. A variety of different array formats have been developed and are known to those of skill in the art. The arrays of the subject invention find use in a variety of applications, including gene expression analysis, drug screening, mutation analysis and the like, as disclosed in the above-listed exemplary patent documents.

In addition to the above nucleic acid libraries, analogous libraries of polypeptides are also provided, where the where the polypeptides of the library will represent at least a portion of the polypeptides encoded by SEQ ID NOs:1-3351.

25 Use of Polynucleotide Probes in Mapping, and in Tissue Profiling

Polynucleotide probes, generally comprising at least 12 contiguous nt of a polynucleotide as shown in the Sequence Listing, are used for a variety of purposes, such as chromosome mapping of the polynucleotide and detection of transcription levels. Additional disclosure about preferred regions of the disclosed polynucleotide sequences is found in the Examples. A probe that hybridizes specifically to a polynucleotide disclosed herein should provide a detection signal at least 5-, 10-, or 20-fold higher than the background hybridization provided with other unrelated sequences.

Detection of Expression Levels. Nucleotide probes are used to detect expression of a gene corresponding to the provided polynucleotide. In Northern blots,

mRNA is separated electrophoretically and contacted with a probe. A probe is detected as hybridizing to an mRNA species of a particular size. The amount of hybridization is quantitated to determine relative amounts of expression, for example under a particular condition. Probes are used for *in situ* hybridization to cells to detect expression. Probes
5 can also be used *in vivo* for diagnostic detection of hybridizing sequences. Probes are typically labeled with a radioactive isotope. Other types of detectable labels can be used such as chromophores, fluors, and enzymes. Other examples of nucleotide hybridization assays are described in WO92/02526 and U.S. Patent No. 5,124,246.

Alternatively, the Polymerase Chain Reaction (PCR) is another means
10 for detecting small amounts of target nucleic acids (see, *e.g.*, Mullis et al., *Meth. Enzymol.* (1987) 155:335; U.S. Patent No. 4,683,195; and U.S. Patent No. 4,683,202). Two primer polynucleotides nucleotides that hybridize with the target nucleic acids are used to prime the reaction. The primers can be composed of sequence within or 3' and 5' to the polynucleotides of the Sequence Listing. Alternatively, if the primers are 3' and
15 5' to these polynucleotides, they need not hybridize to them or the complements. After amplification of the target with a thermostable polymerase, the amplified target nucleic acids can be detected by methods known in the art, *e.g.*, Southern blot. mRNA or cDNA can also be detected by traditional blotting techniques (*e.g.*, Southern blot, Northern blot, *etc.*) described in Sambrook et al., "Molecular Cloning: A Laboratory
20 Manual" (New York, Cold Spring Harbor Laboratory, 1989) (*e.g.*, without PCR amplification). In general, mRNA or cDNA generated from mRNA using a polymerase enzyme can be purified and separated using gel electrophoresis, and transferred to a solid support, such as nitrocellulose. The solid support is exposed to a labeled probe, washed to remove any unhybridized probe, and duplexes containing the labeled probe
25 are detected.

Mapping. Polynucleotides of the present invention can be used to identify a chromosome on which the corresponding gene resides. Such mapping can be useful in identifying the function of the polynucleotide-related gene by its proximity to other genes with known function. Function can also be assigned to the polynucleotide-
30 related gene when particular syndromes or diseases map to the same chromosome. For example, use of polynucleotide probes in identification and quantification of nucleic acid sequence aberrations is described in U.S. Patent No. 5,783,387. An exemplary mapping method is fluorescence *in situ* hybridization (FISH), which facilitates comparative genomic hybridization to allow total genome assessment of changes in
35 relative copy number of DNA sequences (see, *e.g.*, Valdes et al., *Methods in Molecular*

Biology (1997) 68:1). Polynucleotides can also be mapped to particular chromosomes using, for example, radiation hybrids or chromosome-specific hybrid panels. See Leach et al., *Advances in Genetics*, (1995) 33:63-99; Walter et al., *Nature Genetics* (1994) 7:22; Walter and Goodfellow, *Trends in Genetics* (1992) 9:352. Panels for radiation hybrid mapping are available from Research Genetics, Inc., Huntsville, Alabama, USA. The statistical program RHMAP can be used to construct a map based on the data from radiation hybridization with a measure of the relative likelihood of one order versus another. RHMAP is available via the world wide web at <http://www.sph.umich.edu/group/statgen/software>. In addition, commercial programs are available for identifying regions of chromosomes commonly associated with disease, such as cancer.

Tissue Typing or Profiling. Expression of specific mRNA corresponding to the provided polynucleotides can vary in different cell types and can be tissue-specific. This variation of mRNA levels in different cell types can be exploited with nucleic acid probe assays to determine tissue types. For example, PCR, branched DNA probe assays, or blotting techniques utilizing nucleic acid probes substantially identical or complementary to polynucleotides listed in the Sequence Listing can determine the presence or absence of the corresponding cDNA or mRNA.

Tissue typing can be used to identify the developmental organ or tissue source of a metastatic lesion by identifying the expression of a particular marker of that organ or tissue. If a polynucleotide is expressed only in a specific tissue type, and a metastatic lesion is found to express that polynucleotide, then the developmental source of the lesion has been identified. Expression of a particular polynucleotide can be assayed by detection of either the corresponding mRNA or the protein product.

Use of Polymorphisms. A polynucleotide of the invention can be used in forensics, genetic analysis, mapping, and diagnostic applications where the corresponding region of a gene is polymorphic in the human population. Any means for detecting a polymorphism in a gene can be used, including, but not limited to electrophoresis of protein polymorphic variants, differential sensitivity to restriction enzyme cleavage, and hybridization to allele-specific probes.

30 Antibody Production

Expression products of a polynucleotide of the invention, as well as the corresponding mRNA, cDNA, or complete gene, can be prepared and used for raising antibodies for experimental, diagnostic, and therapeutic purposes. For polynucleotides to which a corresponding gene has not been assigned, this provides an additional

method of identifying the corresponding gene. The polynucleotide or related cDNA is expressed as described above, and antibodies are prepared. These antibodies are specific to an epitope on the polypeptide encoded by the polynucleotide, and can precipitate or bind to the corresponding native protein in a cell or tissue preparation or
5 in a cell-free extract of an *in vitro* expression system.

Methods for production of monoclonal and polyclonal antibodies that specifically bind a selected antigen are well known in the art. The antibodies specifically bind to epitopes present in the polypeptides encoded by polynucleotides disclosed in the Sequence Listing. Typically, at least 6, 8, 10, or 12 contiguous amino
10 acids are required to form an epitope. Epitopes that involve non-contiguous amino acids may require a longer polypeptide, *e.g.*, at least 15, 25, or 50 amino acids. Antibodies that specifically bind to human polypeptides encoded by the provided polynucleotides should provide a detection signal at least 5-, 10-, or 20-fold higher than a detection signal provided with other proteins when used in Western blots or other
15 immunochemical assays. Preferably, antibodies that specifically polypeptides of the invention do not bind to other proteins in immunochemical assays at detectable levels and can immunoprecipitate the specific polypeptide from solution.

The invention also contemplates naturally occurring antibodies specific for a polypeptide of the invention. For example, serum antibodies to a polypeptide of
20 the invention in a human population can be purified by methods well known in the art, *e.g.*, by passing antiserum over a column to which the corresponding selected polypeptide or fusion protein is bound. The bound antibodies can then be eluted from the column, for example using a buffer with a high salt concentration.

In addition to the antibodies discussed above, the invention also
25 contemplates genetically engineered antibodies, antibody derivatives (*e.g.*, single chain antibodies, antibody fragments (*e.g.*, Fab, *etc.*)), according to methods well known in the art.

Other embodiments of the present invention include humanized monoclonal antibodies capable of binding to the polypeptides of the invention. The
30 phrase "humanized antibody" refers to an antibody derived from a non-human antibody - typically a mouse monoclonal antibody. Alternatively, a humanized antibody may be derived from a chimeric antibody that retains or substantially retains the antigen-binding properties of the parental, non-human, antibody but which exhibits diminished immunogenicity as compared to the parental antibody when administered to humans.
35 The phrase "chimeric antibody," as used herein, refers to an antibody containing

sequence derived from two different antibodies (*see, e.g.,* U.S. Patent No. 4,816,567) which typically originate from different species. Most typically, chimeric antibodies comprise human and murine antibody fragments, generally human constant and mouse variable regions.

5 Because humanized antibodies are far less immunogenic in humans than the parental mouse monoclonal antibodies, they can be used for the treatment of humans with far less risk of anaphylaxis. Thus, these antibodies may be preferred in therapeutic applications that involve *in vivo* administration to a human such as, *e.g.,* use as radiation sensitizers for the treatment of neoplastic disease or use in methods to reduce the side
10 effects of, *e.g.,* cancer therapy.

Humanized antibodies may be achieved by a variety of methods including, for example: (1) grafting the non-human complementarity determining regions (CDRs) onto a human framework and constant region (a process referred to in the art as "humanizing"), or, alternatively, (2) transplanting the entire non-human
15 variable domains, but "cloaking" them with a human-like surface by replacement of surface residues (a process referred to in the art as "veneering"). In the present invention, humanized antibodies will include both "humanized" and "veneered" antibodies. These methods are disclosed in, *e.g.,* Jones et al., *Nature* 321:522-525 (1986); Morrison et al., *Proc. Natl. Acad. Sci., U.S.A.*, 81:6851-6855 (1984); Morrison and Oi, *Adv. Immunol.*, 44:65-92 (1988); Verhoeyer et al., *Science* 239:1534-1536
20 (1988); Padlan, *Molec. Immunol.* 28:489-498 (1991); Padlan, *Molec. Immunol.* 31(3):169-217 (1994); and Kettleborough, C.A. et al., *Protein Eng.* 4(7):773-83 (1991) each of which is incorporated herein by reference.

The phrase "complementarity determining region" refers to amino acid
25 sequences which together define the binding affinity and specificity of the natural Fv region of a native immunoglobulin binding site. *See, e.g.,* Chothia et al., *J. Mol. Biol.* 196:901-917 (1987); Kabat et al., U.S. Dept. of Health and Human Services NIH Publication No. 91-3242 (1991). The phrase "constant region" refers to the portion of the antibody molecule that confers effector functions. In the present invention, mouse
30 constant regions are substituted by human constant regions. The constant regions of the subject humanized antibodies are derived from human immunoglobulins. The heavy chain constant region can be selected from any of the five isotypes: alpha, delta, epsilon, gamma or mu.

One method of humanizing antibodies comprises aligning the non-
35 human heavy and light chain sequences to human heavy and light chain sequences,

selecting and replacing the non-human framework with a human framework based on such alignment, molecular modeling to predict the conformation of the humanized sequence and comparing to the conformation of the parent antibody. This process is followed by repeated back mutation of residues in the CDR region which disturb the structure of the CDRs until the predicted conformation of the humanized sequence model closely approximates the conformation of the non-human CDRs of the parent non-human antibody. Such humanized antibodies may be further derivatized to facilitate uptake and clearance, *e.g.*, via Ashwell receptors. *See, e.g.*, U.S. Patent Nos. 5,530,101 and 5,585,089 which patents are incorporated herein by reference.

Humanized antibodies can also be produced using transgenic animals that are engineered to contain human immunoglobulin loci. For example, WO 98/24893 discloses transgenic animals having a human Ig locus wherein the animals do not produce functional endogenous immunoglobulins due to the inactivation of endogenous heavy and light chain loci. WO 91/10741 also discloses transgenic non-primate mammalian hosts capable of mounting an immune response to an immunogen, wherein the antibodies have primate constant and/or variable regions, and wherein the endogenous immunoglobulin-encoding loci are substituted or inactivated. WO 96/30498 discloses the use of the Cre/Lox system to modify the immunoglobulin locus in a mammal, such as to replace all or a portion of the constant or variable region to form a modified antibody molecule. WO 94/02602 discloses non-human mammalian hosts having inactivated endogenous Ig loci and functional human Ig loci. U.S. Patent No. 5,939,598 discloses methods of making transgenic mice in which the mice lack endogenous heavy chains, and express an exogenous immunoglobulin locus comprising one or more xenogeneic constant regions.

Using a transgenic animal described above, an immune response can be produced to a selected antigenic molecule, and antibody-producing cells can be removed from the animal and used to produce hybridomas that secrete human monoclonal antibodies. Immunization protocols, adjuvants, and the like are known in the art, and are used in immunization of, for example, a transgenic mouse as described in WO 96/33735. This publication discloses monoclonal antibodies against a variety of antigenic molecules including IL-6, IL-8, TNF, human CD4, L-selectin, gp39, and tetanus toxin. The monoclonal antibodies can be tested for the ability to inhibit or neutralize the biological activity or physiological effect of the corresponding protein. WO 96/33735 discloses that monoclonal antibodies against IL-8, derived from immune cells of transgenic mice immunized with IL-8, blocked IL-8-induced functions of

neutrophils. Human monoclonal antibodies with specificity for the antigen used to immunize transgenic animals are also disclosed in WO 96/34096.

Polynucleotides or Arrays for Diagnostics

- 5 Polynucleotide arrays are created by spotting polynucleotide probes onto a substrate (*e.g.*, glass, nitrocellulose, *etc.*) in a two-dimensional matrix or array having bound probes. The probes can be bound to the substrate by either covalent bonds or by non-specific interactions, such as hydrophobic interactions. Samples of polynucleotides can be detectably labeled (*e.g.*, using radioactive or fluorescent labels) and then
- 10 hybridized to the probes. Double stranded polynucleotides, comprising the labeled sample polynucleotides bound to probe polynucleotides, can be detected once the unbound portion of the sample is washed away. Techniques for constructing arrays and methods of using these arrays are described in EP 799 897; WO 97/29212; WO 97/27317; EP 785 280; WO 97/02357; U.S. Patent No. 5,593,839; U.S. Patent No.
- 15 5,578,832; EP 728 520; U.S. Patent No. 5,599,695; EP 721 016; U.S. Patent No. 5,556,752; WO 95/22058; and U.S. Patent No. 5,631,734. Arrays can be used to, for example, examine differential expression of genes and can be used to determine gene function. For example, arrays can be used to detect differential expression of a polynucleotide between a test cell and control cell (*e.g.*, cancer cells and normal cells).
- 20 For example, high expression of a particular message in a cancer cell, which is not observed in a corresponding normal cell, can indicate a cancer specific gene product. Exemplary uses of arrays are further described in, for example, Pappalarado et al., *Sem. Radiation Oncol.* (1998) 8:217; and Ramsay, *Nature Biotechnol.* (1998) 16:40.

Differential Expression in Diagnosis

- 25 The polynucleotides of the invention can also be used to detect differences in expression levels between two cells, *e.g.*, as a method to identify abnormal or diseased tissue in a human. For polynucleotides corresponding to profiles of protein families, the choice of tissue can be selected according to the putative biological function. In general, the expression of a gene corresponding to a specific
- 30 polynucleotide is compared between a first tissue that is suspected of being diseased and a second, normal tissue of the human. The tissue suspected of being abnormal or diseased can be derived from a different tissue type of the human, but preferably it is derived from the same tissue type; for example an intestinal polyp or other abnormal growth should be compared with normal intestinal tissue. The normal tissue can be the

same tissue as that of the test sample, or any normal tissue of the patient, especially those that express the polynucleotide-related gene of interest (e.g., brain, thymus, testis, heart, prostate, placenta, spleen, small intestine, skeletal muscle, pancreas, and the mucosal lining of the colon). A difference between the polynucleotide-related gene,
5 mRNA, or protein in the two tissues which are compared, for example in molecular weight, amino acid or nucleotide sequence, or relative abundance, indicates a change in the gene, or a gene which regulates it, in the tissue of the human that was suspected of being diseased. Examples of detection of differential expression and its use in diagnosis of cancer are described in U.S. Patent Nos. 5,688,641 and 5,677,125.

10 A genetic predisposition to disease in a human can also be detected by comparing expression levels of an mRNA or protein corresponding to a polynucleotide of the invention in a fetal tissue with levels associated in normal fetal tissue. Fetal tissues that are used for this purpose include, but are not limited to, amniotic fluid, chorionic villi, blood, and the blastomere of an *in vitro*-fertilized embryo. The
15 comparable normal polynucleotide-related gene is obtained from any tissue. The mRNA or protein is obtained from a normal tissue of a human in which the polynucleotide-related gene is expressed. Differences such as alterations in the nucleotide sequence or size of the same product of the fetal polynucleotide-related gene or mRNA, or alterations in the molecular weight, amino acid sequence, or relative abundance of fetal
20 protein, can indicate a germline mutation in the polynucleotide-related gene of the fetus, which indicates a genetic predisposition to disease. In general, diagnostic, prognostic, and other methods of the invention based on differential expression involve detection of a level or amount of a gene product, particularly a differentially expressed gene product, in a test sample obtained from a patient suspected of having or being susceptible to a
25 disease (e.g., breast cancer, lung cancer, colon cancer and/or metastatic forms thereof), and comparing the detected levels to those levels found in normal cells (e.g., cells substantially unaffected by cancer) and/or other control cells (e.g., to differentiate a cancerous cell from a cell affected by dysplasia). Furthermore, the severity of the disease can be assessed by comparing the detected levels of a differentially expressed
30 gene product with those levels detected in samples representing the levels of differentially gene product associated with varying degrees of severity of disease. It should be noted that use of the term "diagnostic" herein is not necessarily meant to exclude "prognostic" or "prognosis," but rather is used as a matter of convenience.

35 The term "differentially expressed gene" is generally intended to encompass a polynucleotide that can, for example, include an open reading frame

encoding a gene product (e.g., a polypeptide), and/or introns of such genes and adjacent 5' and 3' non-coding nucleotide sequences involved in the regulation of expression, up to about 20 kb beyond the coding region, but possibly further in either direction. The gene can be introduced into an appropriate vector for extrachromosomal maintenance or for integration into a host genome. In general, a difference in expression level associated with a decrease in expression level of at least about 25%, usually at least about 50% to 75%, more usually at least about 90% or more is indicative of a differentially expressed gene of interest, i.e., a gene that is underexpressed or down-regulated in the test sample relative to a control sample. Furthermore, a difference in expression level associated with an increase in expression of at least about 25%, usually at least about 50% to 75%, more usually at least about 90% and can be at least about 1 1/2-fold, usually at least about 2-fold to about 10-fold, and can be about 100-fold to about 1,000-fold increase relative to a control sample is indicative of a differentially expressed gene of interest, i.e., an overexpressed or up-regulated gene.

“Differentially expressed polynucleotide” as used herein means a nucleic acid molecule (RNA or DNA) comprising a sequence that represents a differentially expressed gene, e.g., the differentially expressed polynucleotide comprises a sequence (e.g., an open reading frame encoding a gene product) that uniquely identifies a differentially expressed gene so that detection of the differentially expressed polynucleotide in a sample is correlated with the presence of a differentially expressed gene in a sample. “Differentially expressed polynucleotides” is also meant to encompass fragments of the disclosed polynucleotides, e.g., fragments retaining biological activity, as well as nucleic acids homologous, substantially similar, or substantially identical (e.g., having about 90% sequence identity) to the disclosed polynucleotides.

“Diagnosis” as used herein generally includes determination of a subject's susceptibility to a disease or disorder, determination as to whether a subject is presently affected by a disease or disorder, as well as to the prognosis of a subject affected by a disease or disorder (e.g., identification of pre-metastatic or metastatic cancerous states, stages of cancer, or responsiveness of cancer to therapy). The present invention particularly encompasses diagnosis of subjects in the context of breast cancer (e.g., carcinoma *in situ* (e.g., ductal carcinoma *in situ*), estrogen receptor (ER)-positive breast cancer, ER-negative breast cancer, or other forms and/or stages of breast cancer), lung cancer (e.g., small cell carcinoma, non-small cell carcinoma, mesothelioma, and

other forms and/or stages of lung cancer), and colon cancer (*e.g.*, adenomatous polyp, colorectal carcinoma, and other forms and/or stages of colon cancer).

“Sample” or “biological sample” as used throughout here are generally meant to refer to samples of biological fluids or tissues, particularly samples obtained
5 from tissues, especially from cells of the type associated with the disease for which the diagnostic application is designed (*e.g.*, ductal adenocarcinoma), and the like. “Samples” is also meant to encompass derivatives and fractions of such samples (*e.g.*, cell lysates). Where the sample is solid tissue, the cells of the tissue can be dissociated or tissue sections can be analyzed.

10 Methods of the subject invention useful in diagnosis or prognosis typically involve comparison of the abundance of a selected differentially expressed gene product in a sample of interest with that of a control to determine any relative differences in the expression of the gene product, where the difference can be measured qualitatively and/or quantitatively. Quantitation can be accomplished, for example, by
15 comparing the level of expression product detected in the sample with the amounts of product present in a standard curve. A comparison can be made visually; by using a technique such as densitometry, with or without computerized assistance; by preparing a representative library of cDNA clones of mRNA isolated from a test sample, sequencing the clones in the library to determine that number of cDNA clones
20 corresponding to the same gene product, and analyzing the number of clones corresponding to that same gene product relative to the number of clones of the same gene product in a control sample; or by using an array to detect relative levels of hybridization to a selected sequence or set of sequences, and comparing the hybridization pattern to that of a control. The differences in expression are then
25 correlated with the presence or absence of an abnormal expression pattern. A variety of different methods for determining the nucleic acid abundance in a sample are known to those of skill in the art (see, *e.g.*, WO 97/27317). In general, diagnostic assays of the invention involve detection of a gene product of a the polynucleotide sequence (*e.g.*, mRNA or polypeptide) that corresponds to a sequence of SEQ ID NOs:1-3351. The
30 patient from whom the sample is obtained can be apparently healthy, susceptible to disease (*e.g.*, as determined by family history or exposure to certain environmental factors), or can already be identified as having a condition in which altered expression of a gene product of the invention is implicated.

Diagnosis can be determined based on detected gene product expression
35 levels of a gene product encoded by at least one, preferably at least two or more, at least

3 or more, or at least 4 or more of the polynucleotides having a sequence set forth in SEQ ID NOs:1-3351, and can involve detection of expression of genes corresponding to all of SEQ ID NOs:1-3351 and/or additional sequences that can serve as additional diagnostic markers and/or reference sequences. Where the diagnostic method is
5 designed to detect the presence or susceptibility of a patient to cancer, the assay preferably involves detection of a gene product encoded by a gene corresponding to a polynucleotide that is differentially expressed in cancer. Examples of such differentially expressed polynucleotides are described in the Examples below. Given the provided polynucleotides and information regarding their relative expression levels provided
10 herein, assays using such polynucleotides and detection of their expression levels in diagnosis and prognosis will be readily apparent to the ordinarily skilled artisan.

Any of a variety of detectable labels can be used in connection with the various embodiments of the diagnostic methods of the invention. Suitable detectable labels include fluorochromes, (e.g., fluorescein isothiocyanate (FITC), rhodamine,
15 Texas Red, phycoerythrin, allophycocyanin, 6-carboxyfluorescein (6-FAM), 2',7'-dimethoxy-4',5'-dichloro-6-carboxyfluorescein, 6-carboxy-X-rhodamine (ROX), 6-carboxy-2',4',7',4,7-hexachlorofluorescein (HEX), 5-carboxyfluorescein (5-FAM) or N,N,N',N'-tetramethyl-6-carboxyrhodamine (TAMRA)), radioactive labels, (e.g., ³²P, ³⁵S, ³H, etc.), and the like. The detectable label can involve a two stage systems (e.g.,
20 biotin-avidin, hapten-anti-hapten antibody, etc.)

Reagents specific for the polynucleotides and polypeptides of the invention, such as antibodies and nucleotide probes, can be supplied in a kit for detecting the presence of an expression product in a biological sample. The kit can also contain buffers or labeling components, as well as instructions for using the reagents to
25 detect and quantify expression products in the biological sample. Exemplary embodiments of the diagnostic methods of the invention are described below in more detail.

Polypeptide detection in diagnosis. In one embodiment, the test sample is assayed for the level of a differentially expressed polypeptide. Diagnosis can be
30 accomplished using any of a number of methods to determine the absence or presence or altered amounts of the differentially expressed polypeptide in the test sample. For example, detection can utilize staining of cells or histological sections with labeled antibodies, performed in accordance with conventional methods. Cells can be permeabilized to stain cytoplasmic molecules. In general, antibodies that specifically
35 bind a differentially expressed polypeptide of the invention are added to a sample, and

incubated for a period of time sufficient to allow binding to the epitope, usually at least about 10 minutes. The antibody can be detectably labeled for direct detection (*e.g.*, using radioisotopes, enzymes, fluorescers, chemilumescers, and the like), or can be used in conjunction with a second stage antibody or reagent to detect binding (*e.g.*,
5 biotin with horseradish peroxidase-conjugated avidin, a secondary antibody conjugated to a fluorescent compound, *e.g.*, fluorescein, rhodamine, Texas red, *etc.*). The absence or presence of antibody binding can be determined by various methods, including flow cytometry of dissociated cells, microscopy, radiography, scintillation counting, *etc.* Any suitable alternative methods can of qualitative or quantitative detection of levels or
10 amounts of differentially expressed polypeptide can be used, for example ELISA, western blot, immunoprecipitation, radioimmunoassay, *etc.*

mRNA detection. The diagnostic methods of the invention can also or alternatively involve detection of mRNA encoded by a gene corresponding to a differentially expressed polynucleotides of the invention. Any suitable qualitative or
15 quantitative methods known in the art for detecting specific mRNAs can be used. mRNA can be detected by, for example, *in situ* hybridization in tissue sections, by reverse transcriptase-PCR, or in Northern blots containing poly A+ mRNA. One of skill in the art can readily use these methods to determine differences in the size or amount of mRNA transcripts between two samples. mRNA expression levels in a
20 sample can also be determined by generation of a library of expressed sequence tags (ESTs) from the sample, where the EST library is representative of sequences present in the sample (Adams, et al., (1991) *Science* 252:1651). Enumeration of the relative representation of ESTs within the library can be used to approximate the relative representation of the gene transcript within the starting sample. The results of EST
25 analysis of a test sample can then be compared to EST analysis of a reference sample to determine the relative expression levels of a selected polynucleotide, particularly a polynucleotide corresponding to one or more of the differentially expressed genes described herein. Alternatively, gene expression in a test sample can be performed using serial analysis of gene expression (SAGE) methodology (*e.g.*, Velculescu et al.,
30 *Science* (1995) 270:484) or differential display (DD) methodology (see, *e.g.*, U.S. Patent NOs. 5,776,683 and 5,807,680).

Alternatively, gene expression can be analyzed using hybridization analysis. Oligonucleotides or cDNA can be used to selectively identify or capture DNA or RNA of specific sequence composition, and the amount of RNA or cDNA hybridized
35 to a known capture sequence determined qualitatively or quantitatively, to provide

information about the relative representation of a particular message within the pool of cellular messages in a sample. Hybridization analysis can be designed to allow for concurrent screening of the relative expression of hundreds to thousands of genes by using, for example, array-based technologies having high density formats, including
5 filters, microscope slides, or microchips, or solution-based technologies that use spectroscopic analysis (*e.g.*, mass spectrometry). One exemplary use of arrays in the diagnostic methods of the invention is described below in more detail.

Use of a single gene in diagnostic applications. The diagnostic methods of the invention can focus on the expression of a single differentially expressed gene.
10 For example, the diagnostic method can involve detecting a differentially expressed gene, or a polymorphism of such a gene (*e.g.*, a polymorphism in an coding region or control region), that is associated with disease. Disease-associated polymorphisms can include deletion or truncation of the gene, mutations that alter expression level and/or affect activity of the encoded protein, *etc.*

15 A number of methods are available for analyzing nucleic acids for the presence of a specific sequence, *e.g.*, a disease associated polymorphism. Where large amounts of DNA are available, genomic DNA is used directly. Alternatively, the region of interest is cloned into a suitable vector and grown in sufficient quantity for analysis. Cells that express a differentially expressed gene can be used as a source of
20 mRNA, which can be assayed directly or reverse transcribed into cDNA for analysis. The nucleic acid can be amplified by conventional techniques, such as the polymerase chain reaction (PCR), to provide sufficient amounts for analysis, and a detectable label can be included in the amplification reaction (*e.g.*, using a detectably labeled primer or detectably labeled oligonucleotides) to facilitate detection. Alternatively, various
25 methods are also known in the art that utilize oligonucleotide ligation as a means of detecting polymorphisms, see *e.g.*, Riley et al., *Nucl. Acids Res.* (1990) 18:2887; and Delahunty et al., *Am. J. Hum. Genet.* (1996) 58:1239.

The amplified or cloned sample nucleic acid can be analyzed by one of a number of methods known in the art. The nucleic acid can be sequenced by dideoxy or
30 other methods, and the sequence of bases compared to a selected sequence, *e.g.*, to a wild-type sequence. Hybridization with the polymorphic or variant sequence can also be used to determine its presence in a sample (*e.g.*, by Southern blot, dot blot, *etc.*). The hybridization pattern of a polymorphic or variant sequence and a control sequence to an array of oligonucleotide probes immobilized on a solid support, as described in U.S.
35 Patent No. 5,445,934, or in WO 95/35505, can also be used as a means of identifying

polymorphic or variant sequences associated with disease. Single strand conformational polymorphism (SSCP) analysis, denaturing gradient gel electrophoresis (DGGE), and heteroduplex analysis in gel matrices are used to detect conformational changes created by DNA sequence variation as alterations in electrophoretic mobility.

5 Alternatively, where a polymorphism creates or destroys a recognition site for a restriction endonuclease, the sample is digested with that endonuclease, and the products size fractionated to determine whether the fragment was digested. Fractionation is performed by gel or capillary electrophoresis, particularly acrylamide or agarose gels.

10 Screening for mutations in a gene can be based on the functional or antigenic characteristics of the protein. Protein truncation assays are useful in detecting deletions that can affect the biological activity of the protein. Various immunoassays designed to detect polymorphisms in proteins can be used in screening. Where many diverse genetic mutations lead to a particular disease phenotype, functional protein
15 assays have proven to be effective screening tools. The activity of the encoded protein can be determined by comparison with the wild-type protein.

Pattern matching in diagnosis using arrays. In another embodiment, the diagnostic and/or prognostic methods of the invention involve detection of expression of a selected set of genes in a test sample to produce a test expression pattern (TEP).
20 The TEP is compared to a reference expression pattern (REP), which is generated by detection of expression of the selected set of genes in a reference sample (*e.g.*, a positive or negative control sample). The selected set of genes includes at least one of the genes of the invention, which genes correspond to the polynucleotide sequences of SEQ ID NOs:1-3351. Of particular interest is a selected set of genes that includes genes
25 differentially expressed in the disease for which the test sample is to be screened.

"Reference sequences" or "reference polynucleotides" as used herein in the context of differential gene expression analysis and diagnosis/prognosis refers to a selected set of polynucleotides, which selected set includes at least one or more of the differentially expressed polynucleotides described herein. A plurality of reference
30 sequences, preferably comprising positive and negative control sequences, can be included as reference sequences. Additional suitable reference sequences are found in Genbank, Unigene, and other nucleotide sequence databases (including, *e.g.*, expressed sequence tag (EST), partial, and full-length sequences).

"Reference array" means an array having reference sequences for use in
35 hybridization with a sample, where the reference sequences include all, at least one of,

or any subset of the differentially expressed polynucleotides described herein. Usually such an array will include at least 3 different reference sequences, and can include any one or all of the provided differentially expressed sequences. Arrays of interest can further comprise sequences, including polymorphisms, of other genetic sequences, particularly other sequences of interest for screening for a disease or disorder (e.g., cancer, dysplasia, or other related or unrelated diseases, disorders, or conditions). The oligonucleotide sequence on the array will usually be at least about 12 nt in length, and can be of about the length of the provided sequences, or can extend into the flanking regions to generate fragments of 100 nt to 200 nt in length or more. Reference arrays can be produced according to any suitable methods known in the art. For example, methods of producing large arrays of oligonucleotides are described in U.S. Patent NOs. 5,134,854 and 5,445,934 using light-directed synthesis techniques. Using a computer controlled system, a heterogeneous array of monomers is converted, through simultaneous coupling at a number of reaction sites, into a heterogeneous array of polymers. Alternatively, microarrays are generated by deposition of pre-synthesized oligonucleotides onto a solid substrate, for example as described in PCT published application no. WO 95/35505.

A "reference expression pattern" or "REP" as used herein refers to the relative levels of expression of a selected set of genes, particularly of differentially expressed genes, that is associated with a selected cell type, e.g., a normal cell, a cancerous cell, a cell exposed to an environmental stimulus, and the like. A "test expression pattern" or "TEP" refers to relative levels of expression of a selected set of genes, particularly of differentially expressed genes, in a test sample (e.g., a cell of unknown or suspected disease state, from which mRNA is isolated).

REPs can be generated in a variety of ways according to methods well known in the art. For example, REPs can be generated by hybridizing a control sample to an array having a selected set of polynucleotides (particularly a selected set of differentially expressed polynucleotides), acquiring the hybridization data from the array, and storing the data in a format that allows for ready comparison of the REP with a TEP. Alternatively, all expressed sequences in a control sample can be isolated and sequenced, e.g., by isolating mRNA from a control sample, converting the mRNA into cDNA, and sequencing the cDNA. The resulting sequence information roughly or precisely reflects the identity and relative number of expressed sequences in the sample. The sequence information can then be stored in a format (e.g., a computer-readable format) that allows for ready comparison of the REP with a TEP. The REP can be

normalized prior to or after data storage, and/or can be processed to selectively remove sequences of expressed genes that are of less interest or that might complicate analysis (*e.g.*, some or all of the sequences associated with housekeeping genes can be eliminated from REP data).

5 TEPs can be generated in a manner similar to REPs, *e.g.*, by hybridizing a test sample to an array having a selected set of polynucleotides, particularly a selected set of differentially expressed polynucleotides, acquiring the hybridization data from the array, and storing the data in a format that allows for ready comparison of the TEP with a REP. The REP and TEP to be used in a comparison can be generated simultaneously,
10 or the TEP can be compared to previously generated and stored REPs.

 In one embodiment of the invention, comparison of a TEP with a REP involves hybridizing a test sample with a reference array, where the reference array has one or more reference sequences for use in hybridization with a sample. The reference sequences include all, at least one of, or any subset of the differentially expressed
15 polynucleotides described herein. Hybridization data for the test sample is acquired, the data normalized, and the produced TEP compared with a REP generated using an array having the same or similar selected set of differentially expressed polynucleotides. Probes that correspond to sequences differentially expressed between the two samples will show decreased or increased hybridization efficiency for one of the samples
20 relative to the other.

 Methods for collection of data from hybridization of samples with a reference arrays are well known in the art. For example, the polynucleotides of the reference and test samples can be generated using a detectable fluorescent label, and hybridization of the polynucleotides in the samples detected by scanning the
25 microarrays for the presence of the detectable label using, for example, a microscope and light source for directing light at a substrate. A photon counter detects fluorescence from the substrate, while an x-y translation stage varies the location of the substrate. A confocal detection device that can be used in the subject methods is described in U.S. Patent No. 5,631,734. A scanning laser microscope is described in Shalon et al.,
30 *Genome Res.* (1996) 6:639. A scan, using the appropriate excitation line, is performed for each fluorophore used. The digital images generated from the scan are then combined for subsequent analysis. For any particular array element, the ratio of the fluorescent signal from one sample (*e.g.*, a test sample) is compared to the fluorescent signal from another sample (*e.g.*, a reference sample), and the relative signal intensity
35 determined.

Methods for analyzing the data collected from hybridization to arrays are well known in the art. For example, where detection of hybridization involves a fluorescent label, data analysis can include the steps of determining fluorescent intensity as a function of substrate position from the data collected, removing outliers, *i.e.*, data
5 deviating from a predetermined statistical distribution, and calculating the relative binding affinity of the targets from the remaining data. The resulting data can be displayed as an image with the intensity in each region varying according to the binding affinity between targets and probes.

In general, the test sample is classified as having a gene expression
10 profile corresponding to that associated with a disease or non-disease state by comparing the TEP generated from the test sample to one or more REPs generated from reference samples (*e.g.*, from samples associated with cancer or specific stages of cancer, dysplasia, samples affected by a disease other than cancer, normal samples, *etc.*). The criteria for a match or a substantial match between a TEP and a REP include
15 expression of the same or substantially the same set of reference genes, as well as expression of these reference genes at substantially the same levels (*e.g.*, no significant difference between the samples for a signal associated with a selected reference sequence after normalization of the samples, or at least no greater than about 25% to about 40% difference in signal strength for a given reference sequence. In general, a
20 pattern match between a TEP and a REP includes a match in expression, preferably a match in qualitative or quantitative expression level, of at least one of, all or any subset of the differentially expressed genes of the invention.

Pattern matching can be performed manually, or can be performed using a computer program. Methods for preparation of substrate matrices (*e.g.*, arrays),
25 design of oligonucleotides for use with such matrices, labeling of probes, hybridization conditions, scanning of hybridized matrices, and analysis of patterns generated, including comparison analysis, are described in, for example, U.S. Patent No. 5,800,992.

Diagnosis, Prognosis and Management of Cancer

30 The polynucleotides of the invention and their gene products are of particular interest as genetic or biochemical markers (*e.g.*, in blood or tissues) that will detect the earliest changes along the carcinogenesis pathway and/or to monitor the efficacy of various therapies and preventive interventions. For example, the level of expression of certain polynucleotides can be indicative of a poorer prognosis, and

therefore warrant more aggressive chemo- or radio-therapy for a patient or vice versa. The correlation of novel surrogate tumor specific features with response to treatment and outcome in patients can define prognostic indicators that allow the design of tailored therapy based on the molecular profile of the tumor. These therapies include
5 antibody targeting and gene therapy. Determining expression of certain polynucleotides and comparison of a patients profile with known expression in normal tissue and variants of the disease allows a determination of the best possible treatment for a patient, both in terms of specificity of treatment and in terms of comfort level of the patient. Surrogate tumor markers, such as polynucleotide expression, can also be used
10 to better classify, and thus diagnose and treat, different forms and disease states of cancer. Two classifications widely used in oncology that can benefit from identification of the expression levels of the polynucleotides of the invention are staging of the cancerous disorder, and grading the nature of the cancerous tissue.

The polynucleotides of the invention can be useful to monitor patients
15 having or susceptible to cancer to detect potentially malignant events at a molecular level before they are detectable at a gross morphological level. Furthermore, a polynucleotide of the invention identified as important for one type of cancer can also have implications for development or risk of development of other types of cancer, *e.g.*, where a polynucleotide is differentially expressed across various cancer types. Thus,
20 for example, expression of a polynucleotide that has clinical implications for metastatic colon cancer can also have clinical implications for stomach cancer or endometrial cancer.

Staging. Staging is a process used by physicians to describe how advanced the cancerous state is in a patient. Generally, if a cancer is only detectable in
25 the area of the primary lesion without having spread to any lymph nodes it is called Stage I. If it has spread only to the closest lymph nodes, it is called Stage II. In Stage III, the cancer has generally spread to the lymph nodes in near proximity to the site of the primary lesion. Cancers that have spread to a distant part of the body, such as the liver, bone, brain or other site, are Stage IV, the most advanced stage.

30 The polynucleotides of the invention can facilitate fine-tuning of the staging process by identifying markers for the aggressivity of a cancer, *e.g.*, the metastatic potential, as well as the presence in different areas of the body. Thus, a Stage II cancer with a polynucleotide signifying a high metastatic potential cancer can be used to change a borderline Stage II tumor to a Stage III tumor, justifying more aggressive

therapy. Conversely, the presence of a polynucleotide signifying a lower metastatic potential allows more conservative staging of a tumor.

Grading of cancers. Grade is a term used to describe how closely a tumor resembles normal tissue of its same type. The microscopic appearance of a tumor is used to identify tumor grade based on parameters such as cell morphology, cellular organization, and other markers of differentiation. As a general rule, the grade of a tumor corresponds to its rate of growth or aggressiveness, with undifferentiated or high-grade tumors being more aggressive than well differentiated or low-grade tumors. The following guidelines are generally used for grading tumors: 1) GX Grade cannot be assessed; 2) G1 Well differentiated; G2 Moderately well differentiated; 3) G3 Poorly differentiated; 4) G4 Undifferentiated. The polynucleotides of the invention can be especially valuable in determining the grade of the tumor, as they not only can aid in determining the differentiation status of the cells of a tumor, they can also identify factors other than differentiation that are valuable in determining the aggressivity of a tumor, such as metastatic potential.

Detection of lung cancer. The polynucleotides of the invention can be used to detect lung cancer in a subject. Although there are more than a dozen different kinds of lung cancer, the two main types of lung cancer are small cell and nonsmall cell, which encompass about 90% of all lung cancer cases. Small cell carcinoma (also called oat cell carcinoma) usually starts in one of the larger bronchial tubes, grows fairly rapidly, and is likely to be large by the time of diagnosis. Nonsmall cell lung cancer (NSCLC) is made up of three general subtypes of lung cancer. Epidermoid carcinoma (also called squamous cell carcinoma) usually starts in one of the larger bronchial tubes and grows relatively slowly. The size of these tumors can range from very small to quite large. Adenocarcinoma starts growing near the outside surface of the lung and can vary in both size and growth rate. Some slowly growing adenocarcinomas are described as alveolar cell cancer. Large cell carcinoma starts near the surface of the lung, grows rapidly, and the growth is usually fairly large when diagnosed. Other less common forms of lung cancer are carcinoid, cylindroma, mucoepidermoid, and malignant mesothelioma.

The polynucleotides of the invention, *e.g.*, polynucleotides differentially expressed in normal cells versus cancerous lung cells (*e.g.*, tumor cells of high or low metastatic potential) or between types of cancerous lung cells (*e.g.*, high metastatic versus low metastatic), can be used to distinguish types of lung cancer as well as identifying traits specific to a certain patient's cancer and selecting an appropriate

therapy. For example, if the patient's biopsy expresses a polynucleotide that is associated with a low metastatic potential, it may justify leaving a larger portion of the patient's lung in surgery to remove the lesion. Alternatively, a smaller lesion with expression of a polynucleotide that is associated with high metastatic potential may
5 justify a more radical removal of lung tissue and/or the surrounding lymph nodes, even if no metastasis can be identified through pathological examination.

Detection of breast cancer. The majority of breast cancers are adenocarcinomas subtypes, which can be summarized as follows: 1) ductal carcinoma *in situ* (DCIS), including comedocarcinoma; 2) infiltrating (or invasive) ductal
10 carcinoma (IDC); 3) lobular carcinoma *in situ* (LCIS); 4) infiltrating (or invasive) lobular carcinoma (ILC); 5) inflammatory breast cancer; 6) medullary carcinoma; 7) mucinous carcinoma; 8) Paget's disease of the nipple; 9) Phyllodes tumor; and 10) tubular carcinoma.

The expression of polynucleotides of the invention can be used in the
15 diagnosis and management of breast cancer, as well as to distinguish between types of breast cancer. Detection of breast cancer can be determined using expression levels of any of the appropriate polynucleotides of the invention, either alone or in combination. Determination of the aggressive nature and/or the metastatic potential of a breast cancer can also be determined by comparing levels of one or more polynucleotides of the
20 invention and comparing levels of another sequence known to vary in cancerous tissue, e.g., ER expression. In addition, development of breast cancer can be detected by examining the ratio of expression of a differentially expressed polynucleotide to the levels of steroid hormones (e.g., testosterone or estrogen) or to other hormones (e.g., growth hormone, insulin). Thus expression of specific marker polynucleotides can be
25 used to discriminate between normal and cancerous breast tissue, to discriminate between breast cancers with different cells of origin, to discriminate between breast cancers with different potential metastatic rates, etc.

Detection of colon cancer. The polynucleotides of the invention exhibiting the appropriate expression pattern can be used to detect colon cancer in a
30 subject. Colorectal cancer is one of the most common neoplasms in humans and perhaps the most frequent form of hereditary neoplasia. Prevention and early detection are key factors in controlling and curing colorectal cancer. Colorectal cancer begins as polyps, which are small, benign growths of cells that form on the inner lining of the colon. Over a period of several years, some of these polyps accumulate additional
35 mutations and become cancerous. Multiple familial colorectal cancer disorders have

been identified, which are summarized as follows: 1) Familial adenomatous polyposis (FAP); 2) Gardner's syndrome; 3) Hereditary nonpolyposis colon cancer (HNPCC); and 4) Familial colorectal cancer in Ashkenazi Jews. The expression of appropriate polynucleotides of the invention can be used in the diagnosis, prognosis and management of colorectal cancer. Detection of colon cancer can be determined using expression levels of any of these sequences alone or in combination with the levels of expression. Determination of the aggressive nature and/or the metastatic potential of a colon cancer can be determined by comparing levels of one or more polynucleotides of the invention and comparing total levels of another sequence known to vary in cancerous tissue, *e.g.*, expression of p53, DCC ras, or FAP (see, *e.g.*, Fearon ER, et al., *Cell* (1990) 61(5):759; Hamilton SR et al., *Cancer* (1993) 72:957; Bodmer W, et al., *Nat Genet.* (1994) 4(3):217; Fearon ER, *Ann N Y Acad Sci.* (1995) 768:101). For example, development of colon cancer can be detected by examining the ratio of any of the polynucleotides of the invention to the levels of oncogenes (*e.g.*, ras) or tumor suppressor genes (*e.g.*, FAP or p53). Thus expression of specific marker polynucleotides can be used to discriminate between normal and cancerous colon tissue, to discriminate between colon cancers with different cells of origin, to discriminate between colon cancers with different potential metastatic rates, *etc.*

Use of Polynucleotides to Screen for Peptide Analogs and Antagonists

Polypeptides encoded by the instant polynucleotides and corresponding full length genes can be used to screen peptide libraries to identify binding partners, such as receptors, from among the encoded polypeptides. Peptide libraries can be synthesized according to methods known in the art (see, *e.g.*, U.S. Patent No. 5,010,175, and WO 91/17823). Agonists or antagonists of the polypeptides if the invention can be screened using any available method known in the art, such as signal transduction, antibody binding, receptor binding, mitogenic assays, chemotaxis assays, *etc.* The assay conditions ideally should resemble the conditions under which the native activity is exhibited *in vivo*, that is, under physiologic pH, temperature, and ionic strength. Suitable agonists or antagonists will exhibit strong inhibition or enhancement of the native activity at concentrations that do not cause toxic side effects in the subject. Agonists or antagonists that compete for binding to the native polypeptide can require concentrations equal to or greater than the native concentration, while inhibitors capable of binding irreversibly to the polypeptide can be added in concentrations on the order of the native concentration.

Such screening and experimentation can lead to identification of a novel polypeptide binding partner, such as a receptor, encoded by a gene or a cDNA corresponding to a polynucleotide of the invention, and at least one peptide agonist or antagonist of the novel binding partner. Such agonists and antagonists can be used to modulate, enhance, or inhibit receptor function in cells to which the receptor is native, or in cells that possess the receptor as a result of genetic engineering. Further, if the novel receptor shares biologically important characteristics with a known receptor, information about agonist/antagonist binding can facilitate development of improved agonists/antagonists of the known receptor.

10 Pharmaceutical Compositions and Therapeutic Uses

Pharmaceutical compositions of the invention can comprise polypeptides, antibodies, or polynucleotides (including antisense nucleotides and ribozymes) of the claimed invention in a therapeutically effective amount. The term "therapeutically effective amount" as used herein refers to an amount of a therapeutic agent to treat, ameliorate, or prevent a desired disease or condition, or to exhibit a detectable therapeutic or preventative effect. The effect can be detected by, for example, chemical markers or antigen levels. Therapeutic effects also include reduction in physical symptoms, such as decreased body temperature. The precise effective amount for a subject will depend upon the subject's size and health, the nature and extent of the condition, and the therapeutics or combination of therapeutics selected for administration. Thus, it is not useful to specify an exact effective amount in advance. However, the effective amount for a given situation is determined by routine experimentation and is within the judgment of the clinician. For purposes of the present invention, an effective dose will generally be from about 0.01 mg/kg to 50 mg/kg or 0.05 mg/kg to about 10 mg/kg of the DNA constructs in the individual to which it is administered.

A pharmaceutical composition can also contain a pharmaceutically acceptable carrier. The term "pharmaceutically acceptable carrier" refers to a carrier for administration of a therapeutic agent, such as antibodies or a polypeptide, genes, and other therapeutic agents. The term refers to any pharmaceutical carrier that does not itself induce the production of antibodies harmful to the individual receiving the composition, and which can be administered without undue toxicity. Suitable carriers can be large, slowly metabolized macromolecules such as proteins, polysaccharides, polylactic acids, polyglycolic acids, polymeric amino acids, amino acid copolymers,

and inactive virus particles. Such carriers are well known to those of ordinary skill in the art. Pharmaceutically acceptable carriers in therapeutic compositions can include liquids such as water, saline, glycerol and ethanol. Auxiliary substances, such as wetting or emulsifying agents, pH buffering substances, and the like, can also be present in such vehicles. Typically, the therapeutic compositions are prepared as injectables, either as liquid solutions or suspensions; solid forms suitable for solution in, or suspension in, liquid vehicles prior to injection can also be prepared. Liposomes are included within the definition of a pharmaceutically acceptable carrier. Pharmaceutically acceptable salts can also be present in the pharmaceutical composition, e.g., mineral acid salts such as hydrochlorides, hydrobromides, phosphates, sulfates, and the like; and the salts of organic acids such as acetates, propionates, malonates, benzoates, and the like. A thorough discussion of pharmaceutically acceptable excipients is available in *Remington's Pharmaceutical Sciences* (Mack Pub. Co., New Jersey, 1991).

Delivery Methods. Once formulated, the compositions of the invention can be (1) administered directly to the subject (e.g., as polynucleotide or polypeptides); or (2) delivered *ex vivo*, to cells derived from the subject (e.g., as in *ex vivo* gene therapy). Direct delivery of the compositions will generally be accomplished by parenteral injection, e.g., subcutaneously, intraperitoneally, intravenously or intramuscularly, intratumoral or to the interstitial space of a tissue. Other modes of administration include oral and pulmonary administration, suppositories, and transdermal applications, needles, and gene guns or hyposprays. Dosage treatment can be a single dose schedule or a multiple dose schedule.

Methods for the *ex vivo* delivery and reimplantation of transformed cells into a subject are known in the art and described in e.g., International Publication No. WO 93/14778. Examples of cells useful in *ex vivo* applications include, for example, stem cells, particularly hematopoietic, lymph cells, macrophages, dendritic cells, or tumor cells. Generally, delivery of nucleic acids for both *ex vivo* and *in vitro* applications can be accomplished by, for example, dextran-mediated transfection, calcium phosphate precipitation, polybrene mediated transfection, protoplast fusion, electroporation, encapsulation of the polynucleotide(s) in liposomes, and direct microinjection of the DNA into nuclei, all well known in the art.

Once a gene corresponding to a polynucleotide of the invention has been found to correlate with a proliferative disorder, such as neoplasia, dysplasia, and hyperplasia, the disorder can be amenable to treatment by administration of a

therapeutic agent based on the provided polynucleotide, corresponding polypeptide or other corresponding molecule (e.g., antisense, ribozyme, etc.).

The dose and the means of administration of the inventive pharmaceutical compositions are determined based on the specific qualities of the therapeutic composition, the condition, age, and weight of the patient, the progression of the disease, and other relevant factors. For example, administration of polynucleotide therapeutic compositions agents of the invention includes local or systemic administration, including injection, oral administration, particle gun or catheterized administration, and topical administration. Preferably, the therapeutic polynucleotide composition contains an expression construct comprising a promoter operably linked to a polynucleotide of at least 12, 22, 25, 30, or 35 contiguous nt of the polynucleotide disclosed herein. Various methods can be used to administer the therapeutic composition directly to a specific site in the body. For example, a small metastatic lesion is located and the therapeutic composition injected several times in several different locations within the body of tumor. Alternatively, arteries which serve a tumor are identified, and the therapeutic composition injected into such an artery, in order to deliver the composition directly into the tumor. A tumor that has a necrotic center is aspirated and the composition injected directly into the now empty center of the tumor. The antisense composition is directly administered to the surface of the tumor, for example, by topical application of the composition. X-ray imaging is used to assist in certain of the above delivery methods.

Receptor-mediated targeted delivery of therapeutic compositions containing an antisense polynucleotide, subgenomic polynucleotides, or antibodies to specific tissues can also be used. Receptor-mediated DNA delivery techniques are described in, for example, Findeis et al., *Trends Biotechnol.* (1993) 11:202; Chiou et al., *Gene Therapeutics: Methods And Applications Of Direct Gene Transfer* (J.A. Wolff, ed.) (1994); Wu et al., *J. Biol. Chem.* (1988) 263:621; Wu et al., *J. Biol. Chem.* (1994) 269:542; Zenke et al., *Proc. Natl. Acad. Sci. (USA)* (1990) 87:3655; Wu et al., *J. Biol. Chem.* (1991) 266:338. Therapeutic compositions containing a polynucleotide are administered in a range of about 100 ng to about 200 mg of DNA for local administration in a gene therapy protocol. Concentration ranges of about 500 ng to about 50 mg, about 1 mg to about 2 mg, about 5 mg to about 500 mg, and about 20 mg to about 100 mg of DNA can also be used during a gene therapy protocol. Factors such as method of action (e.g., for enhancing or inhibiting levels of the encoded gene product) and efficacy of transformation and expression are considerations which will

affect the dosage required for ultimate efficacy of the antisense subgenomic polynucleotides. Where greater expression is desired over a larger area of tissue, larger amounts of antisense subgenomic polynucleotides or the same amounts readministered in a successive protocol of administrations, or several administrations to different adjacent or close tissue portions of, for example, a tumor site, may be required to effect a positive therapeutic outcome. In all cases, routine experimentation in clinical trials will determine specific ranges for optimal therapeutic effect. For polynucleotide-related genes encoding polypeptides or proteins with anti-inflammatory activity, suitable use, doses, and administration are described in U.S. Patent No. 5,654,173.

10 The therapeutic polynucleotides and polypeptides of the present invention can be delivered using gene delivery vehicles. The gene delivery vehicle can be of viral or non-viral origin (see generally, Jolly, *Cancer Gene Therapy* (1994) 1:51; Kimura, *Human Gene Therapy* (1994) 5:845; Connelly, *Human Gene Therapy* (1995) 1:185; and Kaplitt, *Nature Genetics* (1994) 6:148). Expression of such coding sequences can be induced using endogenous mammalian or heterologous promoters. Expression of the coding sequence can be either constitutive or regulated.

15 Viral-based vectors for delivery of a desired polynucleotide and expression in a desired cell are well known in the art. Exemplary viral-based vehicles include, but are not limited to, recombinant retroviruses (see, e.g., WO 90/07936; WO 94/03622; WO 93/25698; WO 93/25234; U.S. Patent No. 5, 219,740; WO 93/11230; WO 93/10218; U.S. Patent No. 4,777,127; GB Patent No. 2,200,651; EP 0 345 242; and WO 91/02805), alphavirus-based vectors (e.g., Sindbis virus vectors, Semliki forest virus (ATCC VR-67; ATCC VR-1247), Ross River virus (ATCC VR-373; ATCC VR-1246) and Venezuelan equine encephalitis virus (ATCC VR-923; ATCC VR-1250; 25 ATCC VR 1249; ATCC VR-532), and adeno-associated virus (AAV) vectors (see, e.g., WO 94/12649, WO 93/03769; WO 93/19191; WO 94/28938; WO 95/11984 and WO 95/00655). Administration of DNA linked to killed adenovirus as described in Curiel, *Hum. Gene Ther.* (1992) 3:147 can also be employed.

30 Non-viral delivery vehicles and methods can also be employed, including, but not limited to, polycationic condensed DNA linked or unlinked to killed adenovirus alone (see, e.g., Curiel, *Hum. Gene Ther.* (1992) 3:147); ligand-linked DNA (see, e.g., Wu, *J. Biol. Chem.* 264:16985 (1989)); eukaryotic cell delivery vehicles cells (see, e.g., U.S. Patent No. 5,814,482; WO 95/07994; WO 96/17072; WO 95/30763; and WO 97/42338) and nucleic charge neutralization or fusion with cell 35 membranes. Naked DNA can also be employed. Exemplary naked DNA introduction

methods are described in WO 90/11092 and U.S. Patent No. 5,580,859. Liposomes that can act as gene delivery vehicles are described in U.S. Patent No. 5,422,120; WO 95/13796; WO 94/23697; WO 91/14445; and EP 0524968. Additional approaches are described in Philip, *Mol. Cell Biol.* 14:2411 (1994), and in Woffendin, *Proc. Natl. Acad. Sci.* (1994) 91:1581.

Further non-viral delivery suitable for use includes mechanical delivery systems such as the approach described in Woffendin et al., *Proc. Natl. Acad. Sci. USA* 91(24):11581 (1994). Moreover, the coding sequence and the product of expression of such can be delivered through deposition of photopolymerized hydrogel materials or use of ionizing radiation (see, e.g., U.S. Patent No. 5,206,152 and WO 92/11033). Other conventional methods for gene delivery that can be used for delivery of the coding sequence include, for example, use of hand-held gene transfer particle gun (see, e.g., U.S. Patent No. 5,149,655); use of ionizing radiation for activating transferred gene (see, e.g., U.S. Patent No. 5,206,152 and WO 92/11033).

The present invention will now be illustrated by reference to the following examples which set forth particularly advantageous embodiments. However, it should be noted that these embodiments are illustrative and are not to be construed as restricting the invention in any way.

EXAMPLES

EXAMPLE 1

SOURCE OF BIOLOGICAL MATERIALS AND OVERVIEW OF NOVEL POLYNUCLEOTIDES EXPRESSED BY THE BIOLOGICAL MATERIALS

5

Cell lines and human normal and tumor tissue were used to construct cDNA libraries from mRNA isolated from the cells and tissues. Most sequences were about 275-300 nucleotides in length. The cells lines include Km12L4-A cell line, a high metastatic colon cancer cell line (Morika, W. A. K. et al., *Cancer Research* (1988) 48:6863). The KM12L4-A cell line is derived from the KM12C cell line. The KM12C cell line, which is poorly metastatic (low metastatic) was established in culture from a Dukes' stage B2 surgical specimen (Morikawa et al. *Cancer Res.* (1988) 48:6863). The KML4-A is a highly metastatic subline derived from KM12C (Yeatman et al. *Nucl. Acids. Res.* (1995) 23:4007; Bao-Ling et al. *Proc. Annu. Meet. Am. Assoc. Cancer. Res.* (1995) 21:3269). The KM12C and KM12C-derived cell lines (e.g., KM12L4, KM12L4-A, etc.) are well-recognized in the art as model cell lines for the study of colon cancer (see, e.g., Moriakawa et al., *supra*; Radinsky et al. *Clin. Cancer Res.* (1995) 1:19; Yeatman et al., (1995) *supra*; Yeatman et al., *Clin. Exp. Metastasis* (1996) 14:246). These and other cell lines and tissue are described in Table 6.

20

The sequences of the isolated polynucleotides were first masked to eliminate low complexity sequences using the XBLAST masking program (Claverie "Effective Large-Scale Sequence Similarity Searches," In: Computer Methods for Macromolecular Sequence Analysis, Doolittle, ed., *Meth. Enzymol.* 266:212-227 Academic Press, NY, NY (1996); see particularly Claverie, in "Automated DNA Sequencing and Analysis Techniques" Adams et al., eds., Chap. 36, p. 267 Academic Press, San Diego, 1994 and Claverie et al. *Comput. Chem.* (1993) 17:191). Generally, masking does not influence the final search results, except to eliminate sequences of relative little interest due to their low complexity, and to eliminate multiple "hits" based on similarity to repetitive regions common to multiple sequences, e.g., Alu repeats. The sequences remaining after masking were then used in a BLASTN vs. Genbank search; sequences that exhibited greater than 70% overlap, 99% identity, and a p value of less than 1×10^{-40} were discarded. Sequences from this search also were discarded if the inclusive parameters were met, but the sequence was ribosomal or vector-derived.

30

The resulting sequences from the previous search were classified into three groups (1, 2 and 3 below) and searched in a BLASTX vs. NRP (non-redundant proteins) database search: (1) unknown (no hits in the Genbank search), (2) weak similarity (greater than 45% identity and p value of less than 1×10^{-5}), and (3) high similarity (greater than 60% overlap, greater than 80% identity, and p value less than 1×10^{-5}). Sequences having greater than 70% overlap, greater than 99% identity, and p value of less than 1×10^{-40} were discarded.

The remaining sequences were classified as unknown (no hits), weak similarity, and high similarity (parameters as above). Two searches were performed on these sequences. First, a BLAST vs. EST database search was performed and sequences with greater than 99% overlap, greater than 99% similarity and a p value of less than 1×10^{-40} were discarded. Sequences with a p value of less than 1×10^{-65} when compared to a database sequence of human origin were also excluded. Second, a BLASTN vs. Patent GeneSeq database was performed and sequences having greater than 99% identity, p value less than 1×10^{-40} , and greater than 99% overlap were discarded.

The remaining sequences were subjected to screening using other rules and redundancies in the dataset. Sequences with a p value of less than 1×10^{-111} in relation to a database sequence of human origin were specifically excluded. The final result provided the 3351 sequences listed in the accompanying Sequence Listing. Each identified polynucleotide represents sequence from at least a partial mRNA transcript. Polynucleotides that were determined to be novel were assigned a sequence identification number.

The novel polynucleotides were assigned sequence identification numbers SEQ ID NOs:1-3351. The first 1847 DNA sequences corresponding to the novel polynucleotides are provided in the Sequence Listing in Table 1. DNA sequences corresponding to the novel polynucleotides of SEQ ID NOs:1848-3351 are provided in the Sequence Listing in Table 2. The DNA sequences of Table 2, while numbered SEQ ID 1-1504, correspond to SEQ ID NOs:1848-3351 in the Sequence Listing, *e.g.*, Table 2 SEQ ID 1 is SEQ ID NO:1848, Table 2 SEQ ID 2 is SEQ ID NO:1849, *etc.* Each DNA sequence in Table 4 is uniquely identified by a number that is 1847 less than its SEQ ID NO in the Sequence Listing. Tables 1 and 2 provide: 1) the SEQ ID NO assigned to each sequence for use in the present specification or a corresponding number; 2) the sequence name used as an internal identifier of the sequence; 3) the name assigned to the clone from which the

sequence was isolated; and 4) the number of the cluster to which the sequence is assigned (Cluster ID; where the cluster ID is 0, the sequence was not assigned to any cluster).

Because the provided polynucleotides represent partial mRNA transcripts, two or more polynucleotides of the invention may represent different regions of the same mRNA transcript and the same gene. Thus, if two or more SEQ ID NOs: are identified as belonging to the same clone, then either sequence can be used to obtain the full-length mRNA or gene.

EXAMPLE 2

RESULTS OF PUBLIC DATABASE SEARCH TO IDENTIFY FUNCTION OF GENE PRODUCTS

10

SEQ ID NOs:1-3351 were translated in all three reading frames to determine the best alignment with the individual sequences. These amino acid sequences and nucleotide sequences are referred to, generally, as query sequences, which are aligned with the individual sequences. Query and individual sequences were aligned using the BLAST programs, available over the world wide web at <http://www.ncbi.nlm.nih.gov/BLAST/>. Again the sequences were masked to various extents to prevent searching of repetitive sequences or poly-A sequences, using the XBLAST program for masking low complexity as described above in Example 1.

Tables 3 and 4 (inserted before the claims) show the results of the alignments. Table 3 contains alignment information for SEQ ID NOs:1-1847 and Table 4 contains alignment information for SEQ ID NOs:1848-3351. The DNA sequences of Table 4, while numbered SEQ ID 1-1504, correspond to SEQ ID NOs:1848-3351. Each DNA sequence in Table 4 is uniquely identified by a number that is 1847 less than its SEQ ID NO. Tables 3 and 4 refer to each sequence by its SEQ ID NO or a corresponding number, the accession numbers and descriptions of nearest neighbors from the Genbank and Non-Redundant Protein searches, and the p values of the search results.

For each of SEQ ID NOs:1-1847, the best alignment to a protein or DNA sequence is included in Table 3, and the best alignment for each of SEQ ID NOs:1848-3351 is included in Table 4. The activity of the polypeptide encoded by SEQ ID NOs:1-3351 is the same or similar to the nearest neighbor reported in Table 3 or 4. The accession number of the nearest neighbor is reported, providing a reference to the activities exhibited by the nearest neighbor. The search program and database used for the alignment also are indicated as well as a calculation of the p value.

Full length sequences or fragments of the polynucleotide sequences of the nearest neighbors can be used as probes and primers to identify and isolate the full length sequence of SEQ ID NOs:1-3351. The nearest neighbors can indicate a tissue or cell type to be used to construct a library for the full-length sequences of SEQ ID
5 NOs:1-3351.

EXAMPLE 3

MEMBERS OF PROTEIN FAMILIES

The sequences (SEQ ID NOs:1-3351) were used to conduct a profile
10 search as described in the specification above. Several of the polynucleotides of the invention were found to encode polypeptides having characteristics of a polypeptide belonging to a known protein families (and thus represent new members of these protein families) and/or comprising a known functional domain (Table 5). "Start" and "stop" in Table 3 indicate the position within the individual sequences that align with
15 the query sequence having the indicated SEQ ID NO. The direction indicates the orientation of the query sequence with respect to the individual sequence, where forward (for) indicates that the alignment is in the same direction (left to right) as the sequence provided in the Sequence Listing and reverse (rev) indicates that the alignment is with a sequence complementary to the sequence provided in the Sequence
20 Listing.

Some polynucleotides exhibited multiple profile hits because, for example, the particular sequence contains overlapping profile regions, and/or the sequence contains two different functional domains. These profile hits are described in more detail below.

25 Ank Repeats (ANK). SEQ ID NOs:187, 1268, 1804, 1819, 1830, 1839, 2652, 3015 and 3267 represent polynucleotides encoding an Ank repeat-containing protein. The ankyrin motif is a 33 amino acid sequence named for the protein ankyrin which has 24 tandem 33-amino-acid motifs. Ank repeats were originally identified in the cell-cycle-control protein cdc10 (Breedon et al., *Nature* (1987) 329:651). Proteins
30 containing ankyrin repeats include ankyrin, myotropin, I-kappaB proteins, cell cycle protein cdc10, the Notch receptor (Matsuno et al., *Development* (1997) 124(21):4265); G9a (or BAT8) of the class III region of the major histocompatibility complex (*Biochem J.* 290:811-818, 1993), FABP, GABP, 53BP2, Lin12, glp-1, SW14, and SW16. The functions of the ankyrin repeats are compatible with a role in protein-

protein interactions (Bork, *Proteins* (1993) 17(4):363; Lambert and Bennet, *Eur. J. Biochem.* (1993) 211:1; Kerr et al., *Current Op. Cell Biol.* (1992) 4:496; Bennet et al., *J. Biol. Chem.* (1980) 255:6424).

ATPases Associated with Various Cellular Activities (ATPases).

- 5 Sequences within SEQ ID NOs:431, 639, 2135, 2684, 2859, 3197 and 3266 correspond to a sequence that encodes a novel member of the "ATPases Associated with diverse cellular Activities" (AAA) protein family. The AAA protein family is composed of a large number of ATPases that share a conserved region of about 220 amino acids that contains an ATP-binding site (Froehlich et al., *J. Cell Biol.* (1991) 114:443; Erdmann et al., *Cell* (1991) 64:499; Peters et al., *EMBO J.* (1990) 9:1757; Kunau et al., *Biochimie* (1993) 75:209-224; Confalonieri et al., *BioEssays* (1995) 17:639; <http://yeamob.pci.chemie.uni-tuebingen.de/AAA/Description.html>). The proteins that belong to this family either contain one or two AAA domains. In general, the AAA domains in these proteins act as ATP-dependent protein clamps (Confalonieri et al. 15 (1995) *BioEssays* 17:639). In addition to the ATP-binding 'A' and 'B' motifs, which are located in the N-terminal half of this domain, there is a highly conserved region located in the central part of the domain which was used in the development of the signature pattern. The consensus pattern is: [LIVMT]-x-[LIVMT]-[LIVMF]-x-[GATMC]-[ST]-[NS]-x(4)-[LIVM]-D-x-A-[LIFA]-x-R.

- 20 Bromodomain (bromodomain). SEQ ID NO:1814 represents a polynucleotide encoding a polypeptide having a bromodomain region (Haynes et al., 1992, *Nucleic Acids Res.* 20:2693-2603, Tamkun et al., 1992, *Cell* 68:561-572, and Tamkun, 1995, *Curr. Opin. Genet. Dev.* 5:473-477), which is a conserved region of about 70 amino acids. The bromodomain is thought to be involved in protein-protein 25 interactions and may be important for the assembly or activity of multicomponent complexes involved in transcriptional activation. The consensus pattern, which spans a major part of the bromodomain, is: [STANVF]-x(2)-F-x(4)-[DNS]-x(5,7)-[DENQTF]-Y-[HFY]-x(2)-[LIVMFY]-x(3)-[LIVM]-x(4)-[LIVM]-x(6,8)-Y-x(12,13)-[LIVM]-x(2)-N-[SACF]-x(2)-[FY].

- 30 Basic Region Plus Leucine Zipper Transcription Factors (BZIP). SEQ ID NOs:410, 552, 768, 822, 836, 1288, 1365, 1454, 1540, 1549, 1556, 1557, 1563, 1622, 1630, 1704, 1808, 2363, 2424, 3147, 3152, 3158 and 3208 represent polynucleotides encoding a novel member of the family of basic region plus leucine zipper transcription factors. The bZIP superfamily (Hurst, *Protein Prof.* (1995) 2:105; 35 and Ellenberger, *Curr. Opin. Struct. Biol.* (1994) 4:12) of eukaryotic DNA-binding

transcription factors encompasses proteins that contain a basic region mediating sequence-specific DNA-binding followed by a leucine zipper required for dimerization. The consensus pattern for this protein family is: [KR]-x(1,3)-[RKSAQ]-N-x(2)-[SAQ](2)-x-[RKTAENQ]-x-R-x-[RK].

- 5 EF Hand (EFhand). SEQ ID NOs:820, 1755 and 3285 correspond to polynucleotides encoding a novel protein in the family of EF-hand proteins. Many calcium-binding proteins belong to the same evolutionary family and share a type of calcium-binding domain known as the EF-hand (Kawasaki et al., *Protein. Prof.* (1995) 2:305-490). This type of domain consists of a twelve residue loop flanked on both sides
10 by a twelve residue alpha-helical domain. In an EF-hand loop the calcium ion is coordinated in a pentagonal bipyramidal configuration. The six residues involved in the binding are in positions 1, 3, 5, 7, 9 and 12; these residues are denoted by X, Y, Z, -Y, -X and -Z. The invariant Glu or Asp at position 12 provides two oxygens for liganding Ca (bidentate ligand). The consensus pattern includes the complete EF-hand loop as
15 well as the first residue which follows the loop and which seem to always be hydrophobic: D-x-[DNS]-{ILVFYW}-[DENSTG]-[DNQGHRK]-{GP}-[LIVMC]-[DENQSTAGC]-x(2)-[DE]-[LIVMFYW].

- Ets Domain (Ets Nterm). SEQ ID NO:1811 represents a polynucleotide encoding a polypeptide with N-terminal homology in ETS domain. Proteins of this
20 family contain a conserved domain, the "ETS-domain," that is involved in DNA binding. The domain appears to recognize purine-rich sequences; it is about 85 to 90 amino acids in length, and is rich in aromatic and positively charged residues (Wasylyk, et al., *Eur. J. Biochem.* (1993) 211:718). The *ets* gene family encodes a novel class of DNA-binding proteins, each of which binds a specific DNA sequence and comprises an
25 *ets* domain that specifically interacts with sequences containing the common core trinucleotide sequence GGA. In addition to an *ets* domain, native *ets* proteins comprise other sequences which can modulate the biological specificity of the protein. *Ets* genes and proteins are involved in a variety of essential biological processes including cell growth, differentiation and development, and three members are implicated in
30 oncogenic process.

- G-Protein Alpha Subunit (G-alpha). SEQ ID NO:1846 represents a polynucleotide encoding a novel polypeptide of the G-protein alpha subunit family. Guanine nucleotide binding proteins (G-proteins) are a family of membrane-associated proteins that couple extracellularly-activated integral-membrane receptors to
35 intracellular effectors, such as ion channels and enzymes that vary the concentration of

second messenger molecules. G-proteins are composed of 3 subunits (alpha, beta and gamma) which, in the resting state, associate as a trimer at the inner face of the plasma membrane. The alpha subunit binds GTP and exhibits GTPase activity. G-protein alpha subunits are 350-400 amino acids in length and have molecular weights in the range 40-45 kDa. Seventeen distinct types of alpha subunit have been identified in mammals, and fall into 4 main groups on the basis of both sequence similarity and function: alpha-s, alpha-q, alpha-i and alpha-12 (Simon et al., *Science* (1993) 252:802). They are often N-terminally acylated, usually with myristate and/or palmitoylate, and these fatty acid modifications can be important for membrane association and high-affinity interactions with other proteins.

Helicases conserved C-terminal domain (helicase C). SEQ ID NOs:1496, 2826 and 2871 represent polynucleotides encoding novel members of the DEAD/H helicase family. A number of eukaryotic and prokaryotic proteins have been characterized (Schmid S.R., et al., *Mol. Microbiol.* (1992) 6:283; Linder P., et al., *Nature* (1989) 337:121; Wassarman D.A., et al., *Nature* (1991) 349:463) on the basis of their structural similarity. All are involved in ATP-dependent, nucleic-acid unwinding. All DEAD box family members of the above proteins share a number of conserved sequence motifs, some of which are specific to the DEAD family while others are shared by other ATP-binding proteins or by proteins belonging to the helicases 'superfamily' (Hodgman T.C., *Nature* (1988) 333:22 and *Nature* (1988) 333:578 (Errata). One of these motifs, called the "D-E-A-D-box", represents a special version of the B motif of ATP-binding proteins. Some other proteins belong to a subfamily which have His instead of the second Asp and are thus said to be "D-E-A-H-box" proteins (Wassarman D.A., et al., *Nature* (1991) 349:463; Harosh I., et al., *Nucleic Acids Res.* (1991) 19:6331; Koonin E.V. et al., *J. Gen. Virol.* (1992) 73:989. The following signature patterns are used to identify members of both subfamilies: 1) [LIVMF](2)-D-E-A-D-[RKEN]-x-[LIVMFYGSTN]; and 2) [GSAH]-x-[LIVMF](3)-D-E-[ALIV]-H-[NECR].

Homeobox domain (homeobox). SEQ ID NOs:1676, 1820 and 1821 represent polynucleotides encoding proteins having a homeobox domain. The homeobox is a protein domain of 60 amino acids (Gehring In: Guidebook to the Homeobox Genes, Duboule D., Ed., pp. 1-10, Oxford University Press, Oxford, (1994); Buerklin In: Guidebook to the Homeobox Genes, pp25-72, Oxford University Press, Oxford, (1994); Gehring, *Trends Biochem. Sci.* (1992) 17:277-280; Gehring et al., *Annu. Rev. Genet.* (1986) 20:147-173; Schofield, *Trends Neurosci.* (1987) 10:3-6) first

identified in a number of *Drosophila* homeotic and segmentation proteins. It is extremely well conserved in many other animals, including vertebrates. This domain binds DNA through a helix-turn-helix type of structure. Several proteins that contain a homeobox domain play an important role in development. Most of these proteins are sequence-specific DNA-binding transcription factors. The homeobox domain is also very similar to a region of the yeast mating type proteins. These are sequence-specific DNA-binding proteins that act as master switches in yeast differentiation by controlling gene expression in a cell type-specific fashion.

A schematic representation of the homeobox domain is shown below.

The helix-turn-helix region is shown by the symbols 'H' (for helix), and 't' (for turn).

```

XXXXXXXXXXXXXXXXXXXXXXXXXXXXHHHHHHHHttHHHHHHHHXXXXXXXXXXXX
1                                                                 60

```

The pattern detects homeobox sequences 24 residues long and spans positions 34 to 57 of the homeobox domain. The consensus pattern is as follows: [LIVMFYVG]-[ASLVR]-x(2)-[LIVMSTACN]-x-[LIVM]-x(4)-[LIV]-[RKNQESTAIY]-[LIVFSTNKH]-W-[FYVC]-x-[NDQTAH]-x(5)-[RKNAIMW].

MAP kinase kinase (mkk). SEQ ID NOs:29, 31, 196, 3175, 3190 and 3281 represent novel members of the MAP kinase kinase family. MAP kinases (MAPK) are involved in signal transduction, and are important in cell cycle and cell growth controls. The MAP kinase kinases (MAPKK) are dual-specificity protein kinases which phosphorylate and activate MAP kinases. MAPKK homologues have been found in yeast, invertebrates, amphibians, and mammals. Moreover, the MAPKK/MAPK phosphorylation switch constitutes a basic module activated in distinct pathways in yeast and in vertebrates. MAPKKs are essential transducers through which signals must pass before reaching the nucleus. For review, see, *e.g.*, Biologie *Biol Cell* (1993) 79:193-207; Nishida et al., *Trends Biochem Sci* (1993) 18:128-31; Ruderman, *Curr Opin Cell Biol* (1993) 5:207-13; Dhanasekaran et al., *Oncogene* (1998) 17:1447-55; Kiefer et al., *Biochem Soc Trans* (1997) 25:491-8; and Hill, *Cell Signal* (1996) 8:533-44.

Protein Kinase (prot kinase). SEQ ID NOs:1157, 1478, 1496, 2286, 2969 and 3190 represent polynucleotides encoding protein kinases. Protein kinases catalyze phosphorylation of proteins in a variety of pathways, and are implicated in cancer. Eukaryotic protein kinases (Hanks S.K., et al., *FASEB J.* (1995) 9:576; Hunter T., *Meth. Enzymol.* (1991) 200:3; Hanks S.K., et al., *Meth. Enzymol.* (1991) 200:38; Hanks S.K.,

Curr. Opin. Struct. Biol. (1991) 1:369; Hanks S.K. et al., *Science* (1988) 241:42) are enzymes that belong to a very extensive family of proteins which share a conserved catalytic core common to both serine/threonine and tyrosine protein kinases. There are a number of conserved regions in the catalytic domain of protein kinases. The first region, which is located in the N-terminal extremity of the catalytic domain, is a glycine-rich stretch of residues in the vicinity of a lysine residue, which has been shown to be involved in ATP binding. The second region, which is located in the central part of the catalytic domain, contains a conserved aspartic acid residue which is important for the catalytic activity of the enzyme (Knighton D.R. et al., *Science* (1991) 253:407).

10 The protein kinase profile includes two signature patterns for this second region: one specific for serine/threonine kinases and the other for tyrosine kinases. A third profile is based on the alignment in (Hanks S.K. et al., *FASEB J.* (1995) 9:576) and covers the entire catalytic domain.

The consensus patterns are as follows: 1) [LIV]-G-{P}-G-{P}-[FYWMGSTNH]-[SGA]-{PW}-[LIVCAT]-{PD}-x-[GSTACLIVMFY]-x(5,18)-[LIVMFYWCSTAR]-[AIVP]-[LIVMFAGCKR]-K, where K binds ATP; 2) [LIVMFYC]-x-[HY]-x-D-[LIVMFY]-K-x(2)-N-[LIVMFYCT](3), where D is an active site residue; and 3) [LIVMFYC]-x-[HY]-x-D-[LIVMFY]-[RSTAC]-x(2)-N-[LIVMFYC], where D is an active site residue.

20 If a protein analyzed includes two of the above protein kinase signatures, the probability of it being a protein kinase is close to 100%.

Ras family proteins (ras). SEQ ID NOs:1688 and 3258 represent polynucleotides encoding novel members of the ras family of small GTP/GDP-binding proteins (Valencia et al., 1991, *Biochemistry* 30:4637-4648). Ras family members generally require a specific guanine nucleotide exchange factor (GEF) and a specific GTPase activating protein (GAP) as stimulators of overall GTPase activity. Among ras-related proteins, the highest degree of sequence conservation is found in four regions that are directly involved in guanine nucleotide binding. The first two constitute most of the phosphate and Mg²⁺ binding site (PM site) and are located in the first half of the G-domain. The other two regions are involved in guanosine binding and are located in the C-terminal half of the molecule. Motifs and conserved structural features of the ras-related proteins are described in Valencia et al., 1991, *Biochemistry* 30:4637-4648. A major consensus pattern of ras proteins is: D-T-A-G-Q-E-K-[LF]-G-G-L-R-[DE]-G-Y-Y.

Thioredoxin family active site (Thioredox). SEQ ID NO:1677 represents a polynucleotide encoding a protein having a thioredoxin family active site. Thioredoxins (Holmgren A., *Annu. Rev. Biochem.* (1985) 54:237; Gleason F.K. et al., *FEMS Microbiol. Rev.* (1988) 54:271; Holmgren, A. *J. Biol. Chem.* (1989) 264:13963; 5 Eklund H. et al., *Proteins* (1991) 11:13) are small proteins of approximately one hundred amino- acid residues which participate in various redox reactions via the reversible oxidation of an active center disulfide bond. They exist in either a reduced form or an oxidized form where the two cysteine residues are linked in an intramolecular disulfide bond. Thioredoxin is present in prokaryotes and eukaryotes 10 and the sequence around the redox-active disulfide bond is well conserved. All PDI contains two or three (ERp72) copies of the thioredoxin domain. The consensus pattern is: [LIVMF]-[LIVMSTA]-x-[LIVMFYC]-[FYWSTHE]-x(2)-[FYWGTV]-C-[GATPLVE]-[PHYWSTA]-C-x(6)-[LIVMFYWT] (where the two C's form the redox-active bond).

15 Trypsin (trypsin). SEQ ID NO:1410 corresponds to a novel serine protease of the trypsin family. The catalytic activity of the serine proteases from the trypsin family is provided by a charge relay system involving an aspartic acid residue hydrogen-bonded to a histidine, which itself is hydrogen-bonded to a serine. The sequences in the vicinity of the active site serine and histidine residues are well 20 conserved in this family of proteases (Brenner S., *Nature* (1988) 334:528). The consensus patterns for this trypsin protein family are: 1) [LIVM]-[ST]-A-[STAG]-H-C, where H is the active site residue; and 2) [DNSTAGC]-[GSTAPIMVQH]-x(2)-G-[DE]-S-G-[GS]-[SAPHV]- [LIVMFYWH]-[LIVMFYSTANQH], where S is the active site residue. All sequences known to belong to this family are detected by the above 25 consensus sequences, except for 18 different proteases which have lost the first conserved glycine. If a protein includes both the serine and the histidine active site signatures, the probability of it being a trypsin family serine protease is 100%.

WD Domain, G-Beta Repeats (WD domain). SEQ ID NOs:1336, 1380, 1711, 1762, 1909, 2218, 3047, 3108 and 3292 represent novel members of the WD 30 domain/G-beta repeat family. Beta-transducin (G-beta) is one of the three subunits (alpha, beta, and gamma) of the guanine nucleotide-binding proteins (G proteins) which act as intermediaries in the transduction of signals generated by transmembrane receptors (Gilman, *Annu. Rev. Biochem.* (1987) 56:615). The alpha subunit binds to and hydrolyzes GTP; the functions of the beta and gamma subunits are less clear but 35 they seem to be required for the replacement of GDP by GTP as well as for membrane

anchoring and receptor recognition. In higher eukaryotes, G-beta exists as a small multigene family of highly conserved proteins of about 340 amino acid residues. Structurally, G-beta consists of eight tandem repeats of about 40 residues, each containing a central Trp-Asp motif (this type of repeat is sometimes called a WD-40 repeat). The consensus pattern for the WD domain/G-Beta repeat family is:

5 [LIVMSTAC]-[LIVMFYWSTAGC]-[LIMSTAG]-[LIVMSTAGC]-x(2)-[DN]-x(2)-[LIVMWSTAC]-x-[LIVMFSTAG]-W-[DEN]-[LIVMFSTAGCN].

wnt Family of Developmental Signaling Proteins (Wnt dev sign). SEQ ID NO:1538 corresponds to a novel member of the wnt family of developmental signaling proteins. Wnt-1 (previously known as int-1), the seminal member of this

10 family, (Nusse R., *Trends Genet.* (1988) 4:291) is thought to play a role in intercellular communication and seems to be a signalling molecule important in the development of the central nervous system (CNS). All wnt family proteins share the following features

15 characteristics of secretory proteins: a signal peptide, several potential N-glycosylation sites and 22 conserved cysteines that are probably involved in disulfide bonds. The Wnt proteins seem to adhere to the plasma membrane of the secreting cells and are therefore likely to signal over only few cell diameters. The consensus pattern, which is based upon a highly conserved region including three cysteines, is as follows: C-K-C-H-G-[LIVMT]-S-G-x-C.

20 Protein Tyrosine Phosphatase (Y phosphatase). SEQ ID NO:1417 represents a polynucleotide encoding a protein tyrosine kinase. Tyrosine specific protein phosphatases (EC 3.1.3.48) (PTPase) (Fischer et al., *Science* (1991) 253:401; Charbonneau et al., *Annu. Rev. Cell Biol.* (1992) 8:463; Trowbridge, *J. Biol. Chem.* (1991) 266:23517; Tonks et al., *Trends Biochem. Sci.* (1989) 14:497; and Hunter, *Cell*

25 (1989) 58:1013) catalyze the removal of a phosphate group attached to a tyrosine residue. These enzymes are very important in the control of cell growth, proliferation, differentiation and transformation. Multiple forms of PTPase have been characterized and can be classified into two categories: soluble PTPases and transmembrane receptor proteins that contain PTPase domain(s). Structurally, all known receptor PTPases are

30 made up of a variable length extracellular domain, followed by a transmembrane region and a C-terminal catalytic cytoplasmic domain. PTPase domains consist of about 300 amino acids. The search of two conserved cysteines has been shown to be absolutely required for activity. Furthermore, a number of conserved residues in its immediate vicinity have also been shown to be important. The consensus pattern for PTPases is:

35 [LIVMF]-H-C-x(2)-G-x(3)-[STC]-[STAGP]-x-[LIVMFY]; C is the active site residue.

Zinc Finger, C2H2 Type (Zincfing C2H2). SEQ ID NOs:308, 807, 1324, 1503, 1527, 3081, 3193 and 3306 correspond to polynucleotides encoding novel members of the of the C2H2 type zinc finger protein family. Zinc finger domains (Klug et al., *Trends Biochem. Sci.* (1987) 12:464; Evans et al., *Cell* (1988) 52:1; Payre et al., *FEBS Lett.* (1988) 234:245; Miller et al., *EMBO J.* (1985) 4:1609; and Berg, *Proc. Natl. Acad. Sci. USA* (1988) 85:99) are nucleic acid-binding protein structures. In addition to the conserved zinc ligand residues, it has been shown that a number of other positions are also important for the structural integrity of the C2H2 zinc fingers. (Rosenfeld et al., *J. Biomol. Struct. Dyn.* (1993) 11:557) The best conserved position is found four residues after the second cysteine; it is generally an aromatic or aliphatic residue. The consensus pattern for C2H2 zinc fingers is: C-x(2,4)-C-x(3)-[LIVMFYWC]-x(8)-H-x(3,5)-H. The two C's and two H's are zinc ligands.

Src homology 2. SEQ ID NOs:186, 2591, 3307 and 3339 represent polynucleotides encoding novel members of the family of Src homology 2 (SH2) proteins. The Src homology 2 (SH2) domain is a protein domain of about 100 amino acid residues first identified as a conserved sequence region between the oncoproteins Src and Fps (Sadowski I. et al., *Mol. Cell. Biol.* 6:4396-4408 (1986)). Similar sequences are found in many other intracellular signal-transducing proteins (Russel R.B. et al., *FEBS Lett.* 304:15-20 (1992)). SH2 domains function as regulatory modules of intracellular signalling cascades by interacting with high affinity to phosphotyrosine-containing target peptides in a sequence-specific and phosphorylation-dependent manner (Marangere L.E.M., Pawson T., *J. Cell Sci. Suppl.* 18:97-104 (1994); Pawson T., Schlessinger J., *Curr. Biol.* 3:434-442 (1993); Mayer B.J., Baltimore D., *Trends Cell. Biol.* 3:8-13 (1993); Pawson T., *Nature* 373:573-580 (1995)).

The SH2 domain has a conserved 3D structure consisting of two alpha helices and six to seven beta-strands. The core of the domain is formed by a continuous beta-meander composed of two connected beta-sheets (Kuriyan J., Cowburn D., *Curr. Opin. Struct. Biol.* 3:828-837(1993)). The profile to detect SH2 domains is based on a structural alignment consisting of 8 gap-free blocks and 7 linker regions totaling 92 match positions.

Src homology 3. SEQ ID NO:234, 1832, and 1835 represent polynucleotides encoding novel members of the family of Src homology 3 (SH3) proteins. The Src homology 3 (SH3) domain is a small protein domain of about 60 amino acid residues first identified as a conserved sequence in the non-catalytic part of several cytoplasmic protein tyrosine kinases (e.g., Src, Abl, Lck) (Mayer B.J. et al.,

Nature 332:272-275 (1988)). Since then, it has been found in a great variety of other intracellular or membrane-associated proteins (Musacchio A. et al., *FEBS Lett.* 307:55-61 (1992); Pawson T., Schlessinger J., *Curr. Biol.* 3:434-442 (1993); Mayer B.J., Baltimore D., *Trends Cell Biol.* 3:8-13 (1993); Pawson T., *Nature* 373:573-580 (1995)).

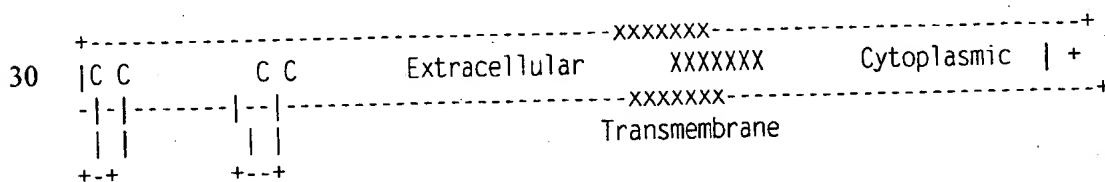
5 The SH3 domain has a characteristic fold which consists of five or six beta strands arranged as two tightly packed anti-parallel beta sheets. The linker regions may contain short helices (Kuriyan J., Cowburn D., *Curr. Opin. Struct. Biol.* 3:828-837 (1993)).

10 The function of the SH3 domain may be to mediate assembly of specific protein complexes via binding to proline-rich peptides (Morton C.J., Campbell I.D., *Curr. Biol.* 4:615-617 (1994)).

In general SH3 domains are found as single copies in a given protein, but there are a significant number of proteins with two SH3 domains and a few with 3 or 4 copies.

15 Fibronectin type III. SEQ ID NOs:746 and 1192 represent polynucleotides encoding novel members of the family of fibronectin type III proteins. A number of receptors for lymphokines, hematopoietic growth factors and growth hormone-related molecules have been found to share a common binding domain. (Bazan J.F., *Biochem. Biophys. Res. Commun.* 164:788-795 (1989); Bazan J.F., *Proc.*
20 *Natl. Acad. Sci. U.S.A.* 87:6934-6938 (1990); Cosman D. et al., *Trends Biochem. Sci.* 15:265-270 (1990); d'Andrea A.D., Fasman G.D., Lodish H.F., *Cell* 58:1023-1024 (1989); d'Andrea A.D., Fasman G.D., Lodish H.F., *Curr. Opin. Cell Biol.* 2:648-651 (1990)).

25 The conserved region constitutes all or part of the extracellular ligand-binding region and is about 200 amino acid residues long. In the N-terminal of this domain there are two pairs of cysteines known, in the growth hormone receptor, to be involved in disulfide bonds.



35 Two patterns detect this family of receptors. The first one is derived from the first N-terminal disulfide loop, the second is a tryptophan-rich pattern located at the C-terminal extremity of the extracellular region.

A consensus for this protein family is: C-[LVFYR]-x(7,8)-[STIVDN]-C-x-W (The two C's are linked by a disulfide bond). A second consensus for this protein family is: [STGL]-x-W-[SG]-x-W-S.

LIM domain containing proteins. SEQ ID NOs:1269, 1309, 1360, and 1386 represent polynucleotides encoding novel members of the family of LIM domain containing proteins. A number of proteins contain a conserved cysteine-rich domain of about 60 amino-acid residues. (Freyd G. et al., *Nature* 344:876-879 (1990); Baltz R. et al., *Plant Cell* 4:1465-1466 (1992); Sanchez-Garcia I., Rabbitts T.H., *Trends Genet.* 10:315-320 (1994)).

In the LIM domain, there are seven conserved cysteine residues and a histidine. The arrangement followed by these conserved residues is C-x(2)-C-x(16,23)-H-x(2)-[CH]-x(2)-C-x(2)-C-x(16,21)-C-x(2,3)-[CHD]. The LIM domain binds two zinc ions (Michelsen J.W. et al., *Proc. Natl. Acad. Sci. U.S.A.* 90:4404-4408 (1993)). LIM does not bind DNA, rather it seems to act as interface for protein-protein interaction. The consensus for this protein family is: C-x(2)-C-x(15,21)-[FYWH]-H-x(2)-[CH]-x(2)-C-x(2)-C-x(3)-[LIVMF]. The 5 C's and the H bind zinc.

C2 domain (protein kinase C like). SEQ ID NOs:1325 and 2282 represent polynucleotides encoding novel members of the family of C2 domain containing proteins. Some isozymes of protein kinase C (PKC) contain a domain, known as C2, of about 116 amino-acid residues, which is located between the two copies of the C1 domain (that bind phorbol esters and diacylglycerol) and the protein kinase catalytic domain. (Azzi A. et al., *Eur. J. Biochem.* 208:547-557 (1992); Stabel S., *Semin. Cancer Biol.* 5:277-284 (1994)).

The C2 domain is involved in calcium-dependent phospholipid binding (Davletov B.A., Suedhof T.C., *J. Biol. Chem.* 268:26386-26390 (1993)). Since domains related to the C2 domain are also found in proteins that do not bind calcium, other putative functions for the C2 domain include binding to inositol-1,3,5-tetraphosphate. (Fukuda M., et al., *J. Biol. Chem.* 269:29206-29211 (1994)).

The consensus pattern for the C2 domain is located in a conserved part of that domain, the connecting loop between beta strands 2 and 3. The profile for the C2 domain covers the total domain. The consensus for this protein family is: [ACG]-x(2)-L-x(2,3)-D-x(1,2)-[NGSTLIF]-[GTMR]-x-[STAP]-D-[PA]-[FY]

Serine proteases, trypsin family, active sites. SEQ ID NO:1410 represents a polynucleotide encoding a novel member of the family of serine protease, trypsin proteins. The catalytic activity of the serine proteases from the trypsin family is

provided by a charge relay system involving an aspartic acid residue hydrogen-bonded to a histidine, which itself is hydrogen-bonded to a serine. The sequences in the vicinity of the active site serine and histidine residues are well conserved in this family of proteases (Brenner S., *Nature* 334:528-530 (1988)).

5 A consensus for this protein family is: [LIVM]-[ST]-A-[STAG]-H-C [H is the active site residue]. A second consensus for this protein family is: [DNSTAGC]-[GSTAPIMVQH]-x(2)-G-[DE]-S-G-[GS]-[SAPHV]- [LIVMFYWH]-[LIVMFYSTANQH] [S is the active site residue].

RNA Recognition Motif Domain (RRM, RBD, or RNP). SEQ ID NOs:
10 1464 and 1514 represent polynucleotides encoding novel members of the family of RNA recognition motif domain proteins (Bandziulis R.J. et al., *Genes Dev.* 3:431-437 (1989); Dreyfuss G. et al., *Trends Biochem. Sci.* 13:86-91 (1988)).

Inside the putative RNA-binding domain there are two regions which are highly conserved. The first one is a hydrophobic segment of six residues (which is
15 called the RNP-2 motif); the second one is an octapeptide motif (which is called RNP-1 or RNP-CS). The position of both motifs in the domain is shown in the following schematic representation:

20 xxxxxx#####xx#####xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx
RNP-2 RNP-1

As a consensus pattern for this type of domain the RNP-1 motif was used. The consensus for this protein family is: [RK]-G-{EDRKHPCG}-[AGSCI]-[FY]-[LIVA]-x-[FYLM]

25 Phosphatidylinositol-specific phospholipase C, Y Domain. SEQ ID NO: 1707 represents a polynucleotide encoding a novel member of the phosphatidylinositol-specific phospholipase C, Y domain family of proteins. Phosphatidylinositol-specific phospholipase C (EC3.1.4.11), a eukaryotic intracellular enzyme, plays an important role in signal transduction processes (Meldrum E. et al., *Biochim. Biophys. Acta*
30 1092:49-71 (1991)). It catalyzes the hydrolysis of 1-phosphatidyl-D-myo-inositol-3,4,5- triphosphate into the second messenger molecules diacylglycerol and inositol-1,4,5-triphosphate. This catalytic process is tightly regulated by reversible phosphorylation and binding of regulatory proteins (Rhee S.G., Choi K.D., *Adv. Second Messenger Phosphoprotein Res.* 26:35-61 (1992); Rhee S.G., Choi K.D., *J. Biol. Chem.*
35 267:12393-12396 (1992); Sternweis P.C., Smrcka A.V., *Trends Biochem. Sci.* 17:502-506 (1992)).

All eukaryotic PI-PLCs contain two regions of homology, referred to as "X-box" and "Y-box". The order of these two regions is the same (NH₂-X-Y-COOH), but the spacing is variable. In most isoforms, the distance between these two regions is only 50-100 residues but in the gamma isoforms one PH domain, two SH2 domains, and one SH3 domain are inserted between the two PLC-specific domains. The two conserved regions have been shown to be important for the catalytic activity. At the C-terminal of the Y-box, there is a C2 domain possibly involved in Ca-dependent membrane attachment.

Serine Carboxypeptidases. SEQ ID NO:1744 represents a polynucleotide encoding a novel member of the serine carboxypeptidases family of proteins. Carboxypeptidases may be either metallo carboxypeptidases or serine carboxypeptidases (EC 3.4.16.5 and EC 3.4.16.6). The catalytic activity of the serine carboxypeptidases, like that of the trypsin family serine proteases, is provided by a charge relay system involving an aspartic acid residue hydrogen-bonded to a histidine, which is itself hydrogen-bonded to a serine (Liao D.I., Remington S.J., *J. Biol. Chem.* 265:6528-6531 (1990)).

The sequences surrounding the active site serine and histidine residues are highly conserved in all these serine carboxypeptidases. A consensus for this protein family is: [LIVM]-x-[GTA]-E-S-Y-[AG]-[GS] [S is the active site residue]. A second consensus for this protein family is: [LIVF]-x(2)-[LIVSTA]-x-[IVPST]-x-[GSDNQL]-[SAGV]-[SG]-H-x-[IVAQ]-P-x(3)-[PSA] [H is the active site residue].

dsrcm Double-Stranded RNA Binding Motif. SEQ ID NO:1818 represents a polynucleotide encoding a novel member of the dsrcm double-stranded RNA binding motif proteins. In eukaryotic cells, a multitude of RNA-binding proteins play key roles in the posttranscriptional regulation of gene expression. Characterization of these proteins has led to the identification of several RNA-binding motifs. Several human and other vertebrate genetic disorders are caused by aberrant expression of RNA-binding proteins. (C. G. Burd & G. Dreyfuss, *Science* 265: 615-621 (1994)).

Proteins containing double stranded RNA binding motifs bind to specific RNA targets. Double stranded RNA binding motifs are exemplified by interferon-induced protein kinase in humans, which is part of the cellular response to dsRNA.

SEQ ID NOs:2577, 3183 and 3195 encode members of the 4 trans-membrane integral membrane protein family. This family consists of type III proteins, which are integral membrane proteins that contain a N-terminal membrane-anchoring domain that is not cleaved during biosynthesis, and which functions as a translocation

signal and a membrane anchor. The proteins also have three additional transmembrane regions. The consensus pattern is: G-x(3)-[LIVMF]-x(2)-[GSA]-[LIVMF] (2)-G-C-x-[GA]-[STA]-x(20-[eG]-x(20-[CwN]-[LIVM](2).

- 5 SEQ ID NO:2944 encodes a polypeptide having a calpain large subunit, domain III. Calpains are a family of intracellular proteases that play a variety of biological roles. Calpain 3, also known as p94, is predominantly expressed in skeletal muscle and plays a role in limb-girdle muscular dystrophy type 2A. (Sorimachi, H. et al., Biochem. J. 328:721-732, 1997).

- 10 SEQ ID NOs:1911 and 1980 encode polypeptides having a C3HC4 type zinc finger domain (RING finger), which is a cysteine-rich domain of 40 to 60 residues that binds two atoms of zinc, and is believed to be involved in mediating protein-protein interactions. Mammalian proteins of this family include V(D)J recombination activating protein, which activates the rearrangement of immunoglobulin and T-cell receptor genes; breast cancer type 1 susceptibility protein (BRCA1); bmi-1 proto-
15 oncogene; cbl proto-oncogene; and mel-18 protein, which is expressed in a variety of tumor cells and is a transcriptional repressor that recognizes and binds a specific DNA sequence. The consensus pattern is: C-x-H-x-[LIVMFY]-C-x(2)-C-[LIVMYA].

- SEQ ID NO:3274 encodes a eukaryotic transcription factor with a fork head domain, of about 100 amino acid residues. Proteins of this group are transcription
20 factors, including mammalian transcription factors HNF-3-alpha, -beta, and -gamma; interleukin-enhancer binding factor; and HTLF, which binds to a region of human T-cell leukemia virus long terminal repeat. The consensus pattern is [KR]-P-[PTQ]-[FYLVQH]-S-[FY]x(2)-[LIVM]-X(3,4)-[AC]-[LIM].

- SEQ ID NO:3345 encodes a polypeptide having a PDZ domain. Several
25 dozen signaling proteins belong to this group of proteins that have 80-100 residue repeats known as PDZ domains. Several of the proteins interact with the C-terminal tetrapeptide motifs X-Ser/Thr/X-Val-COO- of ion channels and/or receptors. (Ponting, C. P., Protein Sci. 6:464-468, 1997.)

- SEQ ID NO:3351 encodes a polypeptide in the family of phorbol
30 esters/glycerol binding proteins. Phorbol esters (PE) are analogues of diacylglycerol (DAG) and potent tumor promoters. DAG activates a family of serine-threonine protein kinases, known as protein kinase C. The N-terminal region of protein kinase C binds PE and DAG, and contains one or two copies of a cysteine-rich domain of about 50 amino acid residues. Other proteins having this domain include diacylglycerol kinase;
35 the vav oncogene; and N-chimaerin, a brain-specific protein. The DAG/PE binding

domain binds two zinc ions through the six cysteines and two histidines that are conserved in the domain. The consensus pattern is: H-x-[LIVMFYW]-x(8, 11)-C-x(2)-C-x(3)-[LIVMFC]-x(5, 10)-C-x(2)-C-x(4)-[HD]-x(2)-C-x(5, 9)-C.

5 SEQ ID NO:2216 encodes a polypeptide having a WW/rsp5/WWP domain. The protein is named for the presence of conserved aromatic positions, generally tryptophan, as well as a conserved proline. Proteins having the domain include dystrophin, vertebrate YAP protein, and IQGAP, a human GTPase activating protein which acts on ras. The consensus pattern is: W-x(9,11)-[VFY]-[FYW]-x(6,7)-[GSTNE]-[GSTQCR]-[FYW]-x(2)-P.

10 SEQ ID NO:2428 encodes a member of the dual specificity phosphatase family, having a catalytic domain, and SEQ IDS NOs:2281 and 2310 encode members of the protein tyrosine phosphatase family. These families are related and classified as tyrosine specific protein phosphatases. The enzymes catalyze the removal of a phosphate group from a tyrosine residue, and are important in the control of cell growth,
15 proliferation, differentiation, and transformation. The consensus pattern is [LIVMF]-H-C-x(2)-G-x(3)-[STC]-[STAGP]-x-[LIVMFY].

Table 1

SEQ ID	CLUSTER	SEQ NAME	ORIENTATION	CLONE ID	LIBRARY
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2	377708	RTA00002683F.m.01.2.P.Seq	F	M00040089A:G08	CH09LNL
3	427782	RTA00002666F.l.06.1.P.Seq	F	M00032638D:A06	CH08LNH
4	29372	RTA00002712F.a.06.1.P.Seq	F	M00023282A:C02	CH04MAL
5	455003	RTA00002694F.b.02.1.P.Seq	F	M00043419D:A10	CH20COHLV
6	380625	RTA00002684F.d.03.2.P.Seq	F	M00040118D:G10	CH09LNL
7	450959	RTA00002691F.b.05.3.P.Seq	F	M00043306D:B07	CH17COHLV
8	397851	RTA00002680F.b.04.1.P.Seq	F	M00039775A:A09	CH09LNL
9	20652	RTA00002710F.k.01.1.P.Seq	F	M00022440B:E01	CH03MAH
10	97830	RTA00002663F.k.18.1.P.Seq	F	M00022767B:G11	CH03MAH
11	373071	RTA00002670F.j.23.1.P.Seq	F	M00033442A:D06	CH09LNL
12	162369	RTA00002713F.e.01.1.P.Seq	F	M00027292D:F10	CH04MAL
13	401247	RTA00002685F.f.15.2.P.Seq	F	M00039508A:C12	CH12EDT
14	430738	RTA00002669F.l.15.3.P.Seq	F	M00033231D:B09	CH08LNH
15	46779	RTA00002711F.c.14.1.P.Seq	F	M00022860C:G04	CH03MAH
16	375772	RTA00002681F.p.01.2.P.Seq	F	M00039909C:G05	CH09LNL
17	430689	RTA00002669F.j.01.3.P.Seq	F	M00033243B:A05	CH08LNH
18	376546	RTA00002677F.d.07.2.P.Seq	F	M00039345C:C12	CH09LNL
19	450041	RTA00002667F.f.17.1.P.Seq	F	M00032790B:A07	CH08LNH
20	431643	RTA00002669F.l.16.1.P.Seq	F	M00033276D:H09	CH08LNH
21	19422	RTA00002709F.c.02.1.P.Seq	F	M00005449B:B10	CH02COH
22	376802	RTA00002677F.c.18.2.P.Seq	F	M00039344B:G07	CH09LNL
23	376814	RTA00002674F.h.02.1.P.Seq	F	M00039139C:G12	CH09LNL
24	375492	RTA00002677F.m.19.2.P.Seq	F	M00039418B:D08	CH09LNL
25	379114	RTA00002681F.n.24.2.P.Seq	F	M00039903C:F03	CH09LNL
26	380668	RTA00002670F.p.11.1.P.Seq	F	M00033581C:H10	CH09LNL
27	213817	RTA00002664F.l.19.2.P.Seq	F	M00027634A:D11	CH04MAL
28	375749	RTA00002680F.f.23.1.P.Seq	F	M00039795D:G06	CH09LNL
29	430896	RTA00002669F.b.20.4.P.Seq	F	M00033185C:D01	CH08LNH
30	380462	RTA00002670F.o.01.1.P.Seq	F	M00033570B:E06	CH09LNL
31	430896	RTA00002669F.b.20.3.P.Seq	F	M00033185C:D01	CH08LNH
32	376996	RTA00002676F.p.13.2.P.Seq	F	M00039329C:B10	CH09LNL
33	374846	RTA00002677F.k.19.2.P.Seq	F	M00039412D:G06	CH09LNL
34	379075	RTA00002672F.n.13.2.P.Seq	F	M00039039B:E03	CH09LNL
35	374172	RTA00002673F.k.16.2.P.Seq	F	M00039097D:D06	CH09LNL
36	373104	RTA00002683F.o.15.2.P.Seq	F	M00040098D:G12	CH09LNL
37	186302	RTA00002713F.m.21.1.P.Seq	F	M00027591B:C04	CH04MAL
38	427947	RTA00002665F.o.01.1.P.Seq	F	M00032495B:D02	CH08LNH
39	375180	RTA00002673F.d.17.1.P.Seq	F	M00039064D:H09	CH09LNL
40	377584	RTA00002683F.l.22.2.P.Seq	F	M00040083C:E10	CH09LNL
41	377364	RTA00002678F.a.15.2.P.Seq	F	M00039432C:A01	CH09LNL
42	376347	RTA00002675F.l.08.1.P.Seq	F	M00039249C:G11	CH09LNL
43	446747	RTA00002689F.d.16.2.P.Seq	F	M00042740A:E09	CH15CON
44	28092	RTA00002711F.g.12.1.P.Seq	F	M00023032A:B05	CH03MAH
45	378206	RTA00002671F.a.20.3.P.Seq	F	M00033588C:G04	CH09LNL
46	378206	RTA00002671F.a.20.2.P.Seq	F	M00033588C:G04	CH09LNL
47	14940	RTA00002709F.j.11.1.P.Seq	F	M00005623A:G02	CH02COH

SEQ ID	CLUSTER	SEQ NAME	ORIENTATION	CLONE ID	LIBRARY
48	378411	RTA00002672F.g.13.2.P.Seq	F	M00039004B:A06	CH09LNL
49	38120	RTA00002712F.i.14.1.P.Seq	F	M00026927D:F02	CH04MAL
50	375730	RTA00002678F.i.13.2.P.Seq	F	M00039612B:G05	CH09LNL
51	428959	RTA00002667F.h.15.1.P.Seq	F	M00032811B:D02	CH08LNH
52	376851	RTA00002677F.c.03.2.P.Seq	F	M00039541C:H11	CH09LNL
53	373808	RTA00002671F.d.14.2.P.Seq	F	M00038272A:G01	CH09LNL
54	376168	RTA00002675F.n.17.1.P.Seq	F	M00039258B:E06	CH09LNL
55	18653	RTA00002712F.o.08.1.P.Seq	F	M00027135A:B11	CH04MAL
56	187632	RTA00002664F.i.15.1.P.Seq	F	M00027617B:C12	CH04MAL
57	374122	RTA00002673F.i.22.1.P.Seq	F	M00039104D:C09	CH09LNL
58	374946	RTA00002673F.j.24.1.P.Seq	F	M00039096A:E07	CH09LNL
59	375666	RTA00002677F.n.16.2.P.Seq	F	M00039422D:F04	CH09LNL
60	162369	RTA00002713F.d.24.1.P.Seq	F	M00027292D:F10	CH04MAL
61	21480	RTA00002709F.c.18.2.P.Seq	F	M00005531D:F06	CH02COH
62	18560	RTA00002711F.e.20.1.P.Seq	F	M00022938B:F07	CH03MAH
63	96575	RTA00002663F.j.08.1.P.Seq	F	M00022641C:H05	CH03MAH
64	377576	RTA00002682F.f.18.1.P.Seq	F	M00039975C:C11	CH09LNL
65	446747	RTA00002689F.d.16.3.P.Seq	F	M00042740A:E09	CH15CON
66	379311	RTA00002682F.g.01.1.P.Seq	F	M00039976D:A12	CH09LNL
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68	124549	RTA00002713F.c.07.1.P.Seq	F	M00027237C:B08	CH04MAL
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70	375134	RTA00002673F.k.22.2.P.Seq	F	M00039099A:H08	CH09LNL
71	186593	RTA00002713F.n.15.1.P.Seq	F	M00027620D:F11	CH04MAL
72	449831	RTA00002691F.a.17.3.P.Seq	F	M00042518D:A06	CH17COHLV
73	379678	RTA00002676F.b.06.1.P.Seq	F	M00039274B:G07	CH09LNL
74	20599	RTA00002708F.h.06.1.P.Seq	F	M00004264B:A05	CH01COH
75	41115	RTA00002713F.o.11.1.P.Seq	F	M00027652B:F11	CH04MAL
76	21109	RTA00002708F.h.12.1.P.Seq	F	M00004278A:F09	CH01COH
77	455702	RTA00002694F.b.11.1.P.Seq	F	M00043433C:G07	CH20COHLV
78	380643	RTA00002683F.p.09.2.P.Seq	F	M00040103B:H10	CH09LNL
79	374413	RTA00002672F.i.15.2.P.Seq	F	M00039015B:G10	CH09LNL
80	378891	RTA00002672F.i.18.2.P.Seq	F	M00039016A:A02	CH09LNL
81	379374	RTA00002672F.k.11.2.P.Seq	F	M00039028C:B11	CH09LNL
82	17253	RTA00002709F.h.23.1.P.Seq	F	M00006866A:D07	CH02COH
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701	373681	RTA00002671F.d.20.1.P.Seq	F	M00038272D:F11	CH09LNL
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761	374264	RTA00002671F.p.21.2.P.Seq	F	M00038620B:E09	CH09LNL
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955	453501	RTA00002693F.d.14.2.P.Seq	F	M00043162D:C12	CH19COP
956	450845	RTA00002691F.f.10.1.P.Seq	F	M00043410C:A09	CH17COHLV
957	448177	RTA00002690F.e.12.1.P.Seq	F	M00042839B:B11	CH16COP
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990	449794	RTA00002691F.c.22.2.P.Seq	F	M00043361B:A01	CHI7COHLV
991	400921	RTA00002685F.b.18.1.P.Seq	F	M00039371B:H06	CHI2EDT
992	373874	RTA00002672F.c.22.2.P.Seq	F	M00038663D:H10	CH09LNL
993	401050	RTA00002685F.e.09.2.P.Seq	F	M00039499C:A04	CHI2EDT
994	453237	RTA00002693F.c.02.2.P.Seq	F	M00043108A:F06	CHI9COP
995	449294	RTA00002690F.c.13.3.P.Seq	F	M00042770C:C04	CHI6COP
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997	378014	RTA00002680F.g.17.2.P.Seq	F	M00039799A:D10	CH09LNL
998	404726	RTA00002688F.a.18.2.P.Seq	F	M00040371C:H05	CHI4EDT
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1000	401154	RTA00002685F.e.06.2.P.Seq	F	M00039497C:C06	CHI2EDT
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1003	25387	RTA00002711F.f.19.1.P.Seq	F	M00023001C:C08	CH03MAH
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1005	403530	RTA00002688F.a.09.2.P.Seq	F	M00040368A:F01	CHI4EDT
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1012	377085	RTA00002678F.n.14.2.P.Seq	F	M00039619B:D02	CH09LNL
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1017	377632	RTA00002683F.i.18.2.P.Seq	F	M00040087D:F08	CH09LNL
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1027	377186	RTA00002682F.m.07.1.P.Seq	F	M00040014D:F03	CH09LNL
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1040	406092	RTA00002685F.k.11.1.P.Seq	F	M00039584C:C11	CH12EDT
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1115	454132	RTA00002693F.e.18.2.P.Seq	F	M00043191A:A07	CH19COP
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1173	404362	RTA00002687F.o.06.1.P.Seq	F	M00040342B:D12	CH14EDT
1174	403849	RTA00002687F.n.09.1.P.Seq	F	M00040333D:G05	CH14EDT
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1180	403898	RTA00002687F.a.05.1.P.Seq	F	M00039746C:H06	CH14EDT
1181	453512	RTA00002693F.a.21.2.P.Seq	F	M00043078D:D04	CH19COP
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1186	454414	RTA00002693F.f.18.2.P.Seq	F	M00043220B:C04	CH19COP
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1192	403274	RTA00002687F.b.10.1.P.Seq	F	M00039766A:G07	CH14EDT
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1195	402241	RTA00002686F.l.16.1.P.Seq	F	M00040261C:F01	CH13EDT
1196	380451	RTA00002670F.p.12.1.P.Seq	F	M00033581D:D08	CH09LNL
1197	455938	RTA00002694F.d.24.1.P.Seq	F	M00043528C:A02	CH20COHLV
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1213	401655	RTA00002685F.c.22.1.P.Seq	F	M00039378D:H07	CH12EDT
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1216	451600	RTA00002691F.b.19.3.P.Seq	F	M00043328D:H02	CH17COHLV
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1221	451718	RTA00002692F.e.24.1.P.Seq	F	M00043044B:A12	CH18CON
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1225	403541	RTA00002687F.p.20.1.P.Seq	F	M00040364A:E05	CH14EDT
1226	450773	RTA00002691F.d.24.3.P.Seq	F	M00043383D:A02	CH17COHLV
1227	376236	RTA00002685F.l.24.2.P.Seq	F	M00039595C:E05	CH12EDT
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1240	452077	RTA00002692F.c.24.2.P.Seq	F	M00043002A:E05	CH18CON
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1290	425824	RTA00002687F.b.17.2.P.Seq	F	M00039767C:E12	CH14EDT
1291	401266	RTA00002685F.i.11.2.P.Seq	F	M00039535D:D10	CH12EDT
1292	377949	RTA00002674F.p.04.1.P.Seq	F	M00039200A:C10	CH09LNL
1293	12926	RTA00002710F.e.21.1.P.Seq	F	M00022005C:C06	CH03MAH
1294	378242	RTA00002679F.c.20.2.P.Seq	F	M00039664D:G07	CH09LNL
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1296	453101	RTA00002693F.c.16.2.P.Seq	F	M00043143B:A10	CH19COP
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1302	374621	RTA00002675F.p.02.1.P.Seq	F	M00039263D:A12	CH09LNL
1303	19063	RTA00002708F.i.14.1.P.Seq	F	M00004361A:H02	CH01COH
1304	135941	RTA00002713F.g.06.1.P.Seq	F	M00027359B:G05	CH04MAL
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1306	375226	RTA00002677F.m.08.2.P.Seq	F	M00039417C:A01	CH09LNL
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1311	13406	RTA00002709F.l.14.1.P.Seq	F	M00007124D:H10	CH02COH
1312	378364	RTA00002674F.o.17.1.P.Seq	F	M00039192D:A07	CH09LNL
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1314	403548	RTA00002688F.a.10.2.P.Seq	F	M00040363D:E09	CH14EDT
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1320	26017	RTA00002709F.d.04.1.P.Seq	F	M00003601D:D08	CH02COH
1321	380355	RTA00002670F.o.06.1.P.Seq	F	M00033570C:C10	CH09LNL
1322	25232	RTA00002710F.n.22.1.P.Seq	F	M00022667D:B02	CH03MAH
1323	378952	RTA00002683F.h.11.1.P.Seq	F	M00040070B:B07	CH09LNL
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1325	48482	RTA00002712F.p.06.1.P.Seq	F	M00027159D:F03	CH04MAL
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1329	15203	RTA00002710F.a.21.1.P.Seq	F	M00007972B:H12	CH03MAH
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1340	449832	RTA00002691F.e.13.2.P.Seq	F	M00043393A:B08	CH17COHLV
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1348	58005	RTA00002661F.h.14.1.P.Seq	F	M00004222C:E03	CH01COH
1349	451379	RTA00002691F.b.12.3.P.Seq	F	M00043312C:E08	CH17COHLV
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1352	428063	RTA00002666F.i.05.1.P.Seq	F	M00032638C:G08	CH08LNL
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1354	428407	RTA00002665F.p.12.1.P.Seq	F	M00032510D:F12	CH08LNL
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1357	378000	RTA00002681F.j.16.2.P.Seq	F	M00039887D:C04	CH09LNL
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1359	456629	RTA00002694F.d.04.1.P.Seq	F	M00043491C:F04	CH20COHLV
1360	431346	RTA00002669F.g.24.2.P.Seq	F	M00033218A:C04	CH08LNL
1361	377206	RTA00002682F.m.14.1.P.Seq	F	M00040015C:F08	CH09LNL
1362	453036	RTA00002692F.b.11.2.P.Seq	F	M00042960D:H08	CH18CON
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1366	451438	RTA00002691F.d.23.3.P.Seq	F	M00043383C:F12	CH17COHLV
1367	379011	RTA00002681F.n.23.1.P.Seq	F	M00039903C:D01	CH09LNL
1368	404048	RTA00002687F.g.01.1.P.Seq	F	M00040206A:A07	CH14EDT
1369	404048	RTA00002687F.g.01.2.P.Seq	F	M00040206A:A07	CH14EDT
1370	452398	RTA00002692F.f.17.2.P.Seq	F	M00043125C:A11	CH18CON
1371	403686	RTA00002687F.d.03.1.P.Seq	F	M00039946B:F08	CH14EDT
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1373	404048	RTA00002687F.f.24.2.P.Seq	F	M00040206A:A07	CH14EDT
1374	404048	RTA00002687F.f.24.1.P.Seq	F	M00040206A:A07	CH14EDT
1375	450627	RTA00002691F.f.01.2.P.Seq	F	M00043405C:G02	CH17COHLV
1376	375589	RTA00002680F.f.06.2.P.Seq	F	M00039794A:E04	CH09LNL
1377	379011	RTA00002681F.n.23.2.P.Seq	F	M00039903C:D01	CH09LNL
1378	16789	RTA00002709F.b.09.1.P.Seq	F	M00005382B:F08	CH02COH
1379	427346	RTA00002665F.a.24.3.P.Seq	F	M00028066C:D07	CH08LNL
1380	49540	RTA00002712F.e.01.1.P.Seq	F	M00023399C:E10	CH04MAL
1381	14440	RTA00002674F.e.14.2.P.Seq	F	M00039129C:D04	CH09LNL
1382	391401	RTA00002682F.k.11.1.P.Seq	F	M00040004D:B03	CH09LNL
1383	43782	RTA00002662F.d.21.2.P.Seq	F	M00007165B:G11	CH02COH
1384	212635	RTA00002666F.p.01.1.P.Seq	F	M00032688D:D11	CH08LNL
1385	15618	RTA00002710F.o.05.1.P.Seq	F	M00022684A:C02	CH03MAH
1386	18501	RTA00002669F.g.23.3.P.Seq	F	M00033217B:H07	CH08LNL
1387	400510	RTA00002688F.b.05.2.P.Seq	F	M00040375C:B06	CH14EDT
1388	403796	RTA00002687F.h.17.1.P.Seq	F	M00040293D:G04	CH14EDT
1389	452314	RTA00002694F.a.21.1.P.Seq	F	M00043416C:A02	CH20COHLV
1390	119179	RTA00002712F.k.20.1.P.Seq	F	M00027021A:G02	CH04MAL
1391	167451	RTA00002663F.j.11.1.P.Seq	F	M00022646A:H10	CH03MAH
1392	450523	RTA00002691F.e.19.2.P.Seq	F	M00043401D:G08	CH17COHLV
1393	289535	RTA00002693F.i.06.1.P.Seq	F	M00043202B:F01	CH19COP
1394	374736	RTA00002673F.o.08.2.P.Seq	F	M00039112B:C05	CH09LNL
1395	378912	RTA00002672F.n.01.2.P.Seq	F	M00039036C:B05	CH09LNL
1396	134877	RTA00002662F.d.05.2.P.Seq	F	M00007026B:H09	CH02COH
1397	372811	RTA00002670F.c.12.2.P.Seq	F	M00033347C:F02	CH09LNL
1398	373296	RTA00002672F.e.08.2.P.Seq	F	M00038994A:A10	CH09LNL
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1400	452903	RTA00002692F.i.08.2.P.Seq	F	M00043060D:G12	CH18CON
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1402	451013	RTA00002691F.f.08.1.P.Seq	F	M00043409B:B03	CH17COHLV
1403	212635	RTA00002666F.o.24.1.P.Seq	F	M00032688D:D11	CH08LNL
1404	452367	RTA00002692F.c.02.2.P.Seq	F	M00042976A:H04	CH18CON
1405	450627	RTA00002691F.e.24.1.P.Seq	F	M00043405C:G02	CH17COHLV
1406	186438	RTA00002713F.l.15.1.P.Seq	F	M00027462A:D07	CH04MAL
1407	431066	RTA00002669F.c.17.3.P.Seq	F	M00033189D:F08	CH08LNL
1408	378912	RTA00002672F.m.24.2.P.Seq	F	M00039036C:B05	CH09LNL
1409	15731	RTA00002709F.l.13.1.P.Seq	F	M00007116C:G02	CH02COH
1410	377187	RTA00002683F.d.21.2.P.Seq	F	M00040047C:F05	CH09LNL

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1413	379942	RTA00002679F.l.21.1.P.Seq	F	M00039707A:D02	CH09LNL
1414	375589	RTA00002680F.f.06.1.P.Seq	F	M00039794A:E04	CH09LNL
1415	375789	RTA00002674F.a.16.1.P.Seq	F	M00039120C:H03	CH09LNL
1416	456227	RTA00002694F.c.16.1.P.Seq	F	M00043465C:C09	CH20COHLV
1417	455852	RTA00002694F.a.02.1.P.Seq	F	M00042592A:H10	CH20COHLV
1418	25169	RTA00002710F.m.05.1.P.Seq	F	M00022579C:C11	CH03MAH
1419	376524	RTA00002678F.h.23.2.P.Seq	F	M00039477A:B03	CH09LNL
1420	449562	RTA00002690F.b.13.2.P.Seq	F	M00042515C:F08	CH16COP
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1424	380322	RTA00002683F.p.21.1.P.Seq	F	M00040106B:B09	CH09LNL
1425	401603	RTA00002685F.f.23.2.P.Seq	F	M00039510C:G02	CH12EDT
1426	376541	RTA00002678F.d.13.2.P.Seq	F	M00039456A:C08	CH09LNL
1427	449123	RTA00002690F.a.13.3.P.Seq	F	M00042435A:A11	CH16COP
1428	418358	RTA00002686F.m.07.1.P.Seq	F	M00040265D:B07	CH13EDT
1429	380263	RTA00002689F.a.22.1.P.Seq	F	M00042543C:G04	CH13CON
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1431	451679	RTA00002693F.a.04.2.P.Seq	F	M00042612D:F06	CH19COP
1432	396332	RTA00002686F.k.14.1.P.Seq	F	M00040252C:C06	CH13EDT
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1435	402494	RTA00002686F.h.16.1.P.Seq	F	M00040191A:B09	CH13EDT
1436	372798	RTA00002670F.c.18.2.P.Seq	F	M00033349D:F05	CH09LNL
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1455	403200	RTA00002687F.k.01.2.P.Seq	F	M00040318A:B02	CH14EDT
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1463	423432	RTA00002687F.l.10.2.P.Seq	F	M00040323C:G11	CH14EDT
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1558	414331	RTA00002685F.c.14.2.P.Seq	F	M00039376D:H07	CHI2EDT
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1591	446923	RTA00002690F.d.05.3.P.Seq	F	M00042788C:F11	CHI6COP
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1593	452241	RTA00002692F.c.10.2.P.Seq	F	M00042983C:G06	CHI8CON
1594	452455	RTA00002692F.e.10.2.P.Seq	F	M00043029C:A06	CHI8CON
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1745	377183	RTA00002683F.e.15.1.P.Seq	F	M00040052D:F12	CH09LNL
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565	10167	RTA00002916F.k.22.1.P.Seq	F	M00032621A:F11	CH08LNH
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573	13684	RTA00002915F.j.09.1.P.Seq	F	M00031485B:G05	CH08LNH
574	13460	RTA00002898F.f.19.1.P.Seq	F	M00004341C:A09	CH01COH
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1105	13438	RTA00002901F.a.11.1.P.Seq	F	M00005422D:H10	CH02COH
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1108	34364	RTA00002915F.o.09.2.P.Seq	F	M00032515A:B12	CH08LNH
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1122	15748	RTA00002901F.h.12.1.P.Seq	F	M00005515D:F02	CH02COH
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1127	4277	RTA00002927F.h.13.1.P.Seq	F	M00039642A:A08	CH12EDT
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1130	1820	RTA00002922F.n.11.1.P.Seq	F	M00039133C:F12	CH09LNL
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1153	4177	RTA00002902F.h.07.1.P.Seq	F	M00006673A:A03	CH02COH
1154	10430	RTA00002894F.g.21.1.P.Seq	F	M00003996B:H07	CH01COH
1155	31280	RTA00002903F.k.08.1.P.Seq	F	M00007007A:E04	CH02COH
1156	19098	RTA00002925F.e.23.1.P.Seq	F	M00039861C:B12	CH09LNL
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1165	16403	RTA00002935F.p.15.1.P.Seq	F	M00055424D:G05	CH17COHLV
1166	21920	RTA00002886F.j.05.1.P.Seq	F	M00001361A:C12	CH01COH
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1168	45734	RTA00002901F.j.14.1.P.Seq	F	M00005569D:G09	CH02COH
1169	12362	RTA00002929F.i.01.1.P.Seq	F	M00040391A:G05	CH14EDT
1170	9405	RTA00002892F.k.04.1.P.Seq	F	M00003830C:D02	CH01COH
1171	6507	RTA00002922F.o.05.1.P.Seq	F	M00039140A:F05	CH09LNL
1172	10735	RTA00002925F.b.24.1.P.Seq	F	M00039822A:H02	CH09LNL
1173	21177	RTA00002935F.d.18.1.P.Seq	F	M00054542B:A10	CH17COHLV
1174	14950	RTA00002894F.m.18.1.P.Seq	F	M00004047D:F12	CH01COH
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1207	10735	RTA00002925F.c.01.1.P.Seq	F	M00039822A:H02	CH09LNL
1208	3239	RTA00002887F.j.07.1.P.Seq	F	M00001406D:F06	CH01COH
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1213	10256	RTA00002888F.d.16.1.P.Seq	F	M00001449B:H10	CH01COH
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1246	20293	RTA00002888F.j.20.1.P.Seq	F	M00001477D:G09	CH01COH
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1249	25891	RTA00002909F.p.23.1.P.Seq	F	M00022740C:H11	CH03MAH
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1264	2252	RTA00002886F.k.24.1.P.Seq	F	M00001368A:A08	CH01COH
1265	4059	RTA00002935F.f.19.1.P.Seq	F	M00054714B:G10	CH17COHLV
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1309	16	RTA00002935F.a.06.1.P.Seq	F	M00042449B:F05	CH17COHLV
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1316	186798	RTA00002911F.f.11.1.P.Seq	F	M00026914C:H09	CH04MAL
1317	13193	RTA00002886F.l.16.1.P.Seq	F	M00001369A:G06	CH01COH
1318	3554	RTA00002919F.i.14.1.P.Seq	F	M00033149B:E10	CH08LNL
1319	19991	RTA00002908F.h.11.1.P.Seq	F	M00022446C:H06	CH03MAH
1320	173046	RTA00002901F.o.19.1.P.Seq	F	M00005703D:G10	CH02COH
1321	21798	RTA00002932F.b.12.1.P.Seq	F	M00043016B:F09	CH18CON
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1325	12315	RTA00002907F.m.01.1.P.Seq	F	M00022240D:B11	CH03MAH
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1328	15996	RTA00002897F.l.09.1.P.Seq	F	M00004281A:C04	CH01COH
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1335	1425	RTA00002916F.b.19.1.P.Seq	F	M00032541C:G03	CH08LNL
1336	186061	RTA00002911F.e.24.1.P.Seq	F	M00026900A:H07	CH04MAL
1337	20717	RTA00002907F.o.19.1.P.Seq	F	M00022273A:E03	CH03MAH
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1342	6806	RTA00002928F.d.02.1.P.Seq	F	M00040169A:G06	CH13EDT
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1345	6823	RTA00002888F.a.04.1.P.Seq	F	M00001433B:E02	CH01COH
1346	43029	RTA00002897F.d.03.1.P.Seq	F	M00004225D:E03	CH01COH
1347	14789	RTA00002935F.k.11.1.P.Seq	F	M00055055C:F01	CH17COHLV
1348	186061	RTA00002911F.f.01.1.P.Seq	F	M00026900A:H07	CH04MAL
1349	12823	RTA00002921F.g.24.1.P.Seq	F	M00033434D:F05	CH09LNL
1350	25844	RTA00002908F.k.23.1.P.Seq	F	M00022474B:C08	CH03MAH

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1354	25441	RTA00002906F.i.08.1.P.Seq	F	M00021981A:C02	CH03MAH
1355	4303	RTA00002897F.o.20.1.P.Seq	F	M00004295D:C07	CH01COH
1356	5741	RTA00002887F.c.19.1.P.Seq	F	M00001390D:E02	CH01COH
1357	17264	RTA00002900F.a.18.1.P.Seq	F	M00004831C:G11	CH02COH
1358	11766	RTA00002925F.f.20.1.P.Seq	F	M00039871C:G05	CH09LNL
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1360	13903	RTA00002923F.c.18.1.P.Seq	F	M00039204A:E09	CH09LNL
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1362	17412	RTA00002932F.b.11.1.P.Seq	F	M00043015D:D05	CH18CON
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1364	5858	RTA00002923F.i.01.1.P.Seq	F	M00039275B:E02	CH09LNL
1365	2510	RTA00002898F.b.14.1.P.Seq	F	M00004316A:B03	CH01COH
1366	8050	RTA00002900F.n.04.1.P.Seq	F	M00005383A:C11	CH02COH
1367	186538	RTA00002929F.e.18.1.P.Seq	F	M00040329A:H05	CH14EDT
1368	25427	RTA00002935F.n.20.1.P.Seq	F	M00055337B:C04	CH17COHLV
1369	24098	RTA00002901F.a.10.1.P.Seq	F	M00005422D:H02	CH02COH
1370	123823	RTA00002905F.h.08.1.P.Seq	F	M00008071D:H03	CH03MAH
1371	3644	RTA00002901F.c.03.1.P.Seq	F	M00005445D:D04	CH02COH
1372	27783	RTA00002917F.a.17.1.P.Seq	F	M00032666A:C02	CH08LNH
1373	1682	RTA00002910F.b.03.1.P.Seq	F	M00022801D:D09	CH03MAH
1374	3200	RTA00002887F.e.07.1.P.Seq	F	M00001393C:F04	CH01COH
1375	8442	RTA00002917F.h.23.1.P.Seq	F	M00032734B:E12	CH08LNH
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1385	23172	RTA00002896F.b.18.1.P.Seq	F	M00004141B:F08	CH01COH
1386	22510	RTA00002886F.l.05.1.P.Seq	F	M00001363A:C02	CH01COH
1387	17156	RTA00002934F.a.08.1.P.Seq	F	M00043455B:C08	CH20COHLV
1388	4593	RTA00002896F.o.18.1.P.Seq	F	M00004200C:A04	CH01COH
1389	2178	RTA00002901F.m.08.1.P.Seq	F	M00005626D:G11	CH02COH
1390	1015	RTA00002933F.c.11.1.P.Seq	F	M00043213A:D05	CH19COP
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1393	14648	RTA00002898F.j.11.1.P.Seq	F	M00004365C:G11	CH01COH
1394	12585	RTA00002897F.i.20.1.P.Seq	F	M00004269A:F11	CH01COH
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1414	15333	RTA00002888F.c.12.1.P.Seq	F	M00001442C:G12	CH01COH
1415	44436	RTA00002907F.b.17.1.P.Seq	F	M00022117C:A02	CH03MAH
1416	9247	RTA00002930F.a.16.1.P.Seq	F	M00042560C:G06	CH15CON
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1431	12823	RTA00002921F.h.01.1.P.Seq	F	M00033434D:F05	CH09LNL
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1444	8743	RTA00002907F.n.19.1.P.Seq	F	M00022262A:F06	CH03MAH
1445	22251	RTA00002926F.c.10.2.P.Seq	F	M00040079B:F06	CH09LNL
1446	12337	RTA00002928F.d.07.1.P.Seq	F	M00040173D:A04	CH13EDT
1447	13623	RTA00002911F.d.08.2.P.Seq	F	M00026842B:A01	CH04MAL
1448	5521	RTA00002887F.j.06.1.P.Seq	F	M00001406B:H09	CH01COH
1449	2193	RTA00002933F.a.13.1.P.Seq	F	M00043077B:F11	CH19COP
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1456	3662	RTA00002925F.c.07.1.P.Seq	F	M00039826D:E04	CH09LNL
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1458	11214	RTA00002896F.h.01.1.P.Seq	F	M00004161A:E08	CH01COH
1459	22888	RTA00002892F.l.09.1.P.Seq	F	M00003837C:D10	CH01COH
1460	15490	RTA00002925F.k.08.1.P.Seq	F	M00039932B:A07	CH09LNL
1461	112819	RTA00002905F.o.13.1.P.Seq	F	M00021676C:G03	CH03MAH
1462	19688	RTA00002896F.l.02.1.P.Seq	F	M00004179D:A12	CH01COH
1463	15132	RTA00002922F.n.20.1.P.Seq	F	M00039138B:G05	CH09LNL
1464	25022	RTA00002914F.i.21.1.P.Seq	F	M00028219B:H05	CH08LNH
1465	16303	RTA00002888F.b.12.1.P.Seq	F	M00001438A:E01	CH01COH
1466	16828	RTA00002897F.b.04.1.P.Seq	F	M00004214A:E05	CH01COH
1467	14295	RTA00002921F.a.18.1.P.Seq	F	M00033296C:C11	CH09LNL
1468	1979	RTA00002930F.f.06.1.P.Seq	F	M00055725D:D09	CH15CON
1469	36248	RTA00002888F.g.05.1.P.Seq	F	M00001460C:E10	CH01COH
1470	5676	RTA00002926F.b.22.2.P.Seq	F	M00040075B:A05	CH09LNL
1471	1239	RTA00002887F.o.21.1.P.Seq	F	M00001428B:C10	CH01COH
1472	7937	RTA00002917F.g.22.1.P.Seq	F	M00032728D:F01	CH08LNH
1473	4483	RTA00002911F.d.22.2.P.Seq	F	M00026856B:G03	CH04MAL
1474	7796	RTA00002925F.c.05.1.P.Seq	F	M00039826B:F09	CH09LNL
1475	17330	RTA00002915F.a.03.1.P.Seq	F	M00028616C:D09	CH08LNH
1476	25620	RTA00002902F.f.09.1.P.Seq	F	M00006631C:A04	CH02COH
1477	20601	RTA00002923F.l.20.1.P.Seq	F	M00039326A:G07	CH09LNL
1478	6205	RTA00002923F.g.21.1.P.Seq	F	M00039258C:C01	CH09LNL
1479	726	RTA00002913F.b.16.1.P.Seq	F	M00027734D:C03	CH04MAL
1480	104999	RTA00002908F.g.17.1.P.Seq	F	M00022435B:G12	CH03MAH
1481	30321	RTA00002919F.o.17.1.P.Seq	F	M00033264B:E06	CH08LNH
1482	5878	RTA00002913F.a.16.1.P.Seq	F	M00027688C:C01	CH04MAL
1483	5944	RTA00002905F.m.07.1.P.Seq	F	M00021649B:A02	CH03MAH
1484	5796	RTA00002908F.i.21.1.P.Seq	F	M00022457A:G05	CH03MAH
1485	3804	RTA00002935F.m.24.1.P.Seq	F	M00055254A:H03	CH17COHLV
1486	2728	RTA00002918F.a.22.1.P.Seq	F	M00032828A:A06	CH08LNH
1487	3804	RTA00002935F.n.01.1.P.Seq	F	M00055254A:H03	CH17COHLV
1488	3932	RTA00002915F.o.19.2.P.Seq	F	M00032517C:E10	CH08LNH
1489	16691	RTA00002891F.o.03.1.P.Seq	F	M00003780A:G01	CH01COH
1490	15430	RTA00002900F.g.10.1.P.Seq	F	M00005003D:C02	CH02COH
1491	5637	RTA00002925F.b.18.1.P.Seq	F	M00039820B:F06	CH09LNL
1492	16633	RTA00002897F.g.15.1.P.Seq	F	M00004240B:H07	CH01COH
1493	21826	RTA00002898F.g.06.1.P.Seq	F	M00004344A:G11	CH01COH
1494	22193	RTA00002919F.i.09.1.P.Seq	F	M00033140D:A03	CH08LNH
1495	10720	RTA00002898F.c.14.1.P.Seq	F	M00004320C:E07	CH01COH
1496	22491	RTA00002925F.m.06.1.P.Seq	F	M00040003A:G10	CH09LNL
1497	10423	RTA00002915F.n.13.2.P.Seq	F	M00032507D:G08	CH08LNH
1498	4953	RTA00002916F.h.11.1.P.Seq	F	M00032580C:B04	CH08LNH
1499	185567	RTA00002911F.p.08.1.P.Seq	F	M00027178B:A11	CH04MAL
1500	25605	RTA00002924F.m.22.1.P.Seq	F	M00039710B:A01	CH09LNL

SEQ ID	CLUSTER	SEQ NAME	ORIENTATION	CLONE ID	LIBRARY
1501	29446	RTA00002906F.m.24.1.P.S q	F	M00022070B:B04	CH03MAH
1502	9668	RTA00002908F.g.02.1.P.Seq	F	M00022421A:F12	CH03MAH
1503	29446	RTA00002906F.n.01.1.P.Seq	F	M00022070B:B04	CH03MAH
1504	7171	RTA00002887F.m.22.1.P.Seq	F	M00001421B:E07	CH01COH

Table 3

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
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1	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
2	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
3	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
4	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
5	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
6	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
7	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
8	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
9	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
10	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
11	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
12	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
13	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
14	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
15	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
16	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
17	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
18	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
19	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
20	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
21	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
22	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
23	<NONE>	<NONE>	<NONE>	548562	GENOME POLYPROTEIN [CONTAINS: RNA REPLICASE ; HELICASE: COAT PROTEIN] 2.7.7.48) - apple stem grooving virus (strain P-209)	9.2
24	<NONE>	<NONE>	<NONE>	416959	EXCISION REPAIR PROTEIN ERCC-6 DNA repair helicase ERCC6 - human >gil182181 (L04791) excision repair protein [Homo sapiens]	8.9
25	<NONE>	<NONE>	<NONE>	3327096	(AB014541) KIAA0641 protein [Homo sapiens]	8.7
26	<NONE>	<NONE>	<NONE>	861293	(U28741) F35D2.1 gene product [Caenorhabditis elegans]	7.9
27	<NONE>	<NONE>	<NONE>	3297821	(AL031032) extensin-like protein	5.5
28	<NONE>	<NONE>	<NONE>	2119692	transforming growth factor-beta type III receptor - chicken >gil11843 (L01121)	5.1
29	<NONE>	<NONE>	<NONE>	2136028	transforming growth factor-beta type III receptor [Gallus gallus] protein-kinase PRK1 - human	5.0

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
30	<NONE>	<NONE>	<NONE>	2746912	(AF040659) No definition line found [Caenorhabditis elegans]	4.6
31	<NONE>	<NONE>	<NONE>	2358287	(AF010404) ALR [Homo sapiens]	4.5
32	<NONE>	<NONE>	<NONE>	3877816	(Z96048) predicted using Genefinder; cDNA EST. EMBL:D65516 comes from this gene; cDNA EST yk191a5.5 comes from this gene [Caenorhabditis elegans]	4.4
33	<NONE>	<NONE>	<NONE>	4140268	(Y14953) SRCR domain, membrane form 2	4.1
34	<NONE>	<NONE>	<NONE>	1708663	(U51183) transposase [Hydra vulgaris]	4.0
35	<NONE>	<NONE>	<NONE>	1184100	(U45958) pistil extensin-like protein [Nicotiana glauca]	3.9
36	<NONE>	<NONE>	<NONE>	121073	GLUCOCORTICOID RECEPTOR (GR)	3.9
37	<NONE>	<NONE>	<NONE>	1718298	(U75698) ORF 45; contains an extended acidic domain; EBV BKRF4 homolog [Kaposi's sarcoma-associated herpesvirus] homolog, conserved in other gamma-herpesviruses	2.6
38	<NONE>	<NONE>	<NONE>	2352538	(AF006564) alcohol dehydrogenase [Drosophila persimilis] persimilis]	1.4
39	<NONE>	<NONE>	<NONE>	3192897	(AF066071) SP85; PsB [Dictyostelium discoideum]	1.4
40	<NONE>	<NONE>	<NONE>	561645	(L33421) This CDS feature is included to show the translation of the corresponding V_region. Presently translation qualifiers on V_region features are illegal (Z83120) predicted using Genefinder; cDNA EST EMBL:D35016 comes from this gene; cDNA EST EMBL:D32583 comes from this gene; cDNA EST EMBL:D35258 comes from this gene; cDNA EST EMBL:C11471 comes from this gene; cDNA EST EMBL:C...	1.0
41	<NONE>	<NONE>	<NONE>	3878857		1.0

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
42	<NONE>	<NONE>	<NONE>	1658571	(U75903) UGT1A7 [Rattus norvegicus]	1.0
43	<NONE>	<NONE>	<NONE>	2338034	(AF005370) putative immediate early protein [Alcelaphine herpesvirus 1]	0.86
44	<NONE>	<NONE>	<NONE>	3043714	(AB011167) KIAA0595 protein [Homo sapiens]	0.42
45	<NONE>	<NONE>	<NONE>	1723710	HYPOTHETICAL 92.7 KD PROTEIN IN ASN2-PHB1 INTERGENIC REGION >gi 2131678 pir S64439 hypothetical protein YGR130c - yeast (Saccharomyces cerevisiae) >gi 1323215 gnl PID e243523 (Z72915) ORF YGR130c [Saccharomyces cerevisiae]	0.40
46	<NONE>	<NONE>	<NONE>	1723710	HYPOTHETICAL 92.7 KD PROTEIN IN ASN2-PHB1 INTERGENIC REGION >gi 2131678 pir S64439 hypothetical protein YGR130c - yeast (Saccharomyces cerevisiae) >gi 1323215 gnl PID e243523 (Z72915) ORF YGR130c [Saccharomyces cerevisiae]	0.38
47	<NONE>	<NONE>	<NONE>	2996117	(AF046125) immediate early 2 [Rat cytomegalovirus]	0.26
48	<NONE>	<NONE>	<NONE>	4151809	(AF102855) synaptic SAPAP-interacting protein Synamon	0.024
49	<NONE>	<NONE>	<NONE>	2773341	(AF040954) putative protein phosphatase 1 nuclear targeting subunit [Rattus norvegicus]	0.017
50	<NONE>	<NONE>	<NONE>	1653522	(D90914) hypothetical protein	3e-04
51	<NONE>	<NONE>	<NONE>	3219965	HYPOTHETICAL 100.6 KD TRP-ASP REPEATS CONTAINING PROTEIN C2C6.04C IN CHROMOSOME I	3e-06
52	<NONE>	<NONE>	<NONE>	4185567	(AF115480) cAMP-dependent Rap1 guanine-nucleotide exchange factor [Mus musculus]	7e-07

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					HYPOTHETICAL 43.2 KD	
53	<NONE>	<NONE>	<NONE>	1176527	PROTEIN C34E10.1 IN CHROMOSOME III >gi 500724 (U10402) C34E10.1 gene product [Caenorhabditis elegans]	3e-20
54	X85444	G.pallida repetitive DNA element	5.0	2118936	beta-globin - chimpanzee (fragment)	8.6
55	X72961	Synechococcus sp. cpeB, cpeA genes and ORF3	5.0	462569	MICROTUBULE-ASSOCIATED PROTEIN 1A microtubule-associated protein MAP1A - rat >gi 205538 norvegicus]	2.2
56	U94747	Human WD repeat protein HAN11 mRNA. complete cds	5.0	3875538	(Z67990) similar to cuticle collagen	1.3
57	AF032108	Homo sapiens integrin alpha-7 mRNA. complete cds	5.0	2147194	collagen - Paralvinella grasslei	0.002
58	Z50798	G.gallus mRNA for p52	5.0	3122885	ASPARTYL-TRNA SYNTHETASE synthetase [Bacillus subtilis]	3e-11
59	AB002384	Human mRNA for KIAA0386 gene, complete cds	5.0	2632098	(Y15513) Prodos protein [Drosophila melanogaster]	9e-12
60	X14835	Thermofilum pendens DNA for 16S and 23S ribosomal RNA, tRNA-Met, and tRNA Gly	4.9	<NONE>	<NONE>	<NONE>
61	U87149	Hordeum vulgare nucellin gene, complete cds	4.9	128578	NONSTRUCTURAL PROTEIN NS-S spotted wilt virus (strain CPNH1) non-structural protein [Tomato spotted wilt virus]	2.8
62	D87541	Mus musculus gene for integrin alpha v subunit, promoter region	4.9	136956	HYPOTHETICAL PROTEIN UL61 cytomegalovirus (strain AD169) cytomegalovirus]	0.038
63	U72520	Mus musculus mena protein (Mena) mRNA. complete cds	4.9	3413892	(AB007934) KIAA0465 protein [Homo sapiens]	6e-07

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
64	S79797	enzymatic glycosylation-regulating gene [rats, Sprague-Dawley, streptozotocin diabetic, heart, mRNA, 5010 nt]	4.8	<NONE>	<NONE>	<NONE>
65	AB011102	Homo sapiens mRNA for KIAA0530 protein, partial cds	4.8	138022	RECEPTOR RECOGNIZING PROTEIN gp38 - phage Ox2 >gi 15126 (X05675) gene 38 (AA 1-266); pid:g15126 [Bacteriophage Ox2]	3.6
66	AF100985	Penaeus monodon phosphopyruvate hydratase mRNA, complete cds	4.8	500615	(D16221) endochitinase [Oryza sativa]	2.8
67	U31756	Bacillus subtilis gamma-aminobutyrate permease cds	4.8	3880699	(AL021471) similar to Eukaryotic aspartyl proteases [Caenorhabditis elegans] Eukaryotic aspartyl proteases [Caenorhabditis elegans]	2.8
68	U25111	Pisum sativum chloroplast processing enzyme mRNA, nuclear gene encoding chloroplast protein, complete cds.	4.8	1800145	(U83658) FH1/FH2 protein homolog [Emericella nidulans]	1.6
69	U00454	Mus musculus Cdx-2 homeobox protein gene, complete cds.	4.7	<NONE>	<NONE>	<NONE>
70	M84166	Hamster c-Ha-ras protein gene, complete cds.	4.7	1710606	RENIN-BINDING PROTEIN (RNBP) protein [Rattus norvegicus]	0.88
71	AF087516	Mus musculus major sperm fibrous sheath protein Pro-mAKAP82 gene, alternative splice exons 1' and 1"	4.6	<NONE>	<NONE>	<NONE>
72	X74160	M.esculenta mRNA for granule-bound starch synthase	4.6	<NONE>	<NONE>	<NONE>
73	M97487	Haloferax volcanii superoxide dismutase (sod2) gene, complete cds.	4.6	2623307	(AC002409) putative ubiquitin protease [Arabidopsis thaliana]	3.4

Nearest Neighbor (BlastN vs. Genbank)				Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Drosophila				
74	M57889	melanogaster suppressor of sable gene, complete cds.	4.5	<NONE>	<NONE>	<NONE>
75	D49708	Rattus norvegicus mRNA for RNA binding protein	4.5	<NONE>	<NONE>	<NONE>
76	D31853	Yeast GTS1 gene for glycyl-threonin/serine repeat protein, complete cds	4.5	2447195	(U42580) NETTF (7x), DETTS (4x) [Paramecium bursaria Chlorella virus 1]	3.3
77	Z47036	Human partial cDNA sequence, clone bs613;	2.9	<NONE>	<NONE>	<NONE>
78	L19660	Rattus norvegicus gastric inhibitory peptide receptor mRNA, complete cds	2.7	2358279	(AF007871) torsinA [Homo sapiens]	2e-07
79	X82841	A.thaliana Aco gene	2.6	483212	immediate-early protein IE110 - human herpesvirus 1 (strain HFEM) (fragment)	8.4
80	X61931	S.purpurascens famA and famB genes for FAS domain and acyl-CoA-dehydrogenases, respectively	2.6	2290534	(U95031) sublingual gland mucin [Homo sapiens]	0.47
81	U13680	Human lactate dehydrogenase-C (LDH-C) mRNA, complete cds.	2.5	2887449	(AB007874) KIAA0414 [Homo sapiens]	3.1
82	AB007869	Homo sapiens KIAA0409 mRNA, partial cds	2.4	3130157	(AB008859) pheromone receptor [Fugu rubripes]	5.4
83	X97479	H.sapiens mas proto-oncogene, 5' region	2.1	<NONE>	<NONE>	<NONE>
84	X98374	R.norvegicus mRNA for KIS protein	1.9	<NONE>	<NONE>	<NONE>
85	AE000710	Aquifex aeolicus section 42 of 109 of the complete genome	1.9	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Homo sapiens mRNA				
86	D30612	for repressor protein, partial cds	1.9	<NONE>	<NONE>	<NONE>
87	Y14321	Homo sapiens PMP69 gene, exons 8,9,10 & 11	1.9	<NONE>	<NONE>	<NONE>
88	D90773	E.coli genomic DNA, Kohara clone #262(30.3-30.5 min.)	1.9	1536816	(D78305) DNA binding protein [Chlorella virus]	7.9
89	AE000991	Archaeoglobus fulgidus section 116 of 172 of the complete genome	1.9	520645	(X79095) pyruvate,orthophosphate dikinase [Flaveria trinervia]	2.7
90	U39476	Rattus norvegicus p95 Vav (Vav) proto-oncogene mRNA, complete cds.	1.9	4158178	(AL023496) hypothetical protein	1.6
91	U28838	Human transcription factor TFIIIB 90 kDa subunit	1.9	2495730	HYPOTHETICAL PROLINE-RICH PROTEIN KIAA0269 >gi1665805 gnl PID d1014089 (D87459) Similar to Volbox carteri extensin (S22697) [Homo sapiens]	0.23
92	U20106	Rattus norvegicus synaptotagmin VII mRNA, complete cds.	1.9	478380	UL47h protein - Marek's disease virus	0.23
93	AF071010	Mouse mammary tumor virus putative integrase, env polyprotein, and superantigen mRNA, complete cds	1.9	2781386	(AC004010) similar to Leucine-rich transmembrane proteins; 44% similarity to U42767 (PID:g1736918) [Homo sapiens]	4e-33
94	AF061881	Mesocricetus auratus c-fos proto-oncogene protein (c-fos) gene, complete cds	1.8	<NONE>	<NONE>	<NONE>
95	AE001397	Plasmodium falciparum chromosome 2, section 34 of 73 of the complete sequence	1.8	<NONE>	<NONE>	<NONE>

Nearest Neighbor (BlastN vs. Genbank)				Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Horseshoe crab				
96	D14701	mRNA for coagulation factor B, complete cds	1.8	<NONE>	<NONE>	<NONE>
97	M29154	P.falciparum multidrug resistance (MDR) gene, complete cds.	1.8	<NONE>	<NONE>	<NONE>
98	L16532	Rattus norvegicus (clone pCNPII) 2',3'-cyclic nucleotide 3'-phosphodiesterase (CNPII) mRNA, complete cds.	1.8	<NONE>	<NONE>	<NONE>
99	AE001434	Plasmodium falciparum chromosome 2, section 71 of 73 of the complete sequence	1.8	<NONE>	<NONE>	<NONE>
100	Z46785	D.melanogaster gene for protamine (mst35Bb).	1.8	<NONE>	<NONE>	<NONE>
101	X69822	P.sylvestris mRNA for glutamine synthetase	1.8	219896	(D90452) I-caldesmon I [Homo sapiens]	9.7
102	U49055	Rattus norvegicus CTD-binding SR-like protein rA8 mRNA, complete cds	1.8	2497252	INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 4 (IGFBP-4) (IBP-4) (IGF-BINDING PROTEIN 4) factor-binding protein-4 - sheep (fragment) factor-binding protein-4, IGFBP-4 [sheep, liver, Peptide, 237 aa] [Ovis aries]	2.5
103	L28101	Homo sapiens kallistatin (PI4) gene, exons 1-4, complete cds	1.8	4204267	(AC005223) 55585 [Arabidopsis thaliana]	2.4
104	U66987	Pandorina morum internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence	1.8	2635909	(Z99121) permease [Bacillus subtilis]	1.9

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Human polymorphic				
105	X58033	MspI site DNA (D3S3 locus)	1.8	2136878	keratin KAP5.5 - sheep (fragment) >gi 313722	0.65
106	U15780	Human p82 (ST5) mRNA, alternatively spliced, complete cds	1.8	3638957	(AC004877) sco-spondin-mucin-like; similar to P98167 uncertain [Homo sapiens]	0.64
107	AF038535	Homo sapiens synaptotagmin VII mRNA, partial cds	1.8	457927	(U00690) calcium channel alpha 1 subunit [Drosophila melanogaster]	0.51
108	AF052134	Homo sapiens clone 23585 mRNA sequence	1.8	232263	HOMEBOX PROTEIN HOX-D1 (HOX-4.9)	0.28
109	X75208	H.sapiens HEK2 mRNA for protein tyrosine kinase receptor.	1.8	1730198	GROWTH-ARREST-SPECIFIC PROTEIN 1 gene product [Homo sapiens]	0.22
110	AB013896	Xenopus laevis mRNA for SOX-D, complete cds	1.8	2494501	TRANSCRIPTION FACTOR FKH-4 factor [Mus musculus]	0.17
111	D16947	Human HepG2 3' region cDNA, clone hmd6b10	1.8	3413870	(AB007923) KIAA0454 protein [Homo sapiens]	0.002
112	D13547	Mouse DNA, T early alpha (TEA) region	1.8	3393018	(AL031174) hypothetical protein	5e-08
113	M35498	Woodchuck c-myc protein gene, exon 1.	1.8	3183405	HYPOTHETICAL 11.3 KD PROTEIN C2C6.07 IN CHROMOSOME I >gi 2370504 gnl PID e339194 pombe] >gi 3451305 gnl PID e1316730 (AL031324) very hypothetical protein [Schizosaccharomyces pombe]	8e-10
114	M84166	Hamster c-Ha-ras protein gene, complete cds.	1.8	3386622	(AC004665) unknown protein [Arabidopsis thaliana]	2e-10
115	U33135	Mychodea carnosia 18S ribosomal RNA gene, complete sequence	1.8	3334982	(AC005306) R27216_1 [Homo sapiens]	3e-22
116	U84003	Homo sapiens putative tumor suppressor (BIN1) gene, exons 7-12	1.7	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
117	AE001121	<i>Borrelia burgdorferi</i> (section 7 of 70) of the complete genome	1.7	<NONE>	<NONE>	<NONE>
118	AE001114	<i>Archaeoglobus fulgidus</i> section 165 of 172 of the complete genome	1.7	<NONE>	<NONE>	<NONE>
119	U82064	<i>Angiostrongylus cantonensis</i> adult-specific muscle protein-1 gene, partial cds	1.7	<NONE>	<NONE>	<NONE>
120	AF041836	<i>Buchnera aphidicola</i> plasmid pLeu-Sg, complete plasmid sequence	1.7	<NONE>	<NONE>	<NONE>
121	M87479	<i>Lymnaea stagnalis</i> FMRFamide gene, mature peptides.	1.7	<NONE>	<NONE>	<NONE>
122	M55163	<i>Xenopus laevis</i> fibroblast growth factor receptor mRNA, complete cds.	1.7	<NONE>	<NONE>	<NONE>
123	S57565	histamine H2-receptor [rats, Genomic, 1928 nt]	1.7	<NONE>	<NONE>	<NONE>
124	M27256	Simian immunodeficiency virus (SIV) pol region.	1.7	<NONE>	<NONE>	<NONE>
125	U31516	Human chromosome 8 anonymous clone pBS8-165	1.7	<NONE>	<NONE>	<NONE>
126	X12671	Human gene for heterogeneous nuclear ribonucleoprotein (hnRNP) core protein A1	1.7	<NONE>	<NONE>	<NONE>
127	AF009054	<i>Paeonia suffruticosa</i> ssp. <i>spontanea</i> alcohol dehydrogenase 1B (Adh1B) gene, partial cds	1.7	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
128	AF046917	Mus musculus transketolase gene, exon 6 and partial cds	1.7	<NONE>	<NONE>	<NONE>
129	D89053	Homo sapiens mRNA for Acyl-CoA synthetase 3, complete cds	1.7	<NONE>	<NONE>	<NONE>
130	U57968	Staphylothermus marinus surface layer- associated STABLE protease gene, complete cds.	1.7	<NONE>	<NONE>	<NONE>
131	L39072	Bovine herpesvirus 1 (clone p95) UL24 homologue gene, complete cds.	1.7	<NONE>	<NONE>	<NONE>
132	X04980	Drosophila simulans retrotransposon 297 5'-LTR and flanks (pWK1020)	1.7	<NONE>	<NONE>	<NONE>
133	AE001114	Archaeoglobus fulgidus section 165 of 172 of the complete genome	1.7	<NONE>	<NONE>	<NONE>
134	X04434	Human mRNA for insulin-like growth factor I receptor	1.7	<NONE>	<NONE>	<NONE>
135	U07890	Mus musculus C57BL/6J epidermal surface antigen (mesa) mRNA, complete cds.	1.7	<NONE>	<NONE>	<NONE>
136	D26163	Human tyrosinase gene, 5'-flanking region cell-specific transcription)	1.7	<NONE>	<NONE>	<NONE>
137	AF093818	Panorpa nipponensis NADH dehydrogenase subunit 5 gene, mitochondrial gene encoding mitochondrial protein, partial cds	1.7	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Xenopus laevis				
138	D50560	mRNA for cytochrome P-450, complete cds	1.7	<NONE>	<NONE>	<NONE>
139	AF083488	Mus musculus phospholipase D1 (PLD1) gene, exons 18 and 19, complete sequence	1.7	<NONE>	<NONE>	<NONE>
140	AF100694	Mus musculus Pontin52 mRNA, complete cds	1.7	<NONE>	<NONE>	<NONE>
141	M73749	Streptococcus salivarius thermophilus beta-D-galactose (lacZ) gene, complete cds. > :: gb M63636 STRLAC ZZ Streptococcus thermophilus beta-D-galactosidase (lacZ) gene, complete cds.	1.7	<NONE>	<NONE>	<NONE>
142	AE001114	Archaeoglobus fulgidus section 165 of 172 of the complete genome	1.7	2183023	(U84971) unknown [Homo sapiens]	9.2
143	L01983	Human type IV sodium channel alpha polypeptide	1.7	130504	GENOME POLYPROTEIN [CONTAINS: N-TERMINAL PROTEIN (P1); HELPER COMPONENT PROTEINASE INCLUSION PROTEIN (CI); 6 KD PROTEIN 2 (6K2); GENOME-LINKED PROTEIN (VPG); NUCLEAR ... virus (strain D)]	9.2
144	L19731	Plecotus rafinesquii mitochondrial cytochrome b gene, 5' end.	1.7	3327096	(AB014541) KIAA0641 protein [Homo sapiens]	9.1
145	AE001114	Archaeoglobus fulgidus section 165 of 172 of the complete genome	1.7	2183023	(U84971) unknown [Homo sapiens]	8.8

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
146	L27218	Bos taurus serum amine oxidase mRNA, complete cds. > oxidase-amiloride-binding protein homolog [cattle, liver, mRNA, 2664 nt]	1.7	1174459	SIGNAL TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION 6 (IL-4 STAT) >gi 559855 (U16031) IL-4 Stat [Homo sapiens]	7.1
147	Z49868	Caenorhabditis elegans cosmid W07E11, complete sequence [Caenorhabditis elegans]	1.7	4204263	(AC005223) 40409 [Arabidopsis thaliana]	6.7
148	AL022271	Caenorhabditis elegans cosmid F32F2, complete sequence [Caenorhabditis elegans]	1.7	2497969	PERIPLASMIC NITRATE REDUCTASE PRECURSOR >gi 1086107 pir S50163 nitrate reductase large chain precursor, periplasmic - Thiosphaera pantotropha >gi 600093 (Z36773) periplasmic nitrate reductase large subunit [Paracoccus denitrificans]	6.7
149	U43844	Mus musculus cyclin D3 gene, complete cds	1.7	3861490	(AF062037) capsid protein precursor [Thossea asigna virus]	5.1
150	Z25464	S.cerevisiae UNF1, LTV1, MRP8, CYB3 and TGL1 genes, complete CDS's	1.7	1255404	(U53151) weak similarity to cytochrome b [Caenorhabditis elegans]	4.1
151	U77846	Human elastin gene, partial cds and partial 3'UTR	1.7	3355682	(AL031124) putative secreted lyase	4.0
152	X62880	S.scrofa mRNA for calcium release channel (CRC)	1.7	3327080	(AB014533) KIAA0633 protein [Homo sapiens]	4.0
153	Y00067	Human gene for neurofilament subunit M (NF-M)	1.7	479829	heterogeneous ribonuclear particle protein homolog - Caenorhabditis elegans similarity to RNA recognition motifs [Caenorhabditis elegans]	3.9

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
154	X68393	D.melanogaster gene for Beta-tubulin, exons 1 and 2	1.7	2342682	(AC000106) Contains similarity to Rattus AMP-activated protein kinase (gb X95577). [Arabidopsis thaliana]	3.8
155	AB012284	Shuttle vector pAUR123 gene for Aur1-C, complete cds	1.7	417704	POL POLYPROTEIN (ORF1A/1B) [CONTAINS: RNA-DIRECTED RNA POLYMERASE ; HELICASE; PROTEASE]	3.8
156	M96633	Rattus norvegicus mitochondrial intermediate peptidase (MIP) mRNA, complete cds.	1.7	2314209	(AE000613) H. pylori predicted coding region HP1054	3.1
157	U49055	Rattus norvegicus CTD-binding SR-like protein rA8 mRNA, complete cds	1.7	2497252	INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 4 (IGFBP-4) (IBP-4) (IGF-BINDING PROTEIN 4) factor-binding protein-4 - sheep (fragment) factor-binding protein-4, IGFBP-4 [sheep, liver, Peptide, 237 aa] [Ovis aries]	3.0
158	Y15907	Mus musculus mRNA for myc-intron-binding protein-1	1.7	912776	iduronate-2-sulfatase, IDS (EC 3.1.6.13) Peptide Mutant, 550 aa]	3.0
159	U67600	Methanococcus jannaschii section 142 of 150 of the complete genome	1.7	2982355	(AF052252) fork head domain protein FKD9 [Danio rerio]	3.0
160	AF013759	Homo sapiens calumein (Calu) mRNA, complete cds	1.7	2982355	(AF052252) fork head domain protein FKD9 [Danio rerio]	2.9

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
161	AF062915	Arabidopsis thaliana putative transcription factor (MYB90) mRNA, complete cds	1.7	3878065	(U021000) Similarity to Human mRNA product KIAA0077 (TR:Q14997); cDNA EST yk243h8.5 comes from this gene; cDNA EST yk243h8.3 comes from this gene; cDNA EST yk359h4.5 comes from this gene [Caenorhabditis elegans] >gi 3880318 gnl PID e1349839 (Z81133) Similarity to Human mRNA product KIAA0077 (TR:Q14997); cDNA EST yk243h8.5 comes from this gene; cDNA EST yk243h8.3 comes from this gene; cDNA EST yk359h4.5 comes from this gene	2.3
162	X87526	H.sapiens genomic DNA (chromosome 3; clone NL3003R)	1.7	3638957	(AC004877) sco-spondin-mucin-like; similar to P98167 uncertain [Homo.sapiens]	2.3
163	AC005573	Homo sapiens chromosome 5, PAC clone 202e13	1.7	2465540	(AF005632) phosphodiesterase I/nucleotide pyrophosphatase beta [Homo sapiens]	1.8
164	D83402	Homo sapiens gene for prostacyclin synthase, exon 10 and complete cds	1.7	627608	steroid hormone receptor TR3 - human sapiens]	1.7
165	AF053700	Homo sapiens deltex (Dx) mRNA, complete cds	1.7	2662089	(AB007864) KIAA0404 [Homo sapiens]	1.7
166	AF043225	Mus musculus 6-pyruvoyl-tetrahydropterin synthase (Pts) mRNA, complete cds	1.7	2352538	(AF006564) alcohol dehydrogenase [Drosophila persimilis] persimilis]	1.4

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
167	U52917	<i>Thermus aquaticus</i> thermophilus NADH dehydrogenase I subunits NQO7, NQO6, NQO5, NQO4, NQO2, NQO1, NQO3, NQO8, NQO9, NQO10, NQO11, NQO12, NQO13, and NQO14, complete cds.	1.7	2564334	(AB006631) The human homolog of mouse Cux-2 [Homo sapiens]	1.0
168	X72222	<i>M. musculus</i> gene for serotonin 2 receptor	1.7	3875796	(Z73425) Similarity to Yeast hypothetical YIK9 protein (SW:YIK9_YEAST); cDNA EST EMBL:T01252 comes from this gene; cDNA EST EMBL:D33205 comes from this gene; cDNA EST EMBL:D33955 comes from this gene; cDNA EST EMBL:D35484 co...	1.0
169	U23186	<i>Crotalus scutulatus</i> PLA2-like pseudogene	1.7	853971	(X83413) DR5 [Human herpesvirus 6] >gi 853972 (X83413) DR5 [Human herpesvirus 6]	0.99
170	M83118	<i>Mus musculus</i> factor VIII-associated protein (f8a) mRNA, complete cds.	1.7	3201617	(AC004669) hypothetical protein [Arabidopsis thaliana] (AL031282) dJ283E3.3.2 (Cell Division Cycle 2-Like 2 (PITSLRE, p58/GTA, Galactosyltransferase Associated Protein Kinase)) (isoform beta 2-2) [Homo sapiens]	0.80
171	M38347	<i>E. coli</i> ATP-dependent proteinase (lon) gene, complete cds.	1.7	4140322	HYPOTHETICAL PROLINE-RICH PROTEIN KIAA0269 >gi 1665805 gnl PID d1014089 (D87459) Similar to Volbox carteri extensin (S22697) [Homo sapiens]	0.78
172	U28838	Human transcription factor TFIIIB 90 kDa subunit	1.7	2495730		0.62

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
173	U72487	Rattus norvegicus calcium-independent alpha-latrotoxin receptor mRNA, complete cds	1.7	544411	GLYCOPROTEIN GP100 PRECURSOR (P29F8) [discoideum]	0.35
174	AE000718	Aquifex aeolicus section 50 of 109 of the complete genome	1.7	2497569	FIBROBLAST GROWTH FACTOR RECEPTOR 3 PRECURSOR (FGFR-3) (HEPARIN-BINDING GROWTH FACTOR RECEPTOR) >gi 2117851 pir I55363 fibroblast growth factor receptor 3 - mouse >gi 199145 (M81342) fibroblast growth factor receptor 3 [Mus musculus]	0.34
175	AF016897	Oryza sativa GDP dissociation inhibitor protein OsGDI2 (OsGDI2) mRNA, complete cds	1.7	125362	MACROPHAGE COLONY STIMULATING FACTOR I RECEPTOR PRECURSOR (CSF-1-R) (FMS PROTO-ONCOGENE) (C-FMS) factor 1 receptor - cat >gi 163855 (J03149) M-CSF receptor [Felis domesticus]	0.34
176	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	1.7	85058	muscarinic acetylcholine receptor - fruit fly acetylcholine receptor [Drosophila melanogaster]	0.20
177	AF077352	Chlamydomonas reinhardtii myosin heavy chain	1.7	728901	ACROSOMAL PROTEIN SP-10 PRECURSOR SP-10 - western baboon >gi 298488 bbs 127113 (S56458) SP-10=intraacrosomal protein [Papio papio=baboons, Peptide, 285 aa] [Papio hamadryas]	0.20
178	Z92788	Caenorhabditis elegans cosmid F53B8, complete sequence [Caenorhabditis elegans]	1.7	746516	(U23517) D1022.7 [Caenorhabditis elegans] >gil3258651 elegans]	0.068

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
179	AF002217	Ralstonia eutropha megaplasmid pHG1 nitric oxide reductase (norB) gene. complete cds	1.7	1143538	(X87883) mitochondrial capsule selenoprotein [Rattus norvegicus] >gi 1354135 (U48702) mitochondria associated cysteine-rich protein SMCP	0.039
180	D30749	Rat mRNA for protein tyrosine phosphatase	1.7	1228035	(D83776) The KIAA0191 gene is expressed ubiquitously.; The KIAA0191 protein retains the C2H2 zinc-finger at its N-terminal region. [Homo sapiens]	0.008
181	M15202	Rat fast skeletal TnT gene encoding troponin T isoforms. complete cds.	1.7	731172	SKIN SECRETORY PROTEIN XP2 PRECURSOR	4e-04
182	L07592	Human peroxisome proliferator activated receptor mRNA. complete cds.	1.7	4033414	PUTATIVE IMPORTIN BETA-4 SUBUNIT	2e-06
183	U64031	Dendrobium crumenatum ACC synthase gene. complete cds	1.7	3122885	ASPARTYL-TRNA SYNTHETASE synthetase [Bacillus subtilis]	2e-11
184	AF034970	Homo sapiens docking protein (DOK-2) mRNA. complete cds	1.7	2289097	(U78737) alpha(1,3)fucosyltransferase [Cricetulus griseus]	8e-12
185	Z12839	L.longiflorum mRNA encoding calmodulin. > :: gb L18912 LILCALM ODU Lilium longiflorum calmodulin mRNA. complete cds.	1.7	2511747	(AF023270) probable transcriptional regulator dre4	4e-12

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
186	X53459	Equine arteritis virus (EAV) RNA genome > :: emb A45589 A45589 Sequence 1 from Patent WO9519438 > :: emb A58849 A58849 Sequence 1 from Patent WO9700963 > :: gb AR013959 AR013959 Sequence 1 from patent US 5773235	1.7	3979817	(Z70683) Weak similarity to Human tyrosine-protein kinase CSK (SW:CSK_HUMAN); cDNA EST EMBL:C10908 comes from this gene; cDNA EST EMBL:C12822 comes from this gene; cDNA EST yk408c2.3 comes from this gene; cDNA EST yk408c2.5 ... Human tyrosine-protein kinase CSK (SW:CSK_HUMAN); cDNA EST EMBL:C10908 comes from this gene; cDNA EST EMBL:C12822 comes from this gene; cDNA EST yk408c2.3 comes from this gene; cDNA EST yk408c2.5 ...	1e-14
187	K02668	E. coli ddl gene encoding D-alanine:D-alanine ligase and ftsQ and ftsA genes, complete cds, and ftsZ gene, 5' end.	1.7	3879121	(Z70310) predicted using Genefinder; Similarity to Mouse ankyrin (PIR Acc. No. S37771); cDNA EST EMBL:T01923 comes from this gene; cDNA EST EMBL:D32335 comes from this gene; cDNA EST EMBL:D32723 comes from this gene; cDNA ES... Genefinder; Similarity to Mouse ankyrin (PIR Acc. No. S37771); cDNA EST EMBL:T01923 comes from this gene; cDNA EST EMBL:D32335 comes from this gene; cDNA EST EMBL:D32723 comes from this gene; cDNA ES...	2e-19
188	AB008375	Homo sapiens mRNA for osteoblast specific cysteine-rich protein, complete cds	1.7	2496945	HYPOTHETICAL 55.9 KD PROTEIN EEED8.6 IN CHROMOSOME II >gi 733603 (U23484) No definition line found [Caenorhabditis elegans]	1e-19
189	L36603	Pseudomonas cepacia (clone Psudom70-1) heat shock protein 70 (hsp70) gene, complete cds	1.7	2661842	(Y15732) DNA polymerase beta [Xenopus laevis]	6e-20

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
190	Z49760	P.blakesleeanus mRNA GTP cyclohydrolase I	1.7	1731181	HYPOTHETICAL 75.5 KD PROTEIN C14A4.3 IN CHROMOSOME II >gi 3874230 gnl PID c1351618 protein (Swiss Prot accession number P38376); cDNA EST yk220e10.5 comes from this gene [Caenorhabditis elegans] (AF125443) contains similarity to S. pombe phosphatidyl synthase (GB:Z28295) [Caenorhabditis elegans]	3e-21
191	U52428	Human fatty acid synthase gene, partial cds	1.7	4226073		6e-25
192	U12767	Human mitogen induced nuclear orphan receptor	1.6	<NONE>	<NONE>	<NONE>
193	Z63478	H.sapiens CpG DNA, clone 85a12, forward read cpg85a12.ft1a.	1.6	<NONE>	<NONE>	<NONE>
194	AF084375	Homo sapiens inversin protein, exons 8 and 9	1.6	<NONE>	<NONE>	<NONE>
195	AE001114	Archaeoglobus fulgidus section 165 of 172 of the complete genome	1.6	<NONE>	<NONE>	<NONE>
196	AF084375	Homo sapiens inversin protein, exons 8 and 9	1.6	<NONE>	<NONE>	<NONE>
197	U24217	Kluyveromyces lactis RNA polymerase II largest subunit gene, partial cds	1.6	<NONE>	<NONE>	<NONE>
198	AE000580	Helicobacter pylori 26695 section 58 of 134 of the complete genome	1.6	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
199	X62083	H.sapiens mRNA for Drosophila female sterile homeotic (FSH) homologue > :: gb M80613 HUMFS HG Human homolog of Drosophila female sterile homeotic mRNA, complete cds.	1.6	<NONE>	<NONE>	<NONE>
200	M28064	Plasmodium brasilianum DNA homologous to the histidine-rich knob protein region of Plasmodium falciparum.	1.6	457495	(M26647) ORF X [Saccharomyces cerevisiae]	8.4
201	U03114	Streptomyces albus lipase precursor (lip) gene, complete cds, and unidentified 5' ORF and 3' ORF, partial cds.	1.6	3638957	(AC004877) sco-spondin-mucin-like; similar to P98167 uncertain [Homo sapiens]	7.8
202	U88422	Strix varia oocyte maturation factor Mos (c-mos) proto-oncogene, partial cds	1.6	137618	VITAMIN D3 RECEPTOR (VDR) receptor [Rattus norvegicus]	6.4
203	M68519	Human pulmonary surfactant-associated protein SP-A (SFTP1) gene, complete cds.	1.6	3875423	(Z38112) E03A3.6 [Caenorhabditis elegans]	4.9
204	AF044575	Homo sapiens transcription factor POU4F3	1.6	2133625	GABA transport protein - tobacco hornworm	4.7
205	L48476	Homo sapiens (subclone 3_e10 from P1 H21) DNA sequence.	1.6	3687297	(AJ005588) 5-epi-aristolochene synthase	4.6
206	M18630	Rat CNS 2',3'-cyclic nucleotide 3-phosphodiesterase	1.6	3880315	(Z81133) Similarity to Human mRNA product KIAA0077 (TR:Q14997) [Caenorhabditis elegans]	3.7

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
207	AF027174	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-B) mRNA, complete cds	1.6	267068	TUMOR-ASSOCIATED ANTIGEN L6	3.6
208	U53448	Babesia microti heat shock protein 70 (hsp70) gene, complete cds	1.6	1255429	(U53155) strong similarity to the carboxyl two-thirds of valyl-tRNA synthetases [Caenorhabditis elegans]	2.2
209	AF084367	Homo sapiens inversin protein mRNA, complete cds	1.6	1730076	PROBABLE SERINE/THREONINE-PROTEIN KINASE CY49.28 >gi 1370255 gnl PID e247094 (Z73966) pknJ	1.2
210	D55635	Yeast dis1+ gene for p93dis1, complete cds	1.6	3128353	(AF010496) maltose transport inner membrane protein	1.2
211	AF035756	Streptomyces sp. 2-dehydro-3-deoxyphosphoheptonate aldolase gene, partial cds	1.6	853971	(X83413) DR5 [Human herpesvirus 6] >gi 853972 (X83413) DR5 [Human herpesvirus 6]	0.97
212	X73479	O.cuniculus rPTPA mRNA	1.6	3413810	(Y17034) Bassoon [Mus musculus]	0.94
213	X98330	H.sapiens mRNA for ryanodine receptor 2	1.6	2072986	(U95142) putative G-protein-coupled receptor G-protein-coupled receptor [Arabidopsis thaliana]	0.73
214	X64194	P.anserina FMR1 gene exons 1 and 2	1.6	128014	NECDIN >gi 91129 pir JN0148 necdin, brain - mouse >gi 200020 (M80840) necdin [Mus musculus]	0.42
215	Z92788	Caenorhabditis elegans cosmid F53B8, complete sequence [Caenorhabditis elegans]	1.6	746516	(U23517) D1022.7 [Caenorhabditis elegans] >gi 3258651 elegans]	0.19
216	AE000888	Methanobacterium thermoautotrophicum from bases 1098908 to 1112186 (section 94 of 148) of the complete genome	1.6	462415	INTERFERON-ALPHA/BETA RECEPTOR ALPHA CHAIN PRECURSOR (IFN-ALPHA-REC) >gi 346520 pir S27387 interferon alpha receptor type 1 - bovine >gi 432	0.001

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
217	AB008375	Homo sapiens mRNA for osteoblast specific cysteine-rich protein, complete cds	1.6	2496945	HYPOTHETICAL 55.9 KD PROTEIN EEED8.6 IN CHROMOSOME II >gi 733603 (U23484) No definition line found [Caenorhabditis elegans] (Z70750) similar to vanadate resistance protein transmembranous domains [Caenorhabditis elegans]	1e-18
218	M25312	Orang-utan involucrin gene, complete cds.	1.6	3875131		3e-26
219	AB012882	Cyprinus carpio mRNA for MyoD, complete cds	1.5	<NONE>	<NONE>	<NONE>
220	U29487	Caenorhabditis elegans cosmid C09C7	1.5	<NONE>	<NONE>	<NONE>
221	X74760	M.musculus mRNA for Notch 3	1.5	1364094	integral membrane protein - Streptomyces pristinaespiralis >gi 872306 (X84072) integral membrane protein [Streptomyces pristinaespiralis]	4.3
222	U72396	Lycopersicon esculentum class II small heat shock protein Le-HSP17.6 mRNA, complete cds	1.5	121855	EXOGLUCANASE II PRECURSOR cellulose 1,4-beta cellobiosidase (EC 3.2.1.91) II precursor - fungus (Trichoderma reesei) 1,4-beta-cellobiosidase (EC 3.2.1.91) II - fungus cellobiohydrolase II [Trichoderma reesei]	4.3
223	U42391	Human myosin-DXb mRNA, complete cds	1.5	3688428	(AJ011534) sucrose synthase	4.2
224	M92296	Pongo pygmaeus gamma-1 and gamma-2 globin genes, complete cds.	1.5	186413	(M13144) inhibin A [Homo sapiens]	0.22
225	X94144	C.japonica mRNA for QNR-71 protein	1.5	2745737	(AF029791) UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase-II [Mus musculus]	3e-08

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
226	AB014557	Homo sapiens mRNA for KIAA0657 protein, partial cds	1.5	1212992	(X90568) Protein sequence and annotation available soon via Swiss-Prot; available at present via e-mail from LABEIT@EMBL-Heidelberg.DE [Homo sapiens]	4e-13
227	AF000948	Borrelia burgdorferi oligopeptide permease homolog OppAIV (oppAIV) gene, complete cds	1.3	<NONE>	<NONE>	<NONE>
228	AF057287	Mus musculus RAB/Rip protein mRNA, partial cds	1.3	2498005	MYC PROTO-ONCOGENE PROTEIN (C-MYC) proto-oncogene [Sus scrofa]	2.6
229	U38951	Drosophila melanogaster vacuolar ATPase subunit E	1.1	<NONE>	<NONE>	<NONE>
230	AF027148	Homo sapiens myogenic determining factor 3	1.1	3172134	(U90209) RNA polymerase II largest subunit [Bonnemaisonia hamifera]	2.3
231	AF079310	Mus musculus histone deacetylase 3 (Hdac3) gene, exons 4 through 15 and complete cds	1.0	1657601	(U66220) unknown [Nannocystis exedens]	0.25
232	X52134	P.radiata lac gene for laccase	0.95	996020	(X91638) BRM protein [Gallus gallus]	0.31
233	D89016	Human mRNA for Neuroblastoma, complete cds	0.93	<NONE>	<NONE>	<NONE>
234	X76392	C.familiaris VIP36 (vesicular integral-membrane protein of 36 kDa) mRNA	0.93	4176446	(AL022238) dJ1042K10.2.1 (novel protein with probable rabGAP domains and Src homology domain 3)	7e-81
235	AF100694	Mus musculus Pontin52 mRNA, complete cds	0.90	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
236	AE000991	Archaeoglobus fulgidus section 116 of 172 of the complete genome	0.90	1176579	EGT2 PROTEIN PRECURSOR (EARLY GT TRANSCRIPT 2) >gi 1362345 pir S55862 probable membrane protein YNL327w - yeast (Saccharomyces cerevisiae) cerevisiae] >gi 1302445 gnl PID e239572 (Z71603) ORF YNL327w [Saccharomyces cerevisiae]	6.9
237	Z35922	S.cerevisiae chromosome II reading frame ORF YBR053c	0.86	<NONE>	<NONE>	<NONE>
238	U47331	Rattus norvegicus metabotropic glutamate receptor 4b mRNA. complete cds.	0.82	1550703	(Z80225) hypothetical protein Rv2662	4.1
239	X72810	H.sapiens Ig germline kappa-chain gene variable region (L3)	0.69	3023063	(AF052587) F14 [Xylella fastidiosa]	6.7
240	Z11700	Escherichia coli genes faeG, faeH, faeI, faeJ and IS629-like insertion sequence. >:: emb Z11710 ECFAE HU E.coli faeH, faeI and faeJ genes encoding FaeH, FaeI and FaeJ proteins	0.69	2347188	(AC002338) laccase isolog [Arabidopsis thaliana] thaliana]	3.9
241	U71597	Phrynosoma douglassii NADH dehydrogenase subunit 4 (ND4) gene. mitochondrial gene encoding mitochondrial protein. partial cds	0.65	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					GLUTAMYL-tRNA	
242	Z77798	Ammonia species LSU rRNA gene (partial; isolate Tr S 5: clone 16)	0.64	1174506	SYNTHETASE glutamate--tRNA ligase (EC 6.1.1.17) - Haemophilus influenzae (strain Rd KW20) >gi 1573240 (U32713) glutamyl-tRNA synthetase (gltX) [Haemophilus influenzae Rd]	1.2
243	D25542	Human mRNA for golgi antigen gcp372, complete cds	0.64	111230	ultra-high-sulfur keratin 1 - mouse	1e-05
244	M80234	Cow dopamine transporter mRNA, putative cds.	0.64	3874972	(Z99709) similar to Elongation factor Tu family (contains ATP/GTP binding P-loop); cDNA EST EMBL:D76223 comes from this gene; cDNA EST yk478c5.5 comes from this gene [Caenorhabditis elegans]	8e-06
245	AB007918	Homo sapiens mRNA for KIAA0449 protein, partial cds	0.64	2833239	EPIDERMAL GROWTH FACTOR RECEPTOR KINASE SUBSTRATE EPS8 >gi 530823 (U12535) epidermal growth factor receptor kinase substrate [Homo sapiens]	2e-14
246	X51754	Human U266 rearranged DNA for lambda-immunoglobulin light chain	0.63	2072301	(U95102) mitotic phosphoprotein 90 [Xenopus laevis]	1.5
247	AE001554	Helicobacter pylori, strain J99 section 115 of 132 of the complete genome	0.62	<NONE>	<NONE>	<NONE>
248	Z64067	H.sapiens CpG DNA, clone 96e7, reverse read cpg96e7.r1a.	0.62	<NONE>	<NONE>	<NONE>
249	AJ223768	Pinus sylvestris microsatellite DNA, clone SPAC11.5	0.62	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
250	AJ011592	Bacteriophage P1 ban gene	0.62	2493689	PHOTOSYSTEM II 10 KD PHOSPHOPROTEIN [deltoides] >gi 2143326 gnl PID c319090 (Y13328) 10kDa phosphoprotein [Populus deltoides]	7.9
251	AF027151	Xenopus laevis survival of motor neuron protein interacting protein 1 (SIP1) mRNA, complete cds	0.62	4007790	(AL034463) putative single-strand polynucleotide binding protein [Schizosaccharomyces pombe]	2.0
252	AJ000376	Helobdella triserialis mRNA for actin	0.62	1117968	(U40763) CARS-Cyp [Homo sapiens] sapiens]	0.90
253	M69231	Rat thymosin beta 4 gene (pTB4G).intron.	0.62	4176370	(AC005058) similar to calcium-independent phospholipase A2; similar to AC004392 (PID:g3367519) [Homo sapiens]	6e-51
254	AB021638	Homo sapiens X11L2 mRNA for X11-like protein 2, complete cds	0.61	<NONE>	<NONE>	<NONE>
255	D26470	Bacteroides gingivalis DNA for arginyl endopeptidase, complete cds	0.61	<NONE>	<NONE>	<NONE>
256	J04737	A.thaliana ATPase gene, complete cds.	0.61	<NONE>	<NONE>	<NONE>
257	U06756	Bos taurus clone bm1308 microsatellite and are-1p repeat region.	0.61	1922280	(Y09905) snail like protein [Gallus gallus]	0.51
258	S75756	p15=cyclin D-dependent kinases 4 and 6-binding protein/p15 product {exon/intron 1} [human, brain tumors, Genomic, 753 nt]	0.61	484938	hypothetical protein 253 - Streptomyces griseus plasmid pSG1 (fragment)	0.13
259	L39837	Drosophila melanogaster tumor suppressor (warts) mRNA exons 1-8, complete cds.	0.61	3875131	(Z70750) similar to vanadate resistance protein transmembranous domains [Caenorhabditis elegans]	1e-09

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
260	U52428	Human fatty acid synthase gene, partial cds	0.61	4226073	(AF125443) contains similarity to S. pombe phosphatidyl synthase (GB:Z28295) [Caenorhabditis elegans]	2e-26
261	X15292	Plasmodium falciparum gene for heat-shock protein pPf203	0.60	<NONE>	<NONE>	<NONE>
262	AB020663	Homo sapiens mRNA for KIAA0856 protein, partial cds	0.60	470341	(U00043) No definition line found [Caenorhabditis elegans]	5.7
263	U68723	Human checkpoint suppressor 1 mRNA, complete cds	0.60	544375	GALACTOSE-BINDING PROTEIN REGULATOR glucose/galactose binding protein regulator - Agrobacterium tumefaciens >gi 142228 (L10424) glucose/galactose binding protein regulator	5.7
264	M32687	S.griseus sporulation protein genes 1590 and 1422.	0.60	2582017	(AF012871) Mergla' [Mus musculus]	3.3
265	AJ005331	Homo sapiens NKCC2 gene, exon 4, isoform B	0.60	3128353	(AF010496) maltose transport inner membrane protein	1.5
266	U14103	Mus musculus RGL protein mRNA, complete cds.	0.60	4099845	(U90533) serine protease inhibitor [Streptomyces fradiae]	0.098
267	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	0.59	3282851	(AF047897) ankyrin-like protein HGE-ANK [Ehrlichia sp. BDS]	5.5
268	AE000872	Methanobacterium thermoautotrophicum from bases 896604 to 912784 (section 78 of 148) of the complete genome	0.59	401553	HYPOTHETICAL 24.5 KD PROTEIN IN NADB-SRMB INTERGENIC REGION	4.3

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
269	L11871	Gallus gallus achaete-scute homologue (ASH) mRNA, complete cds.	0.59	628110	hypothetical protein - human herpesvirus 4 reading frame 1 [Human herpesvirus 4] 2 [Human herpesvirus 4] >gi 1334838 gnl PID e25079 4 [Human herpesvirus 4] >gi 1334840 gnl PID e25081 6 [Human herpesvirus 4] >gi 1334842 gnl PID e25067 8 [Human herpesvirus 4] >gi 1334844 gnl PID e25069 10 [Human herpesvirus 4] >gi 1334846 gnl PID e25071 12 [Human herpesvirus 4]	4.2
270	AF017114	Oryctolagus cuniculus glycogen synthase mRNA, complete cds	0.59	728856	NITROGENASE IRON-IRON PROTEIN ALPHA CHAIN (NITROGENASE COMPONENT 1) (DINITROGENASE) capsulatus >gi 312238 (X70033) alternative nitrogenase	2.4
271	AF027807	Homo sapiens beta-casein (CSN2) gene, complete cds	0.59	3252932	(AF067155) truncated rev protein [Human immunodeficiency virus type 1]	1.5
272	U81787	Human Wnt10B mRNA, complete cds	0.59	3875538	(Z67990) similar to cuticle collagen	1.4
273	U76036	Apteryx australis 16S ribosomal RNA gene, mitochondrial gene for mitochondrial RNA, partial sequence	0.59	4193356	(AF055088) ATP-binding cassette; PsaB [Streptococcus pneumoniae]	0.83
274	AB014564	Homo sapiens mRNA for KIAA0664 protein, partial cds	0.59	1709851	PTB-ASSOCIATED SPLICING FACTOR (PSF) long form - human >gi 38458 (X70944) PTB-associated splicing factor [Homo sapiens]	0.17
275	AF044171	Homo sapiens cyclin-dependent kinase inhibitor 2D (CDKN2D) gene, partial cds	0.59	3925213	(AL032626) Y37D8A.17 [Caenorhabditis elegans]	3e-10

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
276	L19640	Saccharomyces cerevisiae cdc2/cdc28 related protein kinase gene, complete cds.	0.59	3880115	(Z81130) T23G11.9 [Caenorhabditis elegans]	1e-21
277	Z80999	Human DNA sequence from cosmid E140G5 on chromosome 22, complete sequence [Homo sapiens]	0.58	<NONE>	<NONE>	<NONE>
278	Y11108	H.sapiens WNT8B gene	0.58	<NONE>	<NONE>	<NONE>
279	U80001	Sphyraena idastes lactate dehydrogenase A	0.58	<NONE>	<NONE>	<NONE>
280	Z49637	S.cerevisiae chromosome X reading frame ORF YJR137c	0.58	<NONE>	<NONE>	<NONE>
281	X64467	H.sapiens ALAD gene for porphobilinogen synthase	0.58	<NONE>	<NONE>	<NONE>
282	X74506	G.gallus hox B3 mRNA	0.58	<NONE>	<NONE>	<NONE>
283	U68040	Cochliobolus heterostrophus polyketide synthase	0.58	<NONE>	<NONE>	<NONE>
284	AF089084	Arabidopsis thaliana putative auxin efflux carrier protein (PIN1) mRNA, complete cds	0.58	<NONE>	<NONE>	<NONE>
285	U38481	Rattus norvegicus ROK-alpha mRNA, complete cds	0.58	<NONE>	<NONE>	<NONE>
286	AF017656	Homo sapiens G protein beta 5 subunit mRNA, complete cds	0.58	3236249	(AC004684) hypothetical protein [Arabidopsis thaliana]	9.2
287	M96234	Human glutathione transferase class mu number 4	0.58	1280073	(U55366) Similar to cuticle collagen [Caenorhabditis elegans]	7.1
288	AB002339	Human mRNA for KIAA0341 gene, partial cds	0.58	861293	(U28741) F35D2.1 gene product [Caenorhabditis elegans]	7.1

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
289	U11295	Neisseria gonorrhoeae carbamoyl phosphate synthetase (glutamine) small subunit (carA) and large subunit (carB) genes, complete cds.	0.58	2425135	(AF020283) DG2044 gene product [Dictyostelium discoideum]	5.3
290	D80001	Human mRNA for KIAA0179 gene, partial cds	0.58	4097223	(U49836) gamma-glutamyl transpeptidase precursor [Brugia malayi]	4.1
291	Z11700	Escherichia coli genes faeG, faeH, faeI, faeJ and IS629-like insertion sequence. > :: emb Z11710 ECFAE HIJ E.coli faeH, faeI and faeJ genes encoding FaeH, FaeI and FaeJ proteins	0.58	2347188	(AC002338) laccase isolog [Arabidopsis thaliana] thaliana]	3.2
292	M77350	Mouse hair keratin A1 (MHKA1) gene, complete cds.	0.58	141165	HYPOTHETICAL 8.3 KD PROTEIN >gi 62179	3.2
293	X63787	T.thermophila gene for snRNA U3-2	0.58	2826900	(AB004461) DNA polymerase alpha catalytic subunit [Oryza sativa]	3.1
294	D63881	Human mRNA for KIAA0160 gene, partial cds	0.58	1934730	(U95036) germin-like protein [Arabidopsis thaliana]	3.1
295	U39378	Gymnocarena mexicana 16S ribosomal RNA gene; mitochondrial gene encoding mitochondrial RNA, partial sequence	0.58	2194131	(AC002062) Similar to Synechocystis antiviral protein	3.1
296	X87987	P.pastoris PRC1 gene > :: dbj E12103 E12103 DNA encoding precursor of protease from Pichia pastoris	0.58	3914197	OCCLUDIN >gi 1276983 (U49221) occludin [Canis familiaris] >gi 1589181 prf 2210347D occludin [Canis familiaris]	3.1

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
297	X75782	A.thaliana (L.Heynh.) chloroplast mRNA for recombinant APS-kinase	0.58	1732444	(D38529) DRPLA protein [Homo sapiens]	2.4
298	M64848	Mouse platelet-derived growth factor B chain musculus platelet-derived growth factor beta-chain (sis) gene, exon 5.	0.58	3025832	(AF055985) pyrrolidone-rich antigen [Onchocerca volvulus]	1.4
299	AE001460	Helicobacter pylori, strain J99 section 21 of 132 of the complete genome	0.58	2827198	(AF037454) ubiquitin protein ligase [Mus musculus]	1.1
300	X65720	M.musculus gene for protein kinase C-gamma (exon1 and exon 2)	0.58	418395	CHDI PROTEIN >gi 320737 pir S30818 hypothetical protein YER164w - yeast (Saccharomyces cerevisiae) >gi 603404 (U18917) Chd1p: transcriptional regulator [Saccharomyces cerevisiae]	1.1
301	AF043130	Arabidopsis thaliana lactate dehydrogenase	0.58	3024637	SEX-DETERMINING REGION Y PROTEIN determining protein [Mus	0.62
302	D28116	Human genes for collagen type IV alpha 5 and 6, exon 1 and exon 1'	0.58	1458250	(U64835) T09D3.3 [Caenorhabditis elegans]	0.36
303	AE001075	Archaeoglobus fulgidus section 32 of 172 of the complete genome	0.58	2276333	(Z97991) hypothetical protein Rv0336	0.36
304	AF003948	Rhodococcus opacus chloromuconate cycloisomerase transposase homolog genes. complete cds	0.58	477072	mucin 7 precursor, salivary - human	0.28
305	U10692	Human MAGE-7 antigen (MAGE7) pseudogene, complete cds.	0.58	3287858	HOMEBOX PROTEIN HOX-C11	0.054

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
306	AF003948	Rhodococcus opacus chloromuconate cycloisomerase transposase homolog genes, complete cds	0.58	3551821	(AF058803) mucin 4 [Homo sapiens]	0.041
307	X99350	H.sapiens HFH4 gene, exon 1 and joined CDS	0.58	137483	VAV PROTO-ONCOGENE >gi 55221 (X64361) proto-oncogene [Mus musculus]	0.024
308	AJ234282	Homo sapiens mRNA for Ig heavy chain variable region, clone C	0.58	3264846	(AC003682) R27945_2 [Homo sapiens]	0.018
309	AF079310	Mus musculus histone deacetylase 3 (Hdac3) gene, exons 4 through 15 and complete cds	0.58	1657601	(U66220) unknown [Nannocystis exedens]	0.014
310	AF019367	Human thiopurine methyltransferase (TPMT) gene, exons 6 and 7	0.58	3283352	(AF063020) lens epithelium-derived growth factor [Homo sapiens]	0.011
311	X65720	M.musculus gene for protein kinase C-gamma (exon1 and exon 2)	0.58	1790878	(U38291) microtubule-associated protein 1a [Homo sapiens]	0.008
312	AB011155	Homo sapiens mRNA for KIAA0583 protein, partial cds	0.58	1351166	SYNAPSINS 1A AND 1B >gi 163713	0.006
313	X63692	H.sapiens mRNA for DNA	0.58	1817548	(D84307) phosphoethanolamine cytidyltransferase [Homo sapiens]	0.001
314	U53746	Feline immunodeficiency virus isolate FIV-Pco336-8 pol polyprotein (pol) gene, partial cds	0.58	2246532	(U93872) ORF 73, contains large complex repeat CR 73	2e-05
315	K00436	Rattus norvegicus (clone rt1-1) pseudo-Gly-tRNA gene.	0.58	206712	(M64793) salivary proline-rich protein [Rattus norvegicus]	1e-05

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
316	S79632	HSF2=heat shock factor 2 {alternatively spliced, splice junction region} [mice, CBA/J, testis, Genomic, 120 nt. segment 2 of 3]	0.58	4038594	(AJ222798) tDET1 protein [Lycopersicon esculentum] (U55376) coded for by C. elegans cDNA cm21e6; coded for by C. elegans cDNA cm01e2; similar to melibiose carrier protein (thiomethylgalactoside permease II)	3e-06
317	D43964	Rat liver mRNA for Kan-1, complete cds	0.58	1280135	EPIDERMAL GROWTH FACTOR RECEPTOR KINASE SUBSTRATE EPS8 >gi 530823 (U12535) epidermal growth factor receptor kinase substrate [Homo sapiens]	1e-08
318	AB007918	Homo sapiens mRNA for KIAA0449 protein, partial cds	0.58	2833239	(D45027) 25 kDa trypsin inhibitor [Homo sapiens]	3e-13
319	AB001466	Homo sapiens mRNA for Efs1, complete cds	0.58	2943716	(Z81130) T23G11.9 [Caenorhabditis elegans]	2e-14
320	Z11701	Saccharomyces cerevisiae IRE1 gene for putative protein kinase.	0.58	3880115	(Z83819) dJ146H21.2 (similar to CYTOCHROME B-245 HEAVY CHAIN) [Homo sapiens]	9e-21
321	Z49535	S.cerevisiae chromosome X reading frame ORF YJR035w	0.58	4106562		3e-33
322	M62506	S.cerevisiae DBF20 gene, complete cds.	0.57	<NONE>	<NONE>	<NONE>
323	X05944	Yeast PSS gene for phosphatidylserine synthetase	0.57	<NONE>	<NONE>	<NONE>
324	D38536	Snail gene for ADP-ribosyl cyclase, complete cds	0.57	<NONE>	<NONE>	<NONE>
325	Z75004	S.cerevisiae chromosome XV reading frame ORF YOR096w	0.57	<NONE>	<NONE>	<NONE>
326	L77034	Homo sapiens (subclone 10_e10 from P1 H16) DNA sequence.	0.57	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Cyprinus carpio c-myc gene for c-Myc, complete cds	0.57	<NONE>	<NONE>	<NONE>
327	D37887					
328	AB014562	Homo sapiens mRNA for KIAA0662 protein, partial cds	0.57	197406	(M57576) Ig kappa chain [Mus musculus]	8.9
329	Z69651	Human DNA sequence from cosmid L75B9, Huntington's Disease Region, chromosome 4p16.3	0.57	1079280	chaperonin containing TCP-1 complex gamma chain - African clawed frog >gi 793886 (X84990) Cctg	8.9
330	D89285	Mesocricetus auratus mRNA for inter-alpha trypsin inhibitor heavy chain 1, complete cds	0.57	134132	RYANODINE RECEPTOR, SKELETAL MUSCLE	6.9
331	Z48951	S.cerevisiae chromosome XVI cosmid 9723	0.57	4210432	(AJ130783) APC2 protein [Mus musculus]	5.3
332	X95573	A.thaliana mRNA for salt-tolerance zinc finger protein	0.57	1174828	TYROSINE DECARBOXYLASE 2 4.1.1.25 - parsley >gi 169671 (M96070) tyrosine decarboxylase [Petroselinum	5.2
333	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	0.57	465646	PROBABLE ABC TRANSPORTER ATP-BINDING PROTEIN IN NTRA/RPON 5'REGION (ORF1) Azorhizobium caulinodans >gi 311388 (X69959) ORF1	4.0
334	AE001116	Borrelia burgdorferi (section 2 of 70) of the complete genome	0.57	2314735	(AE000653) Na+/H+ antiporter (nhaA) [Helicobacter pylori 26695]	4.0
335	Z34291	R.norvegicus mRNA for putative chloride channel.	0.57	1350832	DNA-DIRECTED RNA POLYMERASE I SECOND LARGEST SUBUNIT (RNA POLYMERASE I SUBUNIT 2) chain RPA2 - Euplotes octocarinatus (SGC9) >gi 578407 octocarinatus]	3.0

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
336	D88255	Homo sapiens A30 Vk germline gene, partial cds	0.57	3875983	(Z81063) similar to Actinin-type actin-binding domain containing proteins [Caenorhabditis elegans]	3.0
337	AF037261	Homo sapiens SH3-containing adaptor molecule-1 mRNA, complete cds	0.57	1397341	(U61955) Similar to kinesin-like protein; coded for by C. elegans cDNA yk184h5.3; coded for by C. elegans cDNA yk184h5.5; coded for by C. elegans cDNA yk13d7.3; coded for by C. elegans cDNA yk13d7.5; coded for by C. elegans cDNA yk31e1.5; co... >gi 3493541 (AF057567) kinesin-like protein ZEN-4a [Caenorhabditis elegans]	2.3
338	U26595	Rattus norvegicus prostaglandin F2a receptor regulatory protein precursor, mRNA, complete cds	0.57	2773160	(AF039656) neuronal tissue-enriched acidic protein [Homo sapiens]	2.3
339	X69903	R.norvegicus mRNA for interleukin 4 receptor	0.57	2649193	(AE001009) quinone-reactive Ni/Fe-hydrogenase B-type cytochrome subunit (hydC) [Archaeoglobus fulgidus]	1.8
340	Z74825	S.cerevisiae chromosome XV reading frame ORF YOL083w	0.57	1458319	(U64846) F47D2.5 gene product [Caenorhabditis elegans]	1.4
341	AJ131469	Foot-and-mouth disease virus O vp1 gene, strain O/A/58	0.57	91206	proline-rich protein - mouse (fragment) musculus]	1.4
342	AF011360	Mus musculus regulator of G-protein signaling 7 (RGS7) mRNA, complete cds	0.57	542514	gelsolin - American lobster	0.80
343	AF011360	Mus musculus regulator of G-protein signaling 7 (RGS7) mRNA, complete cds	0.57	1078946	gelsolin - American lobster >gi 452313 gelsolin [Homarus americanus]	0.80

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
344	L39210	Homo sapiens inosine monophosphate dehydrogenase type II gene, complete cds	0.57	559526	(X77466) 98.8kD polypeptide [Strawberry latent ringspot virus]	0.79
345	U81523	Human endometrial bleeding associated factor mRNA, complete cds	0.57	211499	(K01702) HMW/LMW collagen subunit precursor [Gallus gallus]	0.79
346	U46561	Tetrahymena thermophila polyubiquitin (TTU3) gene, complete cds, and RNA polymerase II subunit 2 (RPB2) gene, partial cds	0.57	2506493	HYPOTHETICAL 100.5 KD PROTEIN IN IAP-CYSH INTERGENIC REGION >gi 882654 (U29579) alternate gene name ygcB; ORF_f888 [Escherichia coli] >gi 1789119	0.60
347	X95543	C.japonica mRNA for legumin (clone CjLeg31)	0.57	1709261	NEUROFILAMENT TRIPLET M PROTEIN (160 KD NEUROFILAMENT PROTEIN) (NF-M) >gi 1083164 pir S55395 neurofilament protein M - rabbit (fragment) >gi 854353	0.46
348	Y17282	Homo sapiens mRNA for cytokeratin type II	0.57	3044086	(AF055904) unknown [Mycococcus xanthus]	0.45
349	X00716	Frog mRNA fragment for alpha-A2-crystallin	0.57	3406654	(AF079369) transcriptional repressor TUP1 [Dictyostelium discoideum]	0.20
350	X53238	Klebsiella sp. bacteriophage K11 gene 1 for RNA polymerase	0.57	1228093	(Z46913) polyketide synthase	0.16
351	X99012	H.sapiens FUS gene, exon 12	0.57	243898	(S78897) GOR=antigenic epitope [chimpanzees, Peptide, 427 aa] [Pan]	0.090
352	AL008711	Human DNA sequence from PAC 390N22 on chromosome Xp22.2	0.57	1469545	(U53585) fibronectin attachment protein [Mycobacterium avium]	0.053
353	S74506	SOX9 [human, fetal brain, Genomic, 1494 nt, segment 3 of 3]	0.57	1326350	(U58748) similar to potential transmembrane domains in S. cerevisiae nuclear division RFT1 protein (SP:P38206)	0.017

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
354	D25542	Human mRNA for golgi antigen gcp372, complete cds	0.57	4063399	(AF102575) cell surface protein DTFA [Dictyostelium discoideum]	0.005
355	AB015426	Mus musculus mRNA for alpha1,3-fucosyltransferase IX, complete cds	0.57	2661842	(Y15732) DNA polymerase beta [Xenopus laevis]	7e-11
356	X51394	Xenopus mRNA for APEG protein, containing a highly repetitive amino acid sequence	0.57	1929056	(Y12090) putative 3,4-dihydroxy-2-butanone kinase [Lycopersicon esculentum]	9e-12
357	AB007918	Homo sapiens mRNA for KIAA0449 protein, partial cds	0.57	2833239	EPIDERMAL GROWTH FACTOR RECEPTOR KINASE SUBSTRATE EPS8 >gi 530823 (U12535) epidermal growth factor receptor kinase substrate [Homo sapiens]	3e-13
358	AB001466	Homo sapiens mRNA for Efs1, complete cds	0.57	2943716	(D45027) 25 kDa trypsin inhibitor [Homo sapiens]	2e-14
359	Y00760	Rabbit mRNA for adult fast skeletal troponin-C	0.57	2576348	(AC002400) Glutamyl tRNA synthetase [Homo sapiens]	2e-28
360	X95153	H.sapiens brca2 gene exon 3 > :: emb A62778 A62778 Sequence 19 from Patent WO9719110	0.57	3419847	(AC004982) similar to yeast hypothetical protein ybk4; similar to P38164 (PID:g586461) [Homo sapiens]	2e-55
361	X85967	B.vulgaris mRNA for betavulgin	0.56	<NONE>	<NONE>	<NONE>
362	U09251	Mycoplasma genitalium DNA gyrase subunit B complete cds, DNA polymerase III beta subunit (dnaN) and seryl-tRNA synthetase (serS) genes, partial cds.	0.56	<NONE>	<NONE>	<NONE>
363	V00158	Chloroplast Euglena gracilis genes coding for transfer RNAs specific for threonine, glycine, methionine, serine and glutamine.	0.56	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Clostridium				
364	D88151	perfringens DNA for D-alanine:D-alanine ligase, cortical fragment-lytic enzyme	0.56	<NONE>	<NONE>	<NONE>
365	U67478	Methanococcus jannaschii section 20 of 150 of the complete genome	0.56	<NONE>	<NONE>	<NONE>
366	L23800	Tachyglossus aculeatus beta-globin homolog (HBB) gene, complete cds	0.56	<NONE>	<NONE>	<NONE>
367	AB011129	Homo sapiens mRNA for KIAA0557 protein, partial cds	0.56	<NONE>	<NONE>	<NONE>
368	L77034	Homo sapiens (subclone 10_e10 from P1 H16) DNA sequence.	0.56	<NONE>	<NONE>	<NONE>
369	Z47202	C.albicans gene for TFIIIB (BRF1) subunit.	0.56	<NONE>	<NONE>	<NONE>
370	U53868	Clostridium acetobutylicum mannitol-specific phosphotransferase system (PTS) system, mtlA, mtlR, mtlF, and mtlD genes, complete cds	0.56	<NONE>	<NONE>	<NONE>
371	AF041259	Homo sapiens breast cancer putative transcription factor (ZABC1) mRNA, complete cds	0.56	<NONE>	<NONE>	<NONE>
372	L42636	Plasmodium falciparum variant-specific surface protein (var-7) mRNA, complete cds.	0.56	2213557	(Z97052) hypothetical protein	8.8

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
373	U96180	Human protein tyrosine phosphatase (TEP1) mRNA, complete cds	0.56	731016	THIOREDOXIN REDUCTASE thioredoxin reductase (NADPH) [Coxiella burnetii]	8.7
374	L76259	Homo sapiens PTS gene, complete cds	0.56	2369863	(Y12225) Spi-1/PU.1 transcription factor	6.7
375	AF045946	Mus musculus D16Jhu17 YAC 98B3 acentric end, partial sequence	0.56	2130017	hypothetical protein - common sunflower protein [Helianthus annuus]	5.1
376	X97986	M.musculus mRNA for desmocollin type 1	0.56	4038031	(AC005936) hypothetical protein [Arabidopsis thaliana]	3.9
377	X79437	M.musculus whey acidic protein (WAP) gene, exon 1	0.56	549670	SPINDLE POLE BODY COMPONENT SPC42 yeast (Saccharomyces cerevisiae) >gi 486054 (Z28042) ORF YKL042w [Saccharomyces cerevisiae] >gi 666098 (X71621) hypothetical 42.3 kD protein [Saccharomyces cerevisiae]	3.9
378	M27902	Rat cardiac specific sodium channel alpha-subunit mRNA, complete cds.	0.56	585234	ENDOGLUCANASE G PRECURSOR 3.2.1.-) CelCCG precursor - Clostridium cellulolyticum cellulolyticum]	3.9
379	AF036696	Caenorhabditis elegans cosmid F15B10	0.56	546071	gp70=envelope protein {endogenous provirus} host=cat lymphoid tissues, Peptide, 445 aa]	3.6
380	Z99102	Caenorhabditis elegans cosmid B0331, complete sequence [Caenorhabditis elegans]	0.56	603664	(U14101) putative reverse transcriptase; ORF2; encodes aa motifs conserved in reverse transcriptases; most closely related reverse transcriptases are those of non-LTR retrotransposons. The 3' 901 bp of this CDS are identical to the 3' 901 bp ...	3.0
381	L27850	Equus caballus (clone T131) T-cell receptor DNA, V-region.	0.56	1079150	transcription factor shn - fruit fly	1.7

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
382	X97986	M.musculus mRNA for desmocollin type 1	0.56	2497227	HYPOTHETICAL 113.1 KD PROTEIN IN PRE5-FET4 INTERGENIC REGION >gi 1072409 (Z54141) unknown (U12964) contains ankyrin-like repeats; similar to human desmoplakin repeat region [Caenorhabditis elegans]	1.7
383	AF087455	Didelphis virginiana G protein receptor kinase 2 mRNA, complete cds	0.56	1213453		1.3
384	D80011	Human mRNA for KIAA0189 gene, complete cds	0.56	226535	protease [Hepatitis B virus]	1.1
385	AJ002272	Mus musculus mRNA for HAP1-A protein, 3' region	0.56	3327158	(AB014572) KIAA0672 protein [Homo sapiens]	1.0
386	L39210	Homo sapiens inosine monophosphate dehydrogenase type II gene, complete cds	0.56	628431	coat protein - strawberry latent ringspot virus	0.77
387	X02770	Mouse Thy-1.2 gene 5' untranslated region and exon 1	0.56	3327046	(AB014516) KIAA0616 protein [Homo sapiens]	0.59
388	AF038575	Schizosaccharomyces pombe Wiskott-Aldrich Syndrome protein homolog (wsp1+) gene, complete cds, and BTF3/beta2-NAC gene, partial sequence	0.56	88466	salivary proline-rich phosphoprotein precursor PRH1 (allele PIF) - human >gi 190484 (K03203) prepro salivary proline-rich protein [Homo sapiens] >gi 190512	0.35
389	X56747	Rat mRNA for fetal intestinal lactase-phlorizin hydrolase precursor, partial	0.56	2072742	(Z48674) chitinase homologue [Sesbania rostrata]	0.23
390	Y12072	G.arboreum mRNA for farnesyl pyrophosphate synthase	0.56	296670	(X07882) Po protein [Homo sapiens]	0.20
391	S75756	p15=cyclin D-dependent kinases 4 and 6-binding protein/p15 product {exon/intron 1} [human, brain tumors, Genomic, 753 nt]	0.56	1082743	protein kinase (EC 2.7.1.37) SPRK - human sapiens] >gi 1090771 prf 2019437A protein Tyr kinase I	0.15

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Equus caballus type				
392	U62528	II collagen mRNA, complete cds	0.56	461671	[Segment 1 of 2] COLLAGEN ALPHA 1(I) CHAIN	0.030
393	X96877	C.reinhardtii mRNA for unknown luminal polypeptide	0.56	3341678	(AC003672) putative zinc finger protein [Arabidopsis thaliana]	5e-09
394	S78788	cGATA-3 [chickens, liver, Genomic, 979 nt, segment 4 of 4]	0.56	2661590	(AL009196) 1-evidence=predicted by content; 1-method=genefinder;084; 1-method_score=59.41; 1-evidence_end; 2-evidence=predicted by match; 2-match_accession=AA950019; 2-match_description=LD29959.5p rime LD Drosophila melanogaster...	2e-11
395	AF006640	Drosophila melanogaster Ste20-like protein kinase mRNA, complete cds	0.56	1109830	(U41534) coded for by C. elegans cDNA CEESI42F; Similar to helicases of SNF2/RAD54 family. [Caenorhabditis elegans]	6e-12
396	AF006640	Drosophila melanogaster Ste20-like protein kinase mRNA, complete cds	0.56	1109830	(U41534) coded for by C. elegans cDNA CEESI42F; Similar to helicases of SNF2/RAD54 family. [Caenorhabditis elegans]	4e-13
397	AE000716	Aquifex aeolicus section 48 of 109 of the complete genome	0.56	3688350	(AL030996) dJ1189B24.4 (novel PUTATIVE protein similar to hypothetical proteins S. pombe C22F3.14C and C. elegans C16A3.8) [Homo sapiens]	3e-66
398	Z36079	S.cerevisiae chromosome II reading frame ORF YBR210w	0.55	<NONE>	<NONE>	<NONE>
399	Y17267	Mus musculus mRNA for ubiquitin conjugating enzyme	0.55	<NONE>	<NONE>	<NONE>
400	AC001461	Homo sapiens (subclone 2_g5 from BAC H107) DNA sequence	0.55	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		<i>Alouatta seniculus</i>				
401	AF019079	breast and ovarian susceptibility (BRCA1) gene, partial cds	0.55	<NONE>	<NONE>	<NONE>
402	M90058	Human serglycin gene, exons 1,2, and 3.	0.55	<NONE>	<NONE>	<NONE>
403	AB013469	Mus musculus CLM2 gene for cytohesin 2, complete and partial cds, alternative splicing	0.55	1729760	(Z68152) chitinase [<i>Gossypium hirsutum</i>]	8.6
404	AJ011592	Bacteriophage P1 ban gene	0.55	2493689	PHOTOSYSTEM II 10 KD PHOSPHOPROTEIN [deltoides] >gi 2143326 gnl PID e319090 (Y13328) 10kDa phosphoprotein [<i>Populus deltoides</i>]	6.6
405	Z15118	<i>T.brucei</i> kinetoplast maxicircle variable region DNA	0.55	2970432	(AF049132) NADH dehydrogenase subunit 5 [<i>Florometra serratissima</i>]	6.5
406	Z48951	<i>S.cerevisiae</i> chromosome XVI cosmid 9723	0.55	4210432	(AJ130783) APC2 protein [<i>Mus musculus</i>]	4.9
407	U78726	Homo sapiens mad protein homolog Smad2 gene, promoter, exon 1a and exon 1b	0.55	3319290	(AF055994) thyroid hormone receptor-associated protein complex component TRAP220 [<i>Homo sapiens</i>]	4.9
408	AG001389	Homo sapiens genomic DNA, 21q region, clone: 9H11Bm42	0.55	125684	KRUEPPEL PROTEIN >gi 72899 pir TWFF Krueppel gap protein - fruit fly (<i>Drosophila sp.</i>) melanogaster] >gi 224875 prf 1202348A Krueppel gene	3.8
409	M27640	Plasmodium vivax major blood stage surface antigen gene, partial cds.	0.55	549453	X-LINKED PEST-CONTAINING TRANSPORTER transporter - human >gi 458255 (U05321) X-linked PEST-containing transporter [<i>Homo sapiens</i>]	3.8

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Fugu rubripes mRNA				
410	D37977	for sodium channel alpha subunit, partial cds	0.55	1435038	(D38024) ORF [Homo sapiens]	3.7
411	M88505	Ostertagia ostertagi cathepsin B-like cysteine protease gene, partial cds.	0.55	3941277	(AF000900) p45 [Rattus norvegicus]	2.9
412	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	0.55	2570154	(AB008376) 17-kDa PKC-potentiated inhibitory protein of PP1 [Sus scrofa]	2.8
413	U89241	Human mibp gene, partial cds	0.55	4097465	(U62253) 16kDa secretory protein [Sus scrofa]	2.2
414	AF027151	Xenopus laevis survival of motor neuron protein interacting protein 1 (SIP1) mRNA, complete cds	0.55	4007790	(AL034463) putative single-strand polynucleotide binding protein [Schizosaccharomyces pombe]	1.7
415	AF006821	Bufo marinus natriuretic peptide receptor C mRNA, partial cds	0.55	2245075	(Z97343) GTP-binding RAB2A protein	1.7
416	Y12736	Lactococcus lactis cremoris plasmid pJW565 DNA, llabiiM, llabiiR genes and orfX	0.55	3386334	(AF035120) type I procollagen pro-alpha 2 chain [Canis familiaris]	1.3
417	U38307	Mus musculus collagen alpha-1 type 1 gene, 5' flanking region, partial sequence.	0.55	1362802	gastric mucin - human (fragment) >gi547517	1.3
418	D13473	Mouse mRNA for Rad51 protein	0.55	1374698	(D83032) nuclear protein, NP220 [Homo sapiens]	1.3
419	AF045238	Bungarus fasciatus acetylcholinesterase gene, alternatively spliced products, partial cds	0.55	3261734	(Z94752) hypothetical protein Rv1004c	0.99
420	AE000795	Methanobacterium thermoautotrophicum from bases 1 to 10208 (section I of 148) of the complete genome	0.55	186396	(M94131) mucin [Homo sapiens]	0.97

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
421	X99537	Y.lipolytica SEC62 gene	0.55	3876397	(Z81068) F25H5.2 [Caenorhabditis elegans]	0.58
422	U08147	Aquilegia sp. phytochrome (PHYB/D) gene, partial cds.	0.55	2338024	(AF005370) ribonucleotide-reductase, large subunit	0.57
423	Z56586	H.sapiens CpG DNA, clone 12c8, reverse read cpg12c8.r1d.	0.55	3320122	(U46007) espin [Rattus norvegicus]	0.44
424	U39442	Mus musculus glutamine:fructose-6-phosphate amidotransferase (GFAT) gene, 5' region and partial cds	0.55	282600	hypothetical protein - Mycoplasma hyorhinis	0.43
425	K02298	Rat chymotrypsin B (chyB) gene, complete cds.	0.55	3413810	(Y17034) Bassoon [Mus musculus]	0.33
426	X84792	M.musculus clusterin gene	0.55	1652475	(D90905) hypothetical protein	0.25
427	U00185	Capra aegagrus Saanen and Weisse Edel breeds DR beta-chain antigen binding domain, MHC class II DRB	0.55	2507136	SUBTILIN BIOSYNTHESIS PROTEIN SPAB	0.19
428	Z54946	H.sapiens CpG DNA, clone 178a12, reverse read cpg178a12.r1a.	0.55	807646	(M17294) unknown protein [Human herpesvirus 4]	0.065
429	AF031650	Oryctolagus cuniculus anion exchanger 3 brain isoform (AE3) mRNA, complete cds	0.55	1778210	(U68412) fibrillar collagen [Arenicola marina]	0.044
430	M25579	Bovine adenylyl cyclase Type I mRNA, complete cds.	0.55	2649040	(AE000997) conserved hypothetical protein [Archaeoglobus fulgidus]	0.023
431	Z48796	H.sapiens Ski-W mRNA for helicase	0.55	330452	(M14708) DNA polymerase [Human cytomegalovirus]	0.023

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
432	M80234	Cow dopamine transporter mRNA, putative cds.	0.55	3874972	(Z99709) similar to Elongation factor Tu family (contains ATP/GTP binding P-loop); cDNA EST EMBL:D76223 comes from this gene; cDNA EST yk478c5.5 comes from this gene [Caenorhabditis elegans]	4e-04
433	U91616	Human I kappa B epsilon (IkBe) mRNA, complete cds	0.55	3875577	(Z68314) similar to G-protein; cDNA EST EMBL:C11959 comes from this gene; cDNA EST EMBL:C10341 comes from this gene; cDNA EST yk494e4.3 comes from this gene; cDNA EST yk448a8.5 comes from this gene comes from this gene; cDNA EST EMBL:C10341 comes from this gene; cDNA EST yk494e4.3 comes from this gene; cDNA EST yk448a8.5 comes from this gene [Caenorhabditis elegans] >gi 3880364 gnl PID e1349948 (Z83016) similar to G-protein; cDNA EST EMBL:C11959 comes from this gene; cDNA EST EMBL:C10341 comes from this gene; cDNA EST yk494e4.3 comes from this gene; cDNA EST yk448a8.5 comes from this gene [Caenorhabditis elegans]	7e-06
434	D10910	Arabidopsis thaliana Atpk7 gene for serine/threonine protein kinase, complete cds	0.55	3876072	(Z81505) Similarity to Metanococcus hypothetical protein 0682 (TR:Q58095) [Caenorhabditis elegans]	4e-42
435	L22013	Swinepox virus complete ORFS C20L-C1L > :: gb I58297 I58297 Sequence 14 from patent US 5651972	0.54	<NONE>	<NONE>	<NONE>
436	Z92653	Human immunodeficiency virus type 1 env gene	0.54	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
437	K01992	E.coli phosphate-repressible periplasmic phosphate-binding protein (phoS), peripheral membrane proteins (pstC, pstB and phoU) and integral membrane protein (pstA) genes, complete cds.	0.54	<NONE>	<NONE>	<NONE>
438	AE001415	Plasmodium falciparum chromosome 2, section 52 of 73 of the complete sequence	0.54	<NONE>	<NONE>	<NONE>
439	AF064030	Helianthus tuberosus lectin 2 mRNA, complete cds	0.54	<NONE>	<NONE>	<NONE>
440	X12591	E.coli plasmid DNA for colicin E9	0.54	<NONE>	<NONE>	<NONE>
441	U73679	Caenorhabditis elegans YNK1-a mRNA, complete cds	0.54	<NONE>	<NONE>	<NONE>
442	Z93990	Unidentified bacterium DNA for 16S ribosomal RNA	0.54	<NONE>	<NONE>	<NONE>
443	X85967	B.vulgaris mRNA for betavulgin	0.54	757836	(Z37980) ORF12 [Escherichia coli]	8.3
444	U76524	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	0.54	151377	(M80653) tetraheme [Pseudomonas stutzeri]	6.2
445	X71800	H.sapiens gene for 5S rRNA (640 bp) > :: emb X71801 HS5SR6-40B H.sapiens gene for 5S rRNA (640 bp)	0.54	3322653	(AE001216) T. pallidum predicted coding region TP0369	2.7
446	U89241	Human mibp gene, partial cds	0.54	4097465	(U62253) 16kDa secretory protein [Sus scrofa]	2.2

186

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
447	L16013	Rattus norvegicus Q-like gene sequence	0.54	3087760	(AJ005583) p75 protein [Cryptocodium cohnii]	0.95
448	U60275	Capra hircus skeletal muscle voltage-gated chloride channel gCIC-1 mRNA, partial cds	0.54	1781344	(Y10438) FK506 polyketide synthase	0.95
449	U36795	Myxococcus xanthus rfbABC O-antigen biosynthesis operon, rfbA, rfbB, and rfbC genes, complete cds.	0.54	3877232	(Z81540) predicted using Genefinder	0.74
450	AF053091	Drosophila melanogaster eyelid (eld) mRNA, complete cds	0.54	2144110	zinc finger protein RIZ - rat >gi 949996	0.14
451	V00602	Genome of the bacteriophage fd (Inoviridae).	0.54	2661620	(AL009197) hypothetical protein	0.11
452	U60800	Human semaphorin (CD100) mRNA, complete cds	0.54	125682	KERATIN, ULTRA HIGH-SULFUR MATRIX PROTEIN (UHS KERATIN) >gi 109116 pir A36686 ultra-high-sulfur keratin - sheep >gi 1306 (X55294) ultra high-sulphur keratin protein [Ovis aries]	0.003
453	X85969	S.coelicolor secD, secF & apt genes	0.54	3874972	(Z99709) similar to Elongation factor Tu family (contains ATP/GTP binding P-loop); cDNA EST EMBL:D76223 comes from this gene; cDNA EST yk478c5.5 comes from this gene [Caenorhabditis elegans]	7e-06
454	Y08265	H.sapiens mRNA for DAN26 protein, partial	0.54	3875131	(Z70750) similar to vanadate resistance protein transmembranous domains [Caenorhabditis elegans]	5e-12

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Hydromantes platycephalus cytochrome b (cytb) gene, mitochondrial gene encoding mitochondrial protein, partial cds	0.53	<NONE>	<NONE>	<NONE>
455	U89613					
		Habrobracon hebetor cytochrome oxidase II gene, partial cds; and tRNA-Asp, tRNA-His, and tRNA-Lys genes, complete sequence, mitochondrial genes for mitochondrial products	0.53	<NONE>	<NONE>	<NONE>
456	AF034597					
		Yeast (S.cerevisiae) tau repetitive element and Cys-tRNA.	0.53	<NONE>	<NONE>	<NONE>
457	K02653					
		Human mRNA for actin-binding protein (filamin)	0.53	2134839	bullous pemphigoid antigen 2 - human	6.2
458	X53416					
		Drosophila subobscura alcohol dehydrogenase (Adh) gene, and alcohol dehydrogenase (Adh-dup) gene, complete cds's.	0.53	2136865	hair keratin cysteine rich protein - sheep	2.1
459	M55545					

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
460	U19362	Methanobacterium thermoautotrophicum methylene-tetrahydromethanopterin dehydrogenase (mtd), imidazoleglycerol-phosphate dehydrogenase (hisB), and putative ferredoxin (fdxA) genes, complete cds, orf9 gene, partial cds, orfs ...	0.53	731969	HYPOTHETICAL 91.6 KD PROTEIN IN HXT8-CRT1 INTERGENIC REGION >gi 1078261 pir S50773 probable membrane protein YJL212c - yeast (Saccharomyces cerevisiae) >gi 496950 (Z34098) ORF [Saccharomyces cerevisiae] >gi 1015596 (Z49487) ORF YJL212c	0.54
461	AB011527	Rattus norvegicus mRNA for MEGF1, complete cds	0.53	417037	GERM CELL-LESS PROTEIN fruit fly (Drosophila melanogaster) >gi 157490 (M97933) germ cell-less protein [Drosophila melanogaster]	3e-06
462	U64313	Bacillus firmus MsyB gene, 5' upstream region and partial cds	0.52	<NONE>	<NONE>	<NONE>
463	AF008590	Caenorhabditis elegans paraquat responsive protein (CePqM132) mRNA, complete cds	0.52	<NONE>	<NONE>	<NONE>
464	L10245	Mus saxicola spermidine/spermine N1-acetyltransferase (SSAT) gene, complete cds.	0.52	<NONE>	<NONE>	<NONE>
465	AF027173	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-A) mRNA, complete cds	0.52	124263	INSULIN-LIKE GROWTH FACTOR IB PRECURSOR (IGF-IB) (SOMATOMEDIN C) >gi 69361 pir IGHU1B insulin-like growth factor IB precursor - human prepropeptide [Homo sapiens]	7.7

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Caenorhabditis elegans cosmid H31B20, complete sequence [Caenorhabditis elegans]	0.52			
466	AL021066			2589162	(D88451) aldehyde oxidase [Zea mays]	6.0
467	AF038588	Porphyra linearis 18S ribosomal RNA gene, 3' partial sequence	0.52	1055055	(U39850) coded for by C. elegans cDNA yk37g1.5; coded for by C. elegans cDNA yk5c9.5; coded for by C. elegans cDNA yk1a9.5; alternatively spliced form of F52C9.8b	4.6
468	AE001125	Borrelia burgdorferi (section 11 of 70) of the complete genome	0.52	4115827	(AB021287) polyprotein [Hepatitis G virus]	2.0
469	AF006640	Drosophila melanogaster Ste20-like protein kinase mRNA, complete cds	0.52	1109830	(U41534) coded for by C. elegans cDNA CEES142F; Similar to helicases of SNF2/RAD54 family. [Caenorhabditis elegans]	0.002
470	U90177	Aplysia californica ubiquitin carboxyl-terminal hydrolase (Ap-uch) mRNA, complete cds	0.51	<NONE>	<NONE>	<NONE>
471	Z28304	S.cerevisiae chromosome XI reading frame ORF YKR079c	0.51	<NONE>	<NONE>	<NONE>
472	Z92837	Caenorhabditis elegans cosmid R03E1, complete sequence [Caenorhabditis elegans]	0.51	123506	HYDROPHOBIC SEED PROTEIN (HPS)	7.6
473	D13803	Mouse mRNA for RecA-like protein MmRad51, complete cds	0.51	3327228	(AB014607) KIAA0707 protein [Homo sapiens]	4.5
474	X07187	Pea hsp21 mRNA	0.51	3328678	(AE001299) hypothetical protein [Chlamydia trachomatis]	4.4

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
475	S63168	CCAAT/enhancer-binding protein delta=transcription factor CRP3 homolog [human, prostate carcinoma cell line LNCaP, Genomic, 1594 nt]	0.51	1653215	(D90911) apolipoprotein N-acyltransferase [Synechocystis sp.]	1.2
476	U67078	Xenopus laevis C2-HC type zinc finger protein X-MyT1 mRNA, complete cds	0.51	3850320	(AF067520) PITSLRE protein kinase beta SV2 isoform [Homo sapiens]	0.17
477	L38933	Homo sapiens GT198 mRNA, complete ORF	0.51	3219965	HYPOTHETICAL 100.6 KD TRP-ASP REPEATS CONTAINING PROTEIN C2C6.04C IN CHROMOSOME I	0.059
478	AF001000	Lycopersicon esculentum polygalacturonase 1	0.50	<NONE>	<NONE>	<NONE>
479	Z28304	S.cerevisiae chromosome XI reading frame ORF YKR079c	0.50	<NONE>	<NONE>	<NONE>
480	X97225	Oncorhynchus keta IGF-II gene	0.50	<NONE>	<NONE>	<NONE>
481	AJ001388	Homo Sapiens, RP58 cDNA for complete mRNA	0.50	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Homo Sapiens. RP58				
481	AJ001388	cDNA for complete mRNA	0.50	<NONE>	<NONE>	<NONE>
482	M86626	P.occultum 23S ribosomal RNA, partial cds.	0.50	<NONE>	<NONE>	<NONE>
483	U76523	Sambucus nigra lectin precursor mRNA, complete cds	0.50	1722856	CHROMOSOME ASSEMBLY PROTEIN XCAP-E African clawed frog >gi 563814 (U13674) XCAP-E [Xenopus laevis]	3.2
484	AF031663	Mus musculus striatin mRNA, complete cds	0.50	179521	(M63730) BPAG2 [Homo sapiens]	3.2
485	U32729	Haemophilus influenzae Rd section 44 of 163 of the complete genome	0.50	3875699	(Z92829) F10A3.15 [Caenorhabditis elegans]	0.65
486	AF067198	Dictyostelium discoideum clone 9.10 Tdd-3 and RED repetitive elements, partial sequence	0.50	2494740	HYPOTHETICAL 28.3 KD PROTEIN IN GBD 5'REGION (ORF4) >gi 2120954 pir I39562 ORF4 - Alcaligenes eutrophus >gi 695274 (L36817) ORF4	0.008
487	M23442	Human interleukin 4 (IL-4) gene, complete cds.	0.49	<NONE>	<NONE>	<NONE>
488	U16367	Caenorhabditis elegans POU homeobox protein CEH-18 (ceh-18) mRNA, complete cds.	0.47	3786409	(AF098499) contains similarity to Saccharomyces cerevisiae MAF1 protein (GB:U19492) [Caenorhabditis elegans]	8.9
489	AF001000	Lycopersicon esculentum polygalacturonase I	0.45	<NONE>	<NONE>	<NONE>
490	Z18920	Yersinia enterocolitica wbb gene cluster	0.41	<NONE>	<NONE>	<NONE>
491	D86983	Human mRNA for KIAA0230 gene, partial cds	0.35	206712	(M64793) salivary proline-rich protein [Rattus norvegicus]	4e-05
492	AF064030	Helianthus tuberosus lectin 2 mRNA, complete cds	0.33	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Vitreoscilla sp. outer				
493	AF067083	membrane protein homolog gene, complete cds; Trp repressor binding protein gene, partial cds; and unknown genes	0.33	401553	HYPOTHETICAL 24.5 KD PROTEIN IN NADB-SRMB INTERGENIC REGION	8.3
494	Y15520	Papio hamadryas anubis gene encoding fertilin alpha-II	0.29	2408049	(Z99164) hypothetical protein	3.1
495	U33475	Alestes sp. ependymin mRNA, partial cds	0.28	3913078	ARYL HYDROCARBON RECEPTOR NUCLEAR TRANSLOCATOR HOMOLOG (DARNT) (TANGO PROTEIN) transcription factor [Drosophila melanogaster]	1.4
496	D88356	Mouse DNA for 8-oxodGTPase, complete cds	0.22	<NONE>	<NONE>	<NONE>
497	U67603	Methanococcus jannaschii section 145 of 150 of the complete genome	0.22	2209261	(U51222) p40 [Streptomyces halstedii]	8.3
498	U82386	Malurus cyaneus microsatellite McyU2	0.22	992631	(U29131) Mg-chelatase subunit [Synechocystis sp.]	0.56
499	Z49625	S.cerevisiae chromosome X reading frame ORF YJR125c	0.21	<NONE>	<NONE>	<NONE>
500	U64830	Dictyostelium discoideum AX2 protein tyrosine kinase gene, complete cds.	0.21	<NONE>	<NONE>	<NONE>
501	M24543	Human prostate-specific antigen (PA) gene, complete cds.	0.21	2764859	(X97918) gene 12.1 [Bacteriophage SPP1]	6.0

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
502	X87618	B.taurus mRNA for thrombospondin (partial) 2162 bp	0.21	2146000	u0002b protein - Mycobacterium tuberculosis tuberculosis] >gi 1694863 gnl PID e283373 (Z83018) hypothetical protein Rv2968c [Mycobacterium tuberculosis]	3.5
503	X71591	B.taurus microsatellite sequence INRA048	0.21	1354453	(U52830) orf [Homo sapiens]	2.7
504	X57808	Human germline immunoglobulin lambda light chain gene	0.21	2119158	procollagen type V alpha 2 - mouse >gi 309181	2.7
505	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	0.21	2497139	HYPOTHETICAL 78.8 KD PROTEIN IN ABF2-CHL12 INTERGENIC REGION >gi 1078003 pir S52835 hypothetical protein YMR075w - yeast (Saccharomyces cerevisiae) >gi 763022 (Z48952) unknown [Saccharomyces cerevisiae]	2.0
506	U84216	Mycobacterium fortuitum plasmid pJAZ38 replication protein Rep (rep) gene, complete cds	0.21	2499087	UDP- GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (DUGT) glucosyltransferase - fruit fly (Drosophila sp.) glucosyltransferase precursor [Drosophila melanogaster]	0.003
507	U31463	Rattus norvegicus nonmuscle myosin heavy chain-A mRNA, complete cds.	0.21	3880111	(Z81130) predicted using Genefinder	0.002
508	X51508	Rabbit mRNA for aminopeptidase N (partial)	0.21	630864	LRR47 protein - fruit fly (Drosophila melanogaster) >gi 415947 (X75760) LRR47 [Drosophila melanogaster]	1e-06
509	AF086476	Homo sapiens full length insert cDNA clone ZD88F12	0.20	<NONE>	<NONE>	<NONE>
510	AF077006	Helicobacter pylori plasmid pHPM186, complete sequence	0.20	<NONE>	<NONE>	<NONE>
511	X75480	E.gunnii CAD gene.	0.20	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		<i>T.aestivum</i>				
512	X75036	mitochondrial nad7 gene for NADH dehydrogenase subunit 7	0.20	<NONE>	<NONE>	<NONE>
513	D90875	E.coli genomic DNA, Kohara clone #422(55.5-55.8 min.)	0.20	<NONE>	<NONE>	<NONE>
514	Z68343	Caenorhabditis elegans cosmid F59B8, complete sequence [Caenorhabditis elegans]	0.20	<NONE>	<NONE>	<NONE>
515	X62486	M.musculus V alpha 11.1 gene 5'-region	0.20	<NONE>	<NONE>	<NONE>
516	AF040651	Caenorhabditis elegans cosmid W04H10	0.20	1170683	PHOSPHORYLASE B KINASE ALPHA REGULATORY CHAIN, SKELETAL MUSCLE ISOFORM (PHOSPHORYLASE KINASE ALPHA M SUBUNIT) >gi 2135923 pir I38111 phosphorylase kinase (EC 2.7.1.38) - human >gi 791043	7.4
517	U10470	Pseudomonas fluorescens PHA depolymerase (phaZ) gene, complete cds.	0.20	3721862	(AB016024) Pfj2 [Plasmodium falciparum]	1.9
518	D83778	Human mRNA for KIAA0194 gene, partial cds	0.20	126363	LAMININ ALPHA-1 CHAIN PRECURSOR precursor - human	0.65
519	S43579	c-scr=pp60c-src, sdr=src downstream region	0.20	4159887	(AC004908) similar to ribosomal protein L23a; similar to P29316 (PID:g132848) [Homo sapiens]	0.52
520	U07357	Mus musculus Balb/c brain-specific kinase (Bsk) mRNA, complete cds.	0.20	206712	(M64793) salivary proline-rich protein [Rattus norvegicus]	0.51

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
521	AF034460	Penicillium thomii internal transcribed spacer 1, 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence	0.20	114136	AMINO-ACID ACETYLTRANSFERASE Pseudomonas aeruginosa >gi 151036 (M38358) N-acetylglutamate synthase [Pseudomonas aeruginosa]	0.39
522	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	0.20	2842674	FOO DOMAIN CLASS 2, ASSOCIATING FACTOR 1 (B-CELL-SPECIFIC COACTIVATOR OBF-1) (OCT BINDING FACTOR 1) (BOB-1) (OCA-B) Bob1, B-cell-specific - mouse >gi 1881818 bbs 179852 mBob1=B-cell specific transcriptional coactivator line J558L, Peptide, 256 aa] >gi 1353792 (U43788) Oct binding factor 1 [Mus musculus] (AL032643) similar to Uncharacterized protein family UPF0054, Double-stranded RNA binding motif; cDNA EST yk489b3.5 comes from this gene; cDNA EST yk439g7.5 comes from this gene [Caenorhabditis elegans]	0.073
523	X95971	S.lividans groEL2 gene	0.20	3925277		4e-19
524	L41502	Ovis aries vasopressin V1 receptor (V1R) gene, complete cds	0.19	<NONE>	<NONE>	<NONE>
525	J03885	K.pneumoniae oxalacetate decarboxylase alpha subunit gene, complete cds.	0.19	<NONE>	<NONE>	<NONE>
526	AE001451	Helicobacter pylori, strain J99 section 12 of 132 of the complete genome	0.19	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
527	D88084	Pedicularis verticillata chloroplast DNA, intergenic region between trnT(UGU) and trnL(UAA)5'exon	0.19	<NONE>	<NONE>	<NONE>
528	U67599	Methanococcus jannaschii section 141 of 150 of the complete genome	0.19	<NONE>	<NONE>	<NONE>
529	J05500	Human beta-spectrin (SPTB) mRNA, complete cds.	0.19	<NONE>	<NONE>	<NONE>
530	Y10137	M.mycoides ftsY gene homologue and gene encoding hypothetical protein	0.19	<NONE>	<NONE>	<NONE>
531	AF027174	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-B) mRNA, complete cds	0.19	<NONE>	<NONE>	<NONE>
532	D43805	Mouse thymic stromal cell mRNA for TLSF-beta, complete cds	0.19	<NONE>	<NONE>	<NONE>
533	AJ012585	Tetrahymena thermophila macronuclear gene encoding ribosomal protein L3, exons 1-2	0.19	<NONE>	<NONE>	<NONE>
534	X51475	Brassica napus 5-enolpyruvylshikimate-3-phosphate synthase gene	0.19	<NONE>	<NONE>	<NONE>
535	AF074386	Sambucus nigra hevein-like protein mRNA, complete cds	0.19	<NONE>	<NONE>	<NONE>
536	Z49625	S.cerevisiae chromosome X reading frame ORF YJR125c	0.19	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		H.sapiens pilor				
537	X63741	mRNA	0.19	<NONE>	<NONE>	<NONE>
538	Y11255	O.latipes mRNA for annexin max4	0.19	<NONE>	<NONE>	<NONE>
539	L63537	Oncorhynchus mykiss (clone Jb-10) beta-2 microglobulin (B2m) mRNA. complete cds.	0.19	<NONE>	<NONE>	<NONE>
540	X70903	N.tobacum T92 gene for auxin-binding protein	0.19	<NONE>	<NONE>	<NONE>
541	U61958	Caenorhabditis elegans cosmid C25A8	0.19	<NONE>	<NONE>	<NONE>
542	U33959	Macaca fascicularis fertilin beta mRNA. complete cds	0.19	<NONE>	<NONE>	<NONE>
543	Z49835	H.sapiens mRNA for protein disulfide isomerase	0.19	2113940	(Z95556) hypothetical protein Rv2507	9.4
544	AF035458	Spinacia oleracea heat shock 70 protein protein. complete cds	0.19	267293	PROBABLE E4 PROTEIN papillomavirus (type 1) >gi 61015 (X62844) E4 gene product [Pygmy chimpanzee papillomavirus type 1]	9.4
545	U23441	Tetrahymena thermophila B internal deletion sequence.	0.19	3877185	(Z66563) F46C3.2 [Caenorhabditis elegans]	9.3
546	U53921	Pneumocystis carinii major surface glycoprotein	0.19	3548901	(AF052502) DA26 homolog [Epiphyas postvittana nucleopolyhedrovirus]	9.3
547	L11002	Rat ankyrin binding glycoprotein-1 related mRNA sequence.	0.19	3337352	(AC004481) putative chromatin structural protein Supt5hp	9.1
548	U67560	Methanococcus jannaschii section 102 of 150 of the complete genome	0.19	3183689	(Y13585) serotonin receptor 4 [Cavia porcellus]	8.7
549	U18424	Mus musculus bacteria binding macrophage receptor MARCO mRNA. complete cds.	0.19	3659853	(AF089083) complement component C1qB like protein	7.1

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
550	X66467	C.albicans sec18 gene	0.19	1326385	(U58751) C07G1.7 gene product [Caenorhabditis elegans]	6.9
551	AF003487	Syngaster lepidus 16S ribosomal RNA gene, partial sequence	0.19	3122039	DIHYDROPYRIMIDINASE (DHPASE) dihydropyrimidinase - rat >gi 1378019 gnl PID d1010479	6.9
552	J05087	Rat calmodulin-sensitive plasma membrane Ca ²⁺ -transporting ATPase (PMCA3) mRNA, complete cds.	0.19	422462	hypothetical protein - fruit fly (Drosophila melanogaster) >gi 296434 (X68408) ORF [Drosophila melanogaster]	5.3
553	AF080464	Homo sapiens glutamate oxaloacetate transaminase	0.19	3024834	PROBABLE E4 PROTEIN >gi 790898 position 3286..3288 is first start codon; putative	5.3
554	U78876	Human MEK kinase 3 mRNA, complete cds	0.19	1710445	(U78083) unknown [Emericella nidulans]	5.3
555	AB009077	Vigna radiata mRNA for proton pyrophosphatase, complete cds	0.19	3256922	(AP000002) 256aa long hypothetical protein [Pyrococcus horikoshii]	5.1
556	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	0.19	4226159	(AF125463) contains similarity to BTB (also known as BR-C/Ttk) domains (Pfam:PF00651, Score=62.8, E=7.6e-15, N=1) [Caenorhabditis elegans]	4.1
557	AE000392	Escherichia coli K-12 MG1655 section 282 of 400 of the complete genome	0.19	3645960	(AL031583) 1-evidence=predicted by content; 1-method=genefinder;084; 1-method_score=47.46; 1-evidence_end; 2-evidence=predicted by match; 2-match_accession=SWISS-PROT:P23792; 2-match_description=DISCONNECTED PROTEIN.; 2-matc...	4.0

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
558	AE000392	Escherichia coli K-12 MG1655 section 282 of 400 of the complete genome	0.19	3645960	(AL051583) 1-evidence=predicted by content; 1-method=genefinder;084; 1-method_score=47.46; 1-evidence_end; 2-evidence=predicted by match; 2-match_accession=SWISS-PROT:P23792; 2-match_description=DISCONNECTED PROTEIN.; 2-matc...	4.0
559	L81774	Homo sapiens (subclone 3_d1 from P1 H25) DNA sequence	0.19	4001725	(AB015981) MnhA [Staphylococcus aureus]	3.0
560	AL021108	Drosophila melanogaster cosmid clone 137E7	0.19	4001688	(AB015718) protein kinase [Homo sapiens]	3.0
561	AB001510	Carabus leptoplesioides mitochondrial DNA for NADH dehydrogenase subunit 5. partial cds	0.19	3758855	(Z98551) MAL3P6.11 [Plasmodium falciparum]	2.4
562	AF069696	Egernia stokesii clone EST1 microsatellite	0.19	3328994	(AE001326) Amino Acid (Branched) Transport [Chlamydia trachomatis]	2.4
563	X64144	F.pringlei ppcA1 gene for phosphoenolpyruvate carboxylase	0.19	3242974	(AF069555) G protein-coupled receptor p2y3 [Meleagris gallopavo]	2.3
564	U56897	Human immunodeficiency virus type 1 gag polyprotein (gag) gene. partial cds	0.19	2257710	(U73041) resolvase-like protein [Thiobacillus ferrooxidans]	2.3
565	U57975	Danio rerio Notch homologue 3 mRNA. complete cds	0.19	3874971	(Z99709) similar to NAD dependant epimerase/dehydratase family; cDNA EST EMBL:C10103 comes from this gene; cDNA EST EMBL:D66400 comes from this gene; cDNA EST EMBL:D70143 comes from this gene; cDNA EST yk493h11.3 comes from ...	1.8

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
566	Y12502	R.norvegicus mRNA for factor XIIIa	0.19	2133693	masquerade precursor - fruit fly (Drosophila melanogaster) >gi 665545 (U18130) masquerade [Drosophila melanogaster] >gi 1095942 prf 2110286A masquerade gene	1.8
567	S82470	BB1=malignant cell expression-enhanced gene/tumor progression-enhanced gene [human, UM-UC-9 bladder carcinoma cell line, mRNA, 1897 nt]	0.19	2444026	(U77783) N-methyl-D-aspartate receptor 2D subunit precursor [Homo sapiens]	1.8
568	U97408	Caenorhabditis elegans cosmid F48A9	0.19	542433	225K protein - Babesia bovis (fragment)	1.8
569	U10470	Pseudomonas fluorescens PHA depolymerase (phaZ) gene, complete cds.	0.19	3721862	(AB016024) Pfj2 [Plasmodium falciparum]	1.7
570	M88160	Ovis aries MAF214 locus polymorphic dinucleotide repeat	0.19	1293816	(U56963) T13A10.5 gene product [Caenorhabditis elegans]	1.4
571	AJ131336	Lolium italicum mRNA for pollen allergen (Lol i 2, group II) > :: emb AJ131339 LIT131339 Lolium italicum mRNA for pollen allergen (Lol i 2, group II) > allergen (Poa p 2, group II) > :: emb AJ131338 TAE131338 Triticum aestivum mRNA for pollen allergen (Tri a 2, group II)	0.19	3880447	(AL032675) predicted using Genefinder	0.82
572	X84036	S.cerevisiae ARG8 and CDC33 genes	0.19	3882041	(AJ010405) hypothetical protein	0.62

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Human WD protein			mucin - human >gi 501033	
573	U57058	IR10 pre-mRNA, partial cds	0.19	631302	(U14383) mucin [Homo sapiens]	0.60
574	AF034460	Penicillium thomii internal transcribed spacer 1, 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence	0.19	114136	AMINO-ACID ACETYLTRANSFERASE Pseudomonas aeruginosa >gi 151036 (M38358) N-acetylglutamate synthase [Pseudomonas aeruginosa]	0.35
575	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	0.19	105270	alpha-2-adrenergic receptor - human name 'ADRA2R' [Homo sapiens]	0.27
576	AG001475	Homo sapiens genomic DNA, 21q region, clone: 125H6N2	0.19	94977	hypothetical protein 3 - Pseudomonas sp. (DSM 6898) plasmid pKB740 >gi 45867 (X66604) ORF3	0.16
577	M63284	Mouse IgG receptor (beta-Fc-gamma-RII) gene, exons 9 and 10, clones lambda-Fc(3.2.93).	0.19	3024681	TRANSCRIPTION INITIATION FACTOR TFIID 135 KD SUBUNIT (TAFII-135) (TAFII135) (TAFII-130) of RNA polymerase II transcription factor TFIID [Homo sapiens]	0.088
578	U38241	Pseudomonas aeruginosa orotate phosphoribosyl transferase (pyrE), catabolite repression control protein (crc) and RNasePH (rph) genes, complete cds	0.19	3044086	(AF055904) unknown [Myxococcus xanthus]	0.052
579	AF039734	Lontra longicaudis transthyretin intron 1, partial sequence	0.19	322759	pistil extensin-like protein (clone pMG14) - common tobacco (fragment) >gi 19927 (Z14015) pistil extensin like protein [Nicotiana tabacum]	0.030
580	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	0.19	2147194	collagen - Paralvinella grasslei	0.002

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
581	AB004232	Drosophila melanogaster mRNA for DAD polypeptide, complete cds	0.19	2498765	PEROXISOMAL MEMBRANE PROTEIN PEX16 lipolytica]	0.002
582	AF098919	Gallus gallus alpha-globin gene domain 5' region	0.19	1086863	(U41272) T03G11.6 gene product [Caenorhabditis elegans]	4e-05
583	AE001457	Helicobacter pylori, strain J99 section 18 of 132 of the complete genome	0.19	2924552	(AL022018) 1-evidence=predicted by content; 1-method=genefinder;084; 1-method_score=165.48; 1-evidence_end; 2-evidence=predicted by match; 2-match_accession=AA264666; 2-match_description=LD08351.5p rime LD Drosophila melanoga...	3e-05
584	L10329	Plasmid RP4 traE gene, 3' end; traD gene, complete cds; traF gene, 5' end.	0.19	3878117	(Z49068) mitochondrial carrier protein	8e-07
585	AE001155	Borrelia burgdorferi (section 41 of 70) of the complete genome	0.19	861276	(U28739) similar to TPR domains in e.g. yeast STI1 protein [Caenorhabditis elegans]	2e-12
586	U49979	Orf virus E10R homolog gene, partial cds, and DNA polymerase gene, complete cds	0.19	3850072	(AL033385) dna-directed rna polymerase iii subunit [Schizosaccharomyces pombe]	1e-15
587	U88155	Xenopus laevis RanGTPase activating protein	0.19	995714	(X91258) pid:e198503 [Saccharomyces cerevisiae]	4e-16
588	AF061854	Schizosaccharomyces pombe Ctr4p (ctr4) gene, complete cds	0.19	3242750	(AC005164) match to ESTs AA731149 (NID:g2140138), AA731908 (NID:g2752719), AA287837 (NID:g1933519), AA262811 (NID:g1898382), and AA825820 (NID:g2899132)	5e-19
589	M23865	S.cerevisiae CHS2 gene encoding chitin synthase.	0.18	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Xenopus laevis XL-				
590	U95094	INCENP (XL-INCENP) mRNA, complete cds	0.18	<NONE>	<NONE>	<NONE>
591	AF067610	Caenorhabditis elegans cosmid F41A4	0.18	<NONE>	<NONE>	<NONE>
592	AF036329	Homo sapiens gonadotropin-releasing hormone precursor, second form (GnRH-II) gene, complete cds	0.18	<NONE>	<NONE>	<NONE>
593	Z49216	H.sapiens mitoxantrone-resistance associated mRNA	0.18	<NONE>	<NONE>	<NONE>
594	X02167	Torulopsis glabrata mitochondrial DNA for tRNA-Thr.-His and -Glu upstream of cytochrome b gene	0.18	<NONE>	<NONE>	<NONE>
595	Z31561	R.communis (Carmencita) ScrI mRNA for sucrose carrier	0.18	<NONE>	<NONE>	<NONE>
596	L81692	Homo sapiens (subclone 2_c9 from P1 H56) DNA sequence	0.18	1346575	55 KD ERYTHROCYTE MEMBRANE PROTEIN	8.4
597	X57310	Nocardia lactamdurans pcbAB and pcbC genes for alpha-aminoadipyl-L-cysteinyl-D-valine synthetase and isopenicillin N synthase	0.18	126404	SEED LIPOXYGENASE-2 (L-2) soybean >gi 170014 (J03211) lipoxigenase (EC 1.13.11.12)	6.5
598	U18315	Sus scrofa parathyroid receptor (PTH) mRNA, complete cds	0.18	1022323	(X04647) collagen alpha-2(IV) chain [Mus musculus]	3.8

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
599	AL010158	Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-85, complete sequence	0.18	2506816	VERSICAN CORE PROTEIN PRECURSOR PROTEOGLYCAN CORE PROTEIN 2) (GLIAL HYALURONATE-BINDING PROTEIN) (GHAP) >gi 608515 (U16306) chondroitin sulfate proteoglycan versican V0 splice-variant precursor peptide u0002b protein -	3.7
600	AB005287	Bos taurus mRNA for thrombospondin 1, complete cds	0.18	2146000	Mycobacterium tuberculosis tuberculosis] >gi 1694863 gnl PID e283373 (Z83018) hypothetical protein Rv2968c [Mycobacterium tuberculosis]	2.9
601	AL021108	Drosophila melanogaster cosmid clone 137E7	0.18	3483032	(AL031371) hypothetical protein SC4G2.06 [Streptomyces coelicolor]	2.9
602	U57975	Danio rerio Notch homologue 3 mRNA, complete cds	0.18	85719	collagen alpha 1'(II) chain precursor - African clawed frog (AL021387) similar to Zinc finger, C4 type (two domains); cDNA EST yk452f4.5 comes from this gene; cDNA EST EMBL:T00774 comes from this gene receptor NHR-3 [Caenorhabditis elegans]	1.7
603	M30124	P.aeruginosa autonomously replicating sequence.	0.18	3878017	STEM CELL PROTEIN chicken >gi 62845 (X63371). transforming capacity [Gallus gallus]	1.3
604	X54965	G.sp alpha 5HR DNA	0.18	134304	(X98893) hTAFII68 [Homo sapiens] splicing [Homo sapiens]	1.3
605	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	0.18	1628403	92 KD TYPE IV COLLAGENASE PRECURSOR IV, 92K, precursor - rat >gi 1022784 (U36476) 92-kDa type IV collagenase [Rattus norvegicus]	1.2
606	U20793	Oryctolagus cuniculus renal sodium-dependent phosphate transporter type II mRNA, complete cds.	0.18	1705984		

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
607	U23427	Human cholecystokinin type A receptor (CCK-A) gene, exons 1 and 2.	0.18	3261734	(Z94752) hypothetical protein Rv1004c	0.97
608	U49953	Rattus norvegicus protein kinase MUK2 mRNA, complete cds	0.18	551238	(X81847) pectate lyase 1 [Erwinia carotovora]	0.43
609	J00182	Human alpha globin gene cluster on chromosome 16: zeta gene.	0.18	1585259	traJ gene [Amycolatopsis methanolica]	0.41
610	X62513	M.gallopavo gene for metallothionein	0.18	2494740	HYPOTHETICAL 28.3 KD PROTEIN IN GBD 5'REGION (ORF4) >gi 2120954 pir I39562 ORF4 - Alcaligenes eutrophus >gi 695274 (L36817) ORF4	0.31
611	X04862	Goat embryonic alpha globin gene zeta exons 2-3	0.18	86837	androgen receptor B - human	0.082
612	M12450	Rat vitamin D binding protein (DBP) mRNA, complete cds.	0.18	4210432	(AJ130783) APC2 protein [Mus musculus]	0.038
613	AF038539	Mus musculus muscle NSP-like 1 (Nspl1) mRNA, complete cds	0.18	3297877	(AJ224868) GNAS1 [Homo sapiens]	0.029
614	X78401	Bacteriophage P22 right operon, orf 48, replication genes 18 and 12, nin region genes, ninG phosphatase, late control gene 23, orf 60, complete cds, late control region, start of lysis gene 13	0.18	1123087	(U42436) C49H3.3 gene product [Caenorhabditis elegans]	0.009
615	D38754	Pig mRNA for inter-alpha-trypsin inhibitor heavy-chain H1, complete cds	0.18	1397275	(U61947) C06G3.8 gene product [Caenorhabditis elegans]	7e-06

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
616	X51508	Rabbit mRNA for aminopeptidase N (partial)	0.18	630864	LRR47 protein - fruit fly (Drosophila melanogaster) >gi 415947 (X75760) LRR47 [Drosophila melanogaster]	6e-07
617	X54850	S.kluyveri linear plasmid pSKL DNA for open reading frames 1-10	0.18	3183405	HYPOTHETICAL 11.3 KD PROTEIN C2C6.07 IN CHROMOSOME I >gi 2370504 gnl PID c339194 pombe] >gi 3451305 gnl PID c1316730 (AL031324) very hypothetical protein [Schizosaccharomyces pombe]	2e-08
618	L21954	Human peripheral benzodiazepine receptor gene, exon 4.	0.18	3925211	(AL052626) cDNA EST EMBL:D70654 comes from this gene; cDNA EST EMBL:Z14359 comes from this gene; cDNA EST EMBL:D33409 comes from this gene; cDNA EST EMBL:D36239 comes from this gene; cDNA EST EMBL:Z14766 comes from this gene...	4e-09
619	U09355	Oryctolagus cuniculus protein phosphatase 2A1 B gamma subunit (skeletal muscle isolate) mRNA, complete cds.	0.18	3947877	(AL034382) putative mitosis and maintenance of ploidy protein [Schizosaccharomyces pombe]	8e-11
620	X58715	T.cruzi hsp70 mRNA for 70 kDa heat shock protein, partial cds	0.18	3024081	MYOSIN LIGHT CHAIN KINASE, SMOOTH MUSCLE AND NON-MUSCLE ISOZYMES (MLCK) (CONTAINS: TELOKIN)	9e-12
621	AF060195	Mus musculus proteasome regulator PA28 beta subunit gene, complete cds	0.18	861276	(U28739) similar to TPR domains in e.g. yeast STI1 protein [Caenorhabditis elegans]	1e-14
622	L27235	Methylobacterium extorquens serine cycle proteins	0.18	2688949	(AF027208) AC133 antigen [Homo sapiens]	1e-14

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
623	AF006573	Drosophila virilis maltase 1 (Mav1) and maltase 2 (Mav2) genes, complete cds	0.18	2500558	PUTATIVE RIBONUCLEASE III (RNASE III) >gi 3876420 gnl PID e1346063 (Z81070) similar to ribonuclease [Caenorhabditis elegans]	2e-23
624	AF001782	Staphylococcus aureus strain SA502A AgrB	0.17	<NONE>	<NONE>	<NONE>
625	AJ223364	Homo sapiens germ-line DNA upstream of Jkappa locus	0.17	<NONE>	<NONE>	<NONE>
626	J03059	Human glucocerebrosidase (GCB) gene, complete cds	0.17	<NONE>	<NONE>	<NONE>
627	AB008860	Fugu rubripes Cal2 gene for pheromone receptor, complete cds	0.17	2198849	(AF004900) EJKARP [Homo sapiens] >gi 2665826 (AF035771) Na+/H+ exchanger regulatory factor 2 [Homo sapiens] factor 2 [Homo sapiens] >gi 3618353 gnl PID d1034182 exchanger isoform A3 [Homo sapiens]	7.8
628	AF027174	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-B) mRNA, complete cds	0.17	539355	SCD25 protein (version 1) - yeast	7.5
629	AF059650	Homo sapiens histone deacetylase 3 (HDAC3) gene, complete cds	0.17	482118	hypothetical protein C15H7.1 - Caenorhabditis elegans	4.5

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
630	AF059650	Homo sapiens histone deacetylase 3 (HDAC3) gene, complete cds	0.17	465932	HYPOTHETICAL 83.2 KD PROTEIN F58A4.11 IN CHROMOSOME III >gi 3874287 gnl PID e1344088 EST EMBL:C12577 comes from this gene; cDNA EST yk227e7.5 comes from this gene; cDNA EST yk303d1.5 comes from this gene; cDNA EST yk314c12.5 comes from this gene; cDNA ... EMBL:C11886 comes from this gene; cDNA EST EMBL:C12577 comes from this gene; cDNA EST yk227e7.5 comes from this gene; cDNA EST yk303d1.5 comes from this gene; cDNA EST yk314c12.5 comes from this gene; cDNA ...	4.4
631	X55065	Chinese hamster metallothionein II gene	0.17	3687237	(AC005169) putative Cys3His zinc-finger protein	1.5
632	U15280	Rattus norvegicus oxytocin receptor (OTR) gene, exon 3 and complete cds	0.17	542565	cyclin E type II - fruit fly (Drosophila melanogaster) >gi 429168 (X75027) Drosophila cyclin E type II [Drosophila melanogaster]	0.45
633	X04862	Goat embryonic alpha globin gene zeta exons 2-3	0.17	86837	androgen receptor B - human	0.080
634	AL010222	Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 4-09, complete sequence	0.17	1177322	(X95466) CPG2 protein [Rattus norvegicus] >gi 1588593 prf 2208498A plasticity-related gene [Rattus norvegicus]	7e-07
635	X60111	H.sapiens mRNA for MRP-1	0.17	3237306	(U92715) breast cancer antiestrogen resistance 3 protein	3e-09
636	U49979	Orf virus E10R homolog gene, partial cds, and DNA polymerase gene, complete cds	0.17	3850072	(AL033385) dna-directed rna polymerase iii subunit [Schizosaccharomyces pombe]	7e-15

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
637	AF006573	<i>Drosophila virilis</i> maltase 1 (Mav1) and maltase 2 (Mav2) genes, complete cds	0.17	2500558	PUTATIVE RIBONUCLEASE III (RNASE III) >gi 3876420 gnl PID e1346063 (Z81070) similar to ribonuclease [Caenorhabditis elegans]	2e-29
638	AE001141	<i>Borrelia burgdorferi</i> (section 27 of 70) of the complete genome	0.16	1850327	(U52370) fertilin beta [Homo sapiens]	2.3
639	M72980	<i>Anthonomus grandis</i> vitellogenin gene (VTG), complete cds.	0.12	3242750	(AC005164) match to ESTs AA731149 (NID:g2140138), AA731908 (NID:g2752719), AA287837 (NID:g1933519), AA262811 (NID:g1898382), and AA825820 (NID:g2899132)	2e-56
640	AF023532	<i>Simulium vittatum</i> ATPase 6 gene, mitochondrial gene encoding mitochondrial protein, partial cds	0.11	<NONE>	<NONE>	<NONE>
641	U76523	<i>Sambucus nigra</i> lectin precursor mRNA, complete cds	0.10	3482965	(AL031369) putative protein	0.49
642	AJ001596	<i>Danio rerio</i> mRNA for opioid receptor homologue	0.099	1706694	LANOSTEROL SYNTHASE 5.4.99.7) - fission yeast (<i>Schizosaccharomyces pombe</i>)	2.3
643	U26341	<i>Oryctolagus cuniculus</i> Na and Cl dependent betaine transporter mRNA, complete cds.	0.099	2645804	(AF033381) betaine homocysteine methyl transferase [<i>Mus musculus</i>]	0.59
644	M11633	Bacteriophage Cp-5 (<i>S.pneumoniae</i>) 3' inverted terminal repeat.	0.082	2314695	(AE000649) type IIS restriction enzyme R and M protein	4.3
645	X74103	<i>Streptomyces</i> sp. gene for alkaline serine protease I	0.073	1314734	(U54641) 220 kDa silk protein [<i>Chironomus thummi</i>]	6.3

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Caenorhabditis				
646	Z72509	elegans cosmid F32G8, complete sequence [Caenorhabditis elegans]	0.072	<NONE>	<NONE>	<NONE>
647	X70282	X.laevis xanf-1 gene Human DNA sequence from cosmid E141E2, on chromosome 22, complete sequence [Homo sapiens]	0.070	3851202	(AC005954) ZO-3 [Homo sapiens] [Homo sapiens]	0.40
648	Z69906		0.069	<NONE>	<NONE>	<NONE>
649	AF056940	Drosophila virilis retrotransposon Tv1, complete sequence	0.069	2246532	(U93872) ORF 73, contains large complex repeat CR 73	5e-12
650	AJ001151	Homo sapiens genomic sequence	0.068	<NONE>	<NONE>	<NONE>
651	X54455	Bacteriophage BF23 gene 17 and gene 18	0.067	<NONE>	<NONE>	<NONE>
652	X87936	P.pinea internal transcribed spacers 1 & 2 of ribosomal DNA	0.067	2459733	(U95374) aldehyde dehydrogenase [Haloferax volcanii]	4.3
653	AF019236	Dictyostelium discoideum TipD (tipD) gene, complete cds	0.067	3882275	(AB018320) KIAA0777 protein [Homo sapiens]	1.1
654	X90592	O.cuniculus mRNA for p53 protein	0.067	1703275	METHIONINE AMINOPEPTIDASE 2 (METAP 2) GLYCOPROTEIN (P67)	0.29
655	U41805	Mus musculus putative T1/ST2 receptor binding protein precursor mRNA, partial cds	0.067	642518	(U17326) neuronal nitric oxide synthase [Homo sapiens]	0.29
656	AB007881	Homo sapiens KIAA0421 mRNA, partial cds	0.066	<NONE>	<NONE>	<NONE>
657	AL010213	Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-109, complete sequence	0.066	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
658	AB014546	Homo sapiens mRNA for KIAA0646 protein, complete cds	0.066	1082461	homeotic protein HB9 - human	0.38
659	AF104156	Rattus exulans isolate huahine30 mitochondrial D-loop, partial sequence	0.066	1002380	(U24189) RRM-type RNA binding protein [Caenorhabditis elegans]	0.29
660	X97581	M.musculus mRNA for spalt transcription factor	0.066	4107313	(AL035075) putative myosin heavy chain	0.28
661	D85378	Human clone H20 N-acetylglucosaminyltransferase III DNA, exon 2	0.066	2114473	(U96963) p140mDia [Mus musculus]	0.22
662	M97561	Human (clone LA179) chromosome 21 sequence.	0.065	<NONE>	<NONE>	<NONE>
663	AE001373	Plasmodium falciparum chromosome 2, section 10 of 73 of the complete sequence	0.065	<NONE>	<NONE>	<NONE>
664	S75479	growth hormone receptor, growth hormone binding protein (GHR/BP gene) [mice, C57 black/6, Genomic, 179 nt, segment 8 of 10]	0.065	<NONE>	<NONE>	<NONE>
665	AF032922	Homo sapiens syntaxin 4 binding protein UNC-18c (UNC-18c) mRNA, complete cds	0.065	3061308	(AB006074) topoisomerase III [Mus musculus]	0.82
666	S80986	svp[40]=svp-related nuclear receptor/retinoid signaling modulator [zebrafishes, mRNA, 3576 nt]	0.065	1326288	(U58734) weak similarity to ankyrin G [Caenorhabditis elegans]	0.12

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
667	X59552	G.domesticus mRNA for ventricular myosin heavy chain	0.065	2497098	HYPOTHETICAL 74.2 KD PROTEIN IN AMD1-RAD52 INTERGENIC REGION >gi 1077180 pir S49745 probable membrane protein YML034w - yeast (Saccharomyces cerevisiae) >gi 575685 (Z46659) unknown orf, len: 656, CAI: 0.13 [Saccharomyces cerevisiae]	0.014
668	M72980	Anthonomus grandis vitellogenin gene (VTG), complete cds.	0.065	3242750	(AC005164) match to ESTs AA731149 (NID:g2140138), AA731908 (NID:g2752719), AA287837 (NID:g1933519), AA262811 (NID:g1898382), and AA825820 (NID:g2899132)	5e-33
669	AB014546	Homo sapiens mRNA for KIAA0646 protein, complete cds	0.064	<NONE>	<NONE>	<NONE>
670	M30039	Sheeppox virus strain KS-1 ORF HM1 gene, partial cds; ORF HM2 and ORF HM3 genes, complete cds; and ORF HM4 gene, partial cds	0.064	<NONE>	<NONE>	<NONE>
671	Z68013	Caenorhabditis elegans cosmid W02H3, complete sequence [Caenorhabditis elegans]	0.064	<NONE>	<NONE>	<NONE>
672	AF041332	Bodo saltans unknown mRNA, kinetoplast gene encoding kinetoplast protein, complete cds	0.064	<NONE>	<NONE>	<NONE>
673	J00451	Mouse germline IgG-3 chain gene, D-J-C region, and switch region.	0.064	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
674	U41289	Dictyostelium discoideum K7 kinesin-like protein mRNA, complete cds	0.064	3482972	(AL031369) putative protein	9.3
675	M37395	L.lactis (strain SK11) proteinase plasmid pSK111 DNA, complete cds.	0.064	993019	(X87246) alternative start codon [Pseudorabies virus]	9.2
676	Z15030	H.sapiens gene for ventricular myosin light chain 2 > :: gb L01652 HUMVM LC Human ventricular myosin light chain 2 gene, seven exons.	0.064	730343	PROLACTIN RECEPTOR PRECURSOR (PRL-R) mouse >gi 220576 gnl PID d1001535 (D10214) prolactin receptor precursor [Mus musculus] >gi 293770 (L14811) prolactin receptor [Mus musculus] >gi 347842 (L13593) prolactin receptor [Mus musculus] receptor:ISOTYPE=long form [Mus musculus]	9.1
677	Z12021	G.max gene for catalase	0.064	2498711	ORIGIN RECOGNITION COMPLEX PROTEIN, SUBUNIT 2 >gi 1185461 (U38472) essential ORC2-related fission replication factor Orp2 [Schizosaccharomyces pombe]	5.3
678	L05668	Entamoeba histolytica protein serine/threonine kinase (pstk1) gene, complete cds.	0.064	733140	(U22453) carboxypeptidase [Simulium vittatum]	5.3

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
679	U50715	Mus musculus alpha-galactosidase A gene, complete cds	0.064	125398	HYGROMYCIN-B KINASE (HYGROMYCIN B PHOSPHOTRANSFERASE) (APH(7")) >gi 66885 pir WGSMMH hygromycin B phosphotransferase (EC 2.7.1.-) - Streptomyces hygroscopicus >gi 581682 (X03615) pot. hyg protein [Streptomyces hygroscopicus] phosphotransferase [synthetic construct] >gi 2739064 cloning vector] >gi 2739068 (AF025747) hygromycin B phosphotransferase [unidentified cloning vector]	2.3
680	Z28182	S.cerevisiae chromosome XI reading frame ORF YKL182w	0.064	1079035	Om(2D) protein - fruit fly (Drosophila ananassae) >gi 443770 gnl PID d1006095 (D26553) ORF	1.8
681	M29917	Human ornithine aminotransferase gene, exon 1.	0.064	2317934	(U97553) unknown [murine herpesvirus 68]	1.4
682	AB020709	Homo sapiens mRNA for KIAA0902 protein, complete cds	0.064	861404	(U29154) T07F12.3 gene product [Caenorhabditis elegans]	0.47
683	AB014546	Homo sapiens mRNA for KIAA0646 protein, complete cds	0.064	1708118	HOMEBOX PROTEIN HB9 >gi 507425	0.35
684	AB010427	Homo sapiens mRNA for NORI-1, complete cds	0.064	2388676	(AF015539) precollagen P [Mytilus edulis]	0.018
685	U34774	Orf virus ankyrin-like repeat protein, F11L homolog, and F12L homolog genes, complete cds.	0.064	731668	SSF1 PROTEIN >gi 626624 pir S46700 SSF1 protein - yeast (Saccharomyces cerevisiae)	1e-05
686	AF022861	Mus musculus neuropilin-2(a5) mRNA, alternatively spliced, complete cds	0.064	4091978	(AF073359) benzaldehyde dehydrogenase [Pseudomonas sp. DJ77]	1e-05

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
687	U14331	Sus scrofa myogenin gene, complete cds	0.064	2781386	(AC004010) similar to Leucine-rich transmembrane proteins; 44% similarity to U42767 (PID:g1736918) [Homo sapiens]	3e-33
688	AF074870	Chironomus pallidivittatus clone 1219 non-telomeric Ssp repeat sequence	0.063	<NONE>	<NONE>	<NONE>
689	Z25523	H.sapiens repeat region DNA.	0.063	<NONE>	<NONE>	<NONE>
690	AE001378	Plasmodium falciparum chromosome 2, section 15 of 73 of the complete sequence	0.063	<NONE>	<NONE>	<NONE>
691	Z72947	S.cerevisiae chromosome VII reading frame ORF YGR162w	0.063	<NONE>	<NONE>	<NONE>
692	Y14723	Choanomphalus incertus mitochondrial cytochrome c oxidase subunit I gene, partial	0.063	<NONE>	<NONE>	<NONE>
693	X74103	Streptomyces sp. gene for alkaline serine protease I	0.063	1730713	HYPOTHETICAL 108.5 KD PROTEIN IN UME3-PUB1 INTERGENIC REGION >gi 2131866 pir S62935 hypothetical protein YNL023c - yeast (Saccharomyces cerevisiae) >gi 1301855 gnl PID e239870 (Z71299) ORF YNL023c [Saccharomyces cerevisiae]	6.7
694	AF039843	Homo sapiens Sprouty 2 (SPRY2) mRNA, complete cds	0.063	232217	GLUTATHIONE S-TRANSFERASE GST-6.0 (GST B1-1) >gi 421198 pir S29772 glutathione transferase (EC 2.5.1.18) - Proteus mirabilis >gi 2126142 pir S71882 glutathione transferase (EC 2.5.1.18) B - Proteus mirabilis >gi 1053076 (U38482)	5.2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
695	M63650	Mouse M-twist gene mRNA. complete cds.	0.063	1730141	FRAGILE X MENTAL RETARDATION SYNDROME RELATED PROTEIN 2 >gi 2135129 pir S60173 fragile X mental retardation syndrome related protein - human >gi 1098637 (U31501) fragile X mental retardation syndrome related protein [Homo sapiens]	1.8
696	Y13298	Homo sapiens GDP dissociation inhibitor beta pseudogene	0.063	1085930	hypothetical protein 4 - fowl adenovirus 1	1.3
697	X56600	Rat SOD-2 gene for manganese-containing superoxide dismutase	0.063	3882143	(AB018254) KIAA0711 protein [Homo sapiens]	0.60
698	Z23107	M.musculus mRNA for 5HTx serotonin receptor	0.063	1708162	HUNTINGTIN (HUNTINGTON'S DISEASE PROTEIN HOMOLOG) (HD PROTEIN)	0.45
699	M20670	Plasmodium vivax circumsporozoite protein gene. 3' end.	0.063	4033395	DNA GYRASE SUBUNIT B subunit [Mycobacterium xanthus]	0.35
700	Z62997	H.sapiens CpG DNA. clone 76g11, reverse read cpg76g11.r1a.	0.063	1350911	RETINOIC ACID RECEPTOR RXR-BETA sapiens >gi 3172498 (AF065396) retinoic X receptor B dJ1033B10.11 (Retinoid X receptor beta (RXRB)) [Homo sapiens] >gi 4249766 (AF120161) retinoic X receptor beta	0.16
701	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA. complete cds	0.063	2981200	(AF048732) cyclin T2b [Homo sapiens]	0.090
702	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA. partial cds	0.063	3877951	(Z81555) predicted using Genefinder	6e-07
703	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA. complete cds	0.063	3393018	(AL031174) hypothetical protein	2e-10

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		E.coli genomic DNA.				
704	D90872	Kohara clone #419(54.7-55.1 min.)	0.063	2498198	CYTOCHROME B561 (CYTOCHROME B-561)	3e-19
705	M25528	M.crystallinum ferredoxin-NADP+ reductase (fnrA) mRNA, complete cds.	0.062	<NONE>	<NONE>	<NONE>
706	U45256	Strongyloides ratti microsatellite B DNA	0.062	<NONE>	<NONE>	<NONE>
707	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	0.062	<NONE>	<NONE>	<NONE>
708	AF044317	Homo sapiens TEL/AML1 fusion gene, partial sequence	0.062	<NONE>	<NONE>	<NONE>
709	Z73975	Caenorhabditis elegans cosmid T06E8, complete sequence [Caenorhabditis elegans]	0.062	3108187	(AC004663) Notch 3 [Homo sapiens]	2.9
710	X54232	Human mRNA for heparan sulfate proteoglycan	0.062	1076741	chitinase (EC 3.2.1.14) precursor - rice precursor - rice >gi S07955 (X87109) chitinase [Oryza sativa]	0.59
711	X03073	Bovine retinal mRNA for transducin beta-subunit	0.062	477578	sialidase - Actinomyces viscosus >gi 141852	0.087
712	Y12573	D.melanogaster Jun and 14-3-3 zeta gene	0.062	3879551	(Z70756) similar to collagen	0.073
713	L26573	Bombus terrestris mitochondrial cytochrome oxidase I, partial cds.	0.062	1684959	(U20600) NADH dehydrogenase subunit [Vanda lamellata]	0.039

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
714	U58994	Human ladinin (LAD) gene, complete cds	0.062	2811078	AMINOPEPTIDASE B (ARGINYL AMINOPEPTIDASE) (ARGININE AMINOPEPTIDASE) (CYTOSOL AMINOPEPTIDASE IV) (AP-B) >gi 2039143 (U61696) aminopeptidase B [Rattus norvegicus]	9e-06
715	AB014553	Homo sapiens mRNA for KIAA0653 protein, partial cds	0.062	1326350	(U58748) similar to potential transmembrane domains in S. cerevisiae nuclear division RFT1 protein (SP:P38206)	5e-10
716	L16898	Mus musculus collagen alpha 1 type XVIII mRNA, 5'end.	0.062	1723657	HYPOTHETICAL 38.5 KD PROTEIN IN ERV1-GLS2 INTERGENIC REGION >gi 2132587 pir S64322 probable membrane protein YGR031w - yeast (Saccharomyces cerevisiae) >gi 1323010 gnl PID e243277 (Z72816) ORF YGR031w [Saccharomyces cerevisiae]	1e-14
717	X99343	M.tuberculosis guaA/B & choD genes	0.062	3873807	(Z49907) B0491.1 [Caenorhabditis elegans]	2e-19
718	AF010193	Homo sapiens MAD-related gene SMAD7 (SMAD7) mRNA, complete cds	0.061	<NONE>	<NONE>	<NONE>
719	L10182	Myrmeleon sp. 18S ribosomal RNA.	0.061	<NONE>	<NONE>	<NONE>
720	Y14723	Choanophalus incertus mitochondrial cytochrome c oxidase subunit I gene, partial	0.061	<NONE>	<NONE>	<NONE>
721	L27840	Bovine respiratory syncytial virus nucleoprotein mRNA, complete cds.	0.061	542955	nucleoporin p62 - human	8.6

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
722	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	0.061	494454	Sus scrofa >gi 494455 pdb IPOS B Sus scrofa Sus scrofa >gi 1421210 pdb 1PCP Porcine Spasmolytic Protein (Psp) (Nmr, 19 Structures) Spasmolytic Polypeptide >gi 1633061 pdb 2PSP B Chain B. Porcine Pancreatic Spasmolytic Polypeptide	2.9
723	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	0.061	3845272	(AE001417) hypothetical protein [Plasmodium falciparum]	1.3
724	U26463	Sporidiobolus salmonicolor NADPH-dependent aldehyde reductase gene, complete cds	0.061	1710288	(U79302) unknown [Homo sapiens]	0.44
725	AF035443	Xenopus laevis weel homolog mRNA, complete cds	0.061	3979720	EMBL:D33048 comes from this gene; cDNA EST EMBL:D35780 comes from this gene; cDNA EST yk442c6.3 comes from this gene; cDNA EST yk442c6.5 comes from this gene; cDNA EST yk398f6.3 comes from this gene; cDNA E... >gi 3979816 gnl PID e1358315 EST EMBL:D35780 comes from this gene; cDNA EST yk442c6.3 comes from this gene; cDNA EST yk442c6.5 comes from this gene; cDNA EST yk398f6.3 comes from this gene; cDNA E...	2e-04
726	Z48584	Caenorhabditis elegans cosmid ZK1321, complete sequence [Caenorhabditis elegans]	0.061	3183491	HYPOTHETICAL 83.8 KD PROTEIN C27F2.7 IN CHROMOSOME III >gi 1065510 (U40419) C27F2.7 gene product [Caenorhabditis elegans]	3e-11

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					HYPOTHETICAL 32.0 KD	
727	X61489	Zea mays pep gene for (C3 type) phosphoenolpyruvate carboxylase	0.061	2496887	PROTEIN C09F5.2 IN CHROMOSOME III >gi 732538 (U22832) C09F5.2 gene product [Caenorhabditis elegans]	1e-15
728	AF025408	Drosophila melanogaster Windbeutel (wind) gene, complete cds	0.061	3702295	(AC005783) R33083_1 [Homo sapiens]	2e-60
729	AB012106	Brassica rapa mRNA for SRK45, complete cds	0.060	<NONE>	<NONE>	<NONE>
730	AF027174	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-B) mRNA, complete cds	0.060	<NONE>	<NONE>	<NONE>
731	Y08682	H.sapiens mRNA for carnitine palmitoyltransferase I type I	0.060	3319446	(AF077541) contains similarity to class-I aminoacyl-tRNA synthetases [Caenorhabditis elegans]	8.1
732	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	0.060	1041119	(D78016) TRAE [Enterococcus faecalis]	8.1
733	AF064030	Helianthus tuberosus lectin 2 mRNA, complete cds	0.060	632209	regulatory protein Rex - primate T-lymphotropic virus PTLV-L (fragment)	3.7
734	AF100694	Mus musculus Pontin52 mRNA, complete cds	0.060	3098348	(AF037401) neuropeptide Y/peptide YY receptor Yc [Danio rerio]	2.1
735	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	0.060	125978	LAR PROTEIN PRECURSOR (LEUKOCYTE ANTIGEN RELATED) >gi 70146 pir TDHULK leukocyte antigen-related protein precursor - human >gi 34267 sapiens]	1.2
736	U76523	Sambucus nigra lectin precursor mRNA, complete cds	0.060	2055394	(U87306) transmembrane receptor UNC5H2 [Rattus norvegicus]	0.32
737	U69668	Human nuclear pore complex-associated protein TPR	0.060	4127854	(Y14063) ChT1 thymocyte antigen [Gallus gallus]	9e-04

221

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
738	AB014553	Homo sapiens mRNA for KIAA0653 protein, partial cds	0.060	1326350	(U58748) similar to potential transmembrane domains in S. cerevisiae nuclear division RFT1 protein (SP:P38206)	1e-09
739	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	0.060	2632098	(Y15513) Prodos protein [Drosophila melanogaster]	5e-10
740	Z96260	H.sapiens telomeric DNA sequence, clone 12QTEL101, read 12QTELOO101.seq	0.059	<NONE>	<NONE>	<NONE>
741	M93128	Mouse homeobox protein (EVX2) mRNA, complete cds	0.059	<NONE>	<NONE>	<NONE>
742	AB012106	Brassica rapa mRNA for SRK45, complete cds	0.059	1652318	(D90904) lysostaphin [Synechocystis sp.]	4.7
743	AB007920	Homo sapiens mRNA for KIAA0451 protein, complete cds	0.059	479491	transcription factor brm-3b - human	0.71
744	M60445	Human histidine decarboxylase (HDC) mRNA, complete cds	0.058	<NONE>	<NONE>	<NONE>
745	U01836	Ustilago maydis exodeoxyribonuclease (REC1) gene, complete cds.	0.058	1171908	OLIGOPEPTIDE TRANSPORT SYSTEM PERMEASE PROTEIN OPPC >gi1075086 pir D64184 oligopeptide transport system permease protein (oppC)C homolog - Haemophilus influenzae (strain Rd KW20) permease protein (oppC) [Haemophilus influenzae Rd]	1.5
746	AF090115	Lycopersicon esculentum cytosolic class II small heat shock protein HCT2 (HSP17.4) mRNA, complete cds	0.058	3193265	(AF069131) chitinase [Bacillus subtilis]	0.002
747	AB012105	Brassica rapa mRNA for SLG45, complete cds	0.057	433385	(U03978) dynein heavy chain isotype 7A [Tripneustes gratilla]	3.4

272

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Arabidopsis thaliana mRNA for neoxanthin cleavage enzyme	0.056	<NONE>	<NONE>	<NONE>
748	AJ005813					
749	Y16828	Lagopus lagopus genomic microsatellite sequence. LLST4	0.056	3328678	(AE001299) hypothetical protein [Chlamydia trachomatis]	4.3
750	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	0.055	<NONE>	<NONE>	<NONE>
751	AF074385	Sambucus nigra hevein-like protein mRNA, complete cds	0.055	137339	69 KD PROTEIN >gi 94375 pir S19150 hypothetical protein, 69K - turnip yellow mosaic virus	0.69
752	U76523	Sambucus nigra lectin precursor mRNA, complete cds	0.035	<NONE>	<NONE>	<NONE>
753	M92069	Human retrovirus-like sequence-isoleucine c	0.034	<NONE>	<NONE>	<NONE>
754	S78516	GIL=ankyrin-like repeat [orf virus OV. NZ2, Genomic. 1608 nt]	0.033	2804465	(AF043700) contains similarity to human RNA-binding protein FUS/TLS (SW:Q28009) [Caenorhabditis elegans]	0.15
755	M15646	Chicken myosin alkali light chain mRNA, complete cds, clone pF1.	0.027	3334221	4-HYDROXYPHENYLPYRUVA TE DIOXYGENASE 4-hydroxyphenylpyruvate dioxygenase [Mycosphaerella graminicola]	6e-17
756	AF027174	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-B) mRNA, complete cds	0.025	3877815	(Z96048) predicted using Genefinder	5.0

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
757	AJ002291	Streptococcus pneumoniae pbplb gene, complete	0.025	3880487	(Z68014) similar to ribose-phosphate pyrophosphokinase; cDNA EST EMBL:D73173 comes from this gene; cDNA EST EMBL:D70909 comes from this gene; cDNA EST EMBL:D73449 comes from this gene; cDNA EST EMBL:D76167 comes from this ge...	1.7
758	X79104	C.borulinum (NCTC 7272 type A) HA-33 and P-21 genes.	0.024	2648615	(AE000970) tungsten formylmethanofuran dehydrogenase, subunit B (fwdB 2) [Archaeoglobus fulgidus]	6.1
759	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	0.024	1663698	(D83785) expressed ubiquitously; product similar to D.melanogaster mam protein. [Homo sapiens]	4.7
760	U36197	Chlamydomonas reinhardtii cobalamin-independent methionine synthase mRNA, complete cds	0.024	585723	PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR GAMMA (PPAR-GAMMA) >gi 283818 pir C42214 peroxisome proliferator-activated receptor gamma chain - African clawed frog >gi 214668 (M84163) peroxisome proliferator activated receptor gamma [Xenopus laevis]	0.42
761	L38865	Macaca mulatta (clone MMVA63) T-cell receptor alpha (TCR A) mRNA, partial cds.	0.023	<NONE>	<NONE>	<NONE>
762	AF035948	Mus musculus insulin receptor substrate-3 S.tuberosum mRNA for inorganic phosphate transporter, SPT1	0.023	2500587	SPLICEOSOME ASSOCIATED PROTEIN 49 spliceosome-associated protein SAP-49 - human >gi 536217	0.40
763	X98890		0.023	110072	proline-rich protein MP4 - mouse >gi 53182	0.18

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
764	X91212	L.esculentum mRNA for HD-ZIP protein	0.022	<NONE>	<NONE>	<NONE>
765	AC004498	Homo sapiens chromosome 5. P1 clone 1209C1 (LBNL H104), complete sequence [Homo sapiens]	0.022	<NONE>	<NONE>	<NONE>
766	U07083	Human prostatic acid phosphatase (ACPP) gene, exon 1	0.022	<NONE>	<NONE>	<NONE>
767	X98890	S.tuberosum mRNA for inorganic phosphate transporter. StPT1	0.022	<NONE>	<NONE>	<NONE>
768	X56488	L.esculentum LAT59 gene 5'flanking region. expressed during pollen maturation	0.022	<NONE>	<NONE>	<NONE>
769	M34651	Pseudorabies virus with upstream and downstream sequences.	0.022	<NONE>	<NONE>	<NONE>
770	X66727	P.taeda gene for protochlorophyllide reductase	0.022	3878517	(Z92806) K10G4.4 [Caenorhabditis elegans]	4.3
771	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA. complete cds	0.022	1854452	(D89501) similar to salivary proline-rich protein P-B [Homo sapiens]	4.3
772	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA. partial cds	0.022	3021699	(AB005298) BAI 2 [Homo sapiens]	0.64
773	X71932	H.sapiens XB gene for tenascin-X. intron 14	0.022	627059	liver stage antigen LSA-1 - Plasmodium falciparum >gi 9916 (X56203) liver stage antigen	0.058
774	X87369	C.perfringens nanH gene & ORF1.2.3 & 4	0.022	2062407	(U78975) poly(ADP-ribose) glycohydrolase [Bos taurus]	0.056

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
775	Y14971	Gallus gallus mRNA for K60 protein	0.022	134091	UI SMALL NUCLEAR RIBONUCLEOPROTEIN 70 KD (U1 SNRNP 70 KD) >gi 85864 pir S02016 U1 snRNP 70K protein - African clawed frog >gi 65179 (X12430) U1 70K [Xenopus laevis]	0.032
776	AF003133	Caenorhabditis elegans cosmid T21E3	0.022	1709997	DNA REPAIR PROTEIN RAD18 >gi 1150622 protein rad18 [Schizosaccharomyces pombe]	2e-08
777	AF003133	Caenorhabditis elegans cosmid T21E3	0.022	1709997	DNA REPAIR PROTEIN RAD18 >gi 1150622 protein rad18 [Schizosaccharomyces pombe]	2e-08
778	U57645	Human helix-loop-helix proteins Id-1 (ID-1) and Id-1' (ID-1) genes, complete cds	0.021	<NONE>	<NONE>	<NONE>
779	U67570	Methanococcus jannaschii section 112 of 150 of the complete genome	0.021	<NONE>	<NONE>	<NONE>
780	L01584	Trypanosoma cruzi calcium-binding protein (CUB2.8) gene, complete cds.	0.021	<NONE>	<NONE>	<NONE>
781	L04787	Borrelia hermsii outer membrane lipoprotein	0.021	<NONE>	<NONE>	<NONE>
782	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	0.021	<NONE>	<NONE>	<NONE>
783	L36890	Saccharomyces cerevisiae mitochondrion transfer RNA-Thr1 (tRNA-Thr) gene; transfer RNA-Val (tRNA-Val) gene; oxi2 gene, complete cds; ORF2 and origin of replication (ori5).	0.021	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
784	M76741	Homo sapiens biliary glycoprotein (BGP) gene, partial cds.	0.021	<NONE>	<NONE>	<NONE>
785	M87504	Tetrahymena thermophila histone H3 (HHT2) gene, complete cds	0.021	<NONE>	<NONE>	<NONE>
786	U94346	Human calpain-like protease (htra-3) mRNA, complete cds	0.021	<NONE>	<NONE>	<NONE>
787	L01584	Trypanosoma cruzi calcium-binding protein (CUB2.8) gene, complete cds.	0.021	<NONE>	<NONE>	<NONE>
788	U36530	Pongo pygmaeus C1 microsatellite, clone #1, from the tandemly repeated genes encoding U2 small nuclear RNA (RNU2 locus)	0.021	<NONE>	<NONE>	<NONE>
789	X03833	Human gene for interleukin 1 alpha (IL-1 alpha)	0.021	416974	EARLY TRANSCRIPTION FACTOR 70 KD SUBUNIT	8.9
790	U20806	Dictyostelium discoideum guanine nucleotide-binding protein alpha subunit 5 (G alpha 5) gene, complete cds.	0.021	1401211	(U58510) RNA helicase homolog [Chlorarachnion CCMP621]	8.8
791	Z59258	H.sapiens CpG DNA, clone 13d2, reverse read cpg13d2.rtlc	0.021	3121732	ACONITATE HYDRATASE (CITRATE HYDRO-LYASE) (ACONITASE) >gi 2183256 (AF002133) aconitase [Mycobacterium avium]	7.0
792	AF030692	Plasmodium falciparum strain 7G8 chloroquine resistance candidate protein (cg2) gene, complete cds	0.021	3024190	NINE PROTEIN >gi 2120251 pir S66581 hypothetical protein 56 - phage S2 >gi 1051114 (X92588) orf56; related to nin60 (ninE) of bacteriophage lambda	5.8
793	U67570	Methanococcus jannaschii section 112 of 150 of the complete genome	0.021	2341037	(AC000104) F19P19.17 [Arabidopsis thaliana]	4.0

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
794	D86566	Human DNA for NOTCH4, partial cds	0.021	1708619	NUCLEAR FACTOR NF-KAPPA-B P100 SUBUNIT (H2TF1) (ONCOGENE LYT-10) (LYT10) [CONTAINS: NUCLEAR FACTOR NF-KAPPA-B P52 SUBUNIT]	3.1
795	L11648	<i>Streptomyces coelicolor</i> sigma factor (rpoX) gene, complete cds.	0.021	79833	hypothetical 119.5K protein (uvrA region) - <i>Micrococcus luteus</i>	1.8
796	U95094	<i>Xenopus laevis</i> XL-INCENP (XL-INCENP) mRNA, complete cds	0.021	128000	NEUROENDOCRINE CONVERTASE 1 PRECURSOR (NEC 1) (PC1) (PROHORMONE CONVERTASE 1) propeptide processing protease [<i>Mus cookii</i>]	1.0
797	U30938	<i>Rattus norvegicus</i> microtubule-associated protein 2	0.021	468600	(X74416) beta-3 integrin [<i>Takifugu rubripes</i>]	1.0
798	D82364	Chicken mRNA for TSC-22 variant, complete cds, clone SLFEST52	0.021	693723	27 kda amelogenin (alternatively spliced)	0.61
799	U40041	<i>Gallus gallus</i> eHAND mRNA, complete cds	0.021	3449308	(AB011541) MEGF8 [<i>Homo sapiens</i>]	0.21
800	X71932	<i>H.sapiens</i> XB gene for tenascin-X, intron 14	0.021	627059	liver stage antigen LSA-1 - <i>Plasmodium falciparum</i> >gi 9916 (X56203) liver stage antigen	0.054
801	AF042333	<i>Oryza sativa</i> 24-methylene lophenol C24(1)methyltransferase mRNA, complete cds	0.021	854065	(X83413) U88 [Human herpesvirus 6]	0.014
802	L37380	Rat apical endosomal glycoprotein mRNA, complete cds.	0.021	3334377	TRANSMEMBRANE PROTEASE, SERINE 2	1e-05
803	AF003133	<i>Caenorhabditis elegans</i> cosmid T21E3	0.021	1709997	DNA REPAIR PROTEIN RAD18 >gi 1150622 protein rad18 [<i>Schizosaccharomyces pombe</i>]	3e-08

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Rabbit mRNA for				
804	X57689	calcium channel BI-2 (lambda CBP109 and CB101)	0.021	2959370	(AL022117) hypothetical protein	1e-10
805	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	0.021	1109830	(U41534) coded for by C. elegans cDNA CEES142F; Similar to helicases of SNF2/RAD54 family. [Caenorhabditis elegans]	5e-11
806	X77753	H.sapiens TROP-2 gene	0.021	1723657	HYPOTHETICAL 38.5 KD PROTEIN IN ERV1-GLS2 INTERGENIC REGION >gi 2132587 pir S64322 probable membrane protein YGR031w - yeast (Saccharomyces cerevisiae) >gi 1323010 gnl PID e243277 (Z72816) ORF YGR031w [Saccharomyces cerevisiae]	5e-11
807	X98890	S.tuberosum mRNA for inorganic phosphate transporter, StPT1	0.021	2137872	zinc finger protein PZF - mouse >gi 453376	2e-19
808	AF027173	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-A) mRNA, complete cds	0.020	<NONE>	<NONE>	<NONE>
809	AJ224935	Homo sapiens Promotor Region and PCK2 gene	0.020	<NONE>	<NONE>	<NONE>
810	U76524	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	0.020	<NONE>	<NONE>	<NONE>
811	X99941	A.thaliana GBF1 gene	0.020	<NONE>	<NONE>	<NONE>
812	X65138	M.musculus mRNA for tyrosine kinase > :: gb S57168 S57168 Sek=Eph-related receptor protein tyrosine kinase [mice. mRNA, 4242 nt]	0.020	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
813	L04787	Borrelia hermsii outer membrane lipoprotein	0.020	<NONE>	<NONE>	<NONE>
814	AJ223633	Enterococcus faecium genes encoding enterocin L50A and enterocin L50B plus 5' and 3' flanking regions	0.020	<NONE>	<NONE>	<NONE>
815	AB012106	Brassica rapa mRNA for SRK45, complete cds	0.020	<NONE>	<NONE>	<NONE>
816	AE001539	Helicobacter pylori, strain J99 section 100 of 132 of the complete genome	0.020	172292	(L11895) transmembrane protein [Saccharomyces cerevisiae]	8.4
817	AF074386	Sambucus nigra hevein-like protein mRNA, complete cds	0.020	94173	pol polyprotein - Chinese hamster intracisternal A-particle CHIAP34	8.0
818	M55264	Herpesvirus saimiri dihydrofolate reductase (DHFR) and snRNA (HSUR) genes, complete cds.	0.020	2924250	(Z98745) dJ29K1.2 [Homo sapiens]	6.5
819	AF052163	Homo sapiens clone 24456 mRNA sequence	0.020	1706288	D(4) DOPAMINE RECEPTOR (D(2C) DOPAMINE RECEPTOR) >gi 2119482 pir I49246 D4 dopamine receptor - mouse >gi 758427 (U19880) D4 dopamine receptor [Mus musculus] >gi 1095539 prf 2109259A dopamine D4 receptor [Mus musculus]	4.9
820	AF074387	Sambucus nigra hevein-like protein mRNA, complete cds	0.020	2113798	(Z83259) AmphiBrf38 [Branchiostoma floridae]	4.7
821	AF052163	Homo sapiens clone 24456 mRNA sequence	0.020	3874733	(Z67754) cDNA EST EMBL:T02354 comes from this gene: cDNA EST EMBL:D32698 comes from this gene: cDNA EST EMBL:D35411 comes from this gene	4.7

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
822	L11002	Rat ankyrin binding glycoprotein-1 related mRNA sequence.	0.020	552132	(K01664) Bkm-like protein [Drosophila melanogaster]	3.8
823	AE001539	Helicobacter pylori, strain J99 section 100 of 132 of the complete genome	0.020	172292	(L11895) transmembrane protein [Saccharomyces cerevisiae]	3.8
824	X98890	S.tuberosum mRNA for inorganic phosphate transporter, StPT1	0.020	3879798	(Z01120) similar to 11K Domain (2 domains); cDNA EST yk390b10.3 comes from this gene; cDNA EST EMBL:D71652 comes from this gene; cDNA EST yk275f8.3 comes from this gene; cDNA EST yk393b9.3 comes from this gene; cDNA EST yk37... >gi 3880220 gnl PID e1349842 yk390b10.3 comes from this gene; cDNA EST EMBL:D71652 comes from this gene; cDNA EST yk275f8.3 comes from this gene; cDNA EST yk393b9.3 comes from this gene; cDNA EST yk37...	1.3
825	U97519	Homo sapiens podocalyxin-like protein mRNA, complete cds	0.020	1345633	C1-TETRAHYDROFOLATE SYNTHASE, CYTOPLASMIC (C1-THF SYNTHASE) (METHYLENETETRAHYDROFOLATE DEHYDROGENASE / METHENYL TETRAHYDROFOLATE CYCLOHYDROLASE C1-tetrahydrofolate synthase [Rattus norvegicus]	0.066
826	AF003133	Caenorhabditis elegans cosmid T21E3	0.020	1709997	DNA REPAIR PROTEIN RAD18 >gi 1150622 protein rad18 [Schizosaccharomyces pombe]	2e-07
827	U32857	Saccharomyces cerevisiae VAR1 gene, mitochondrial gene encoding mitochondrial protein, 3' processing site, partial sequence	0.019	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					NEUROGENIC LOCUS	
828	AF027174	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-B) mRNA, complete cds	0.019	2506381	NOTCH HOMOLOG PROTEIN 4 PRECURSOR (TRANSFORMING PROTEIN INT-3) mammary gene mRNA, complete cds.], gene product [Mus musculus]	3.3
829	AF034099	Laccaria bicolor glyoxal malate synthase protein mRNA, complete cds	0.019	3880930	(AL021481) similar to Phosphoglucomutase and phosphomannomutase phosphoserine; cDNA EST EMBL:D36168 comes from this gene; cDNA EST EMBL:D70697 comes from this gene; cDNA EST yk373h9.5 comes from this gene; cDNA EST EMBL:T008...	6e-15
830	AF100694	Mus musculus Pontin52 mRNA, complete cds	0.018	<NONE>	<NONE>	<NONE>
831	U24578	Human RP1 and complement C4B precursor (C4B) genes, partial cds.	0.013	478673	proline-rich protein precursor - [kidney bean vulgaris]	3.1
832	U76523	Sambucus nigra lectin precursor mRNA, complete cds	0.011	<NONE>	<NONE>	<NONE>
833	U57649	Dibenzofuran-degrading bacterium DPO360 2,3-dihydroxybiphenyl 1,2-dioxygenase (bphC) gene, complete cds and 2-hydroxy-6-oxo-6-phenylhexa-2,4-dienoic acid hydrolase	0.011	<NONE>	<NONE>	<NONE>
834	X15642	Z.mays gene for phosphoenolpyruvate carboxylase	0.011	<NONE>	<NONE>	<NONE>
835	X51623	C.elegans collagen gene col-13	0.010	1695686	(D83706) pyruvate carboxylase [Bacillus stearothermophilus]	3.1
836	U83656	Rattus norvegicus NF-KB gene, promotor region	0.008	4240195	(AB020660) KIAA0853 protein [Homo sapiens]	10.0

232

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
837	AJ222657	Homo sapiens gene encoding retina-specific guanylyl cyclase	0.008	417704	POL POLYPROTEIN (ORF1A/1B) [CONTAINS: RNA-DIRECTED RNA POLYMERASE ; HELICASE; PROTEASE]	7.4
838	AB012106	Brassica rapa mRNA for SRK45, complete cds	0.008	544024	CHLORIDE CHANNEL PROTEIN, SKELETAL MUSCLE (CHLORIDE CHANNEL PROTEIN 1) (CLC-1) human >gi 397143 (Z25587) human CLC-1 muscle chloride channel [Homo sapiens] >gi 398161 (Z25884) human CLC-1 muscle chloride channel [Homo sapiens]	4.6
839	U76524	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	0.008	532468	(U13643) similar to reverse transcriptase; possible pseudogene [Caenorhabditis elegans]	3.8
840	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	0.008	4101160	(AF002589) cytochrome oxidase I [Austrofundulus limnaeus]	2.7
841	AF074385	Sambucus nigra hevein-like protein mRNA, complete cds	0.008	1711520	SRB-8/9 PROTEIN >gi 1334996	1.6
842	U48734	Human non-muscle alpha-actinin mRNA, complete cds	0.008	2829922	(AC002291) extensin [Arabidopsis thaliana]	0.11
843	U66669	Homo sapiens 3-hydroxyisobutyryl-coenzyme A hydrolase mRNA, complete cds	0.007	<NONE>	<NONE>	<NONE>
844	D16492	Mouse mRNA for P100 serine protease of Ra-reactive factor (RaRF), complete cds	0.007	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Human				
845	D90923	immunodeficiency virus type 1 proviral DNA for envelope glycoprotein, partial cds. isolate 03S	0.007	<NONE>	<NONE>	<NONE>
846	AB011087	Homo sapiens mRNA for KIAA0515 protein, partial cds	0.007	<NONE>	<NONE>	<NONE>
847	AE000688	Aquifex aeolicus section 20 of 109 of the complete genome	0.007	<NONE>	<NONE>	<NONE>
848	X63723	B.bovis WC1.1 mRNA	0.007	<NONE>	<NONE>	<NONE>
849	AF074386	Sambucus nigra hevein-like protein mRNA, complete cds	0.007	<NONE>	<NONE>	<NONE>
850	J00097	Human beta globin region Alu repetitive sequence type T.	0.007	<NONE>	<NONE>	<NONE>
851	D90923	Human immunodeficiency virus type 1 proviral DNA for envelope glycoprotein, partial cds. isolate 03S	0.007	<NONE>	<NONE>	<NONE>
852	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	0.007	<NONE>	<NONE>	<NONE>
853	X91618	T.castaneum hunchback gene	0.007	<NONE>	<NONE>	<NONE>
854	X03838	Rat nontranscribed spacer (NTS) downstream of 28S rRNA gene	0.007	<NONE>	<NONE>	<NONE>
855	M55049	Rattus norvegicus interleukin-2 receptor alpha chain (CD25) mRNA, complete cds.	0.007	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
856	Z64318	H.sapiens CpG DNA, clone 9e2, reverse read cpg9e2.r1a.	0.007	<NONE>	<NONE>	<NONE>
857	AF027173	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-A) mRNA, complete cds	0.007	<NONE>	<NONE>	<NONE>
858	AF027174	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-B) mRNA, complete cds	0.007	<NONE>	<NONE>	<NONE>
859	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	0.007	<NONE>	<NONE>	<NONE>
860	X95276	P.falciparum complete gene map of plastid-like DNA	0.007	<NONE>	<NONE>	<NONE>
861	U72396	Lycopersicon esculentum class II small heat shock protein Le-HSP17.6 mRNA, complete cds	0.007	<NONE>	<NONE>	<NONE>
862	AF100694	Mus musculus Pontin52 mRNA, complete cds	0.007	<NONE>	<NONE>	<NONE>
863	AB000383	Leucania seperata nuclear polyhedrosis virus DNA for p13, xe, envelope protein, complete cds	0.007	<NONE>	<NONE>	<NONE>
864	D86566	Human DNA for NOTCH4, partial cds	0.007	<NONE>	<NONE>	<NONE>
865	U76524	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	0.007	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
866	AF027173	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-A) mRNA, complete cds	0.007	3047072	(AF058825) No definition line found [Arabidopsis thaliana]	8.9
867	AF027174	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-B) mRNA, complete cds	0.007	975754	(U29359) SpaO [Salmonella enterica]	8.6
868	U76524	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	0.007	1213557	(U50199) coded for by C. elegans cDNA yk89e9.5; coded for by C. elegans cDNA cm7g5; coded for by C. elegans cDNA cm14b9; coded for by C. elegans cDNA yk52g5.5; coded for by C. elegans cDNA yk76e5.5; coded for by C. elegans cDNA yk131f11.5; c...	8.4
869	AB012106	Brassica rapa mRNA for SRK45, complete cds	0.007	2499568	PROTEIN-L-ISOASPARTATE(D-ASPARTATE) O-METHYLTRANSFERASE (PROTEIN-BETA-ASPARTATE METHYLTRANSFERASE) (PIMT) (PROTEIN L-ISOASPARTYL/D-ASPARTYL METHYLTRANSFERASE) methyltransferase [Drosophila melanogaster] >gi 1171337 melanogaster]	8.3
870	AF093268	Rattus norvegicus homer-1c mRNA, complete cds	0.007	4092077	(AF095353) toll-like receptor 4 mutant [Mus musculus]	6.2
871	AF074386	Sambucus nigra hevein-like protein mRNA, complete cds	0.007	151377	(M80653) tetraheme [Pseudomonas stutzeri]	6.2
872	L42319	Bos taurus (clone Sal3.8) tristetraprolin	0.007	2507337	TRANSCRIPTION TERMINATION FACTOR RHO	5.5

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
873	M59815	Human complement component C4A gene, exons 10 through 41.	0.007	3876769	(Z69637) Similarity to Human Prolyl 4-hydroxylase alpha subunit (SW:P4HA_HUMAN); cDNA EST yk219g12.5 comes from this gene; cDNA EST yk319d8.5 comes from this gene; cDNA EST yk339d11.5 comes from this gene; cDNA EST yk371c9.3...	5.3
874	X63723	B.bovis WC1.1 mRNA	0.007	2969893	(AJ001858) human SIM2 [Homo sapiens]	5.3
875	AB009864	Expression vector pME18S-FL3, complete sequence	0.007	2137618	p45 NF-E2 related factor 2 - mouse musculus]	5.1
876	U76524	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	0.007	2804497	(AF043705) contains similarity to C2H2-type zinc fingers	5.0
877	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	0.007	440298	(L27469) product of alternative splicing [Drosophila melanogaster]	4.7
878	X58869	Chicken mRNA for aldehyde dehydrogenase	0.007	1185062	(L75945) flagellar export protein [Borrelia burgdorferi]	4.1
879	AF027735	Nephila clavipes minor ampullate silk protein MiSp1 mRNA, partial cds	0.007	2394390	(AF017434) pmi-like gene product [Methylobacterium extorquens]	4.0
880	AF105228	Bos taurus tuftelin mRNA, complete cds	0.007	3036802	(AL022373) putative protein	3.9
881	AF100694	Mus musculus Pontin52 mRNA, complete cds	0.007	2500814	HYPOTHETICAL 60.2 KD PROTEIN T27F2.1 IN CHROMOSOME V >gi 3880311 gnl PID e1349855 BX42 (SW:BX42_DROME); cDNA EST EMBL:C07233 comes from this gene; cDNA EST EMBL:C08532 comes from this gene; cDNA EST yk501h10.3 comes from this gene; cDNA EST yk501f1.3...	3.8

237

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
882	X93567	L.major mRNA for beta-tubulin (1404bp)	0.007	2317862	(U78289) tyactone synthase modules 4 & 5 [Streptomyces fradiae]	3.0
883	AB012106	Brassica rapa mRNA for SRK45, complete cds	0.007	3881103	(AL032646) predicted using Genefinder; cDNA EST EMBL:D76407 comes from this gene; cDNA EST EMBL:C08999 comes from this gene; cDNA EST yk199b12.5 comes from this gene; cDNA EST yk282a4.5 comes from this gene; cDNA EST EMBL:C0...	2.7
884	AF041056	Homo sapiens WSCR4 gene, exons 3 and 4	0.007	135817	THROMBIN RECEPTOR PRECURSOR-human >gi 339677 (M62424) thrombin receptor [Homo sapiens]	2.2
885	AF093268	Rattus norvegicus homer-1c mRNA, complete cds	0.007	1723518	HYPOTHETICAL 32.2 KD PROTEIN C22E12.04 IN CHROMOSOME I >gi 1220279 (Z70043) unknown	2.1
886	M74798	Hevea brasiliensis 3-hydroxy-3-methylglutaryl-coenzyme A reductase gene, 3' end.	0.007	1001282	(D64003) polyA polymerase	1.9
887	Z62997	H.sapiens CpG DNA, clone 76g11, reverse read cpg76g11.rta.	0.007	1176532	HYPOTHETICAL 111.9 KD PROTEIN C34E10.8 IN CHROMOSOME III >gi 500731 (U10402) weakly similar to protein C kinase substrate [Caenorhabditis	1.8
888	AF074386	Sambucus nigra hevein-like protein mRNA, complete cds	0.007	2498317	DVA-1 POLYPROTEIN PRECURSOR nematode polyprotein antigen precursor [Dictyocaulus viviparus] >gi 1585421 prf 2124414A polyprotein antigen/allergen [Dictyocaulus viviparus]	1.2
889	L29426	Synechocystis species (strain PCC 6803) drgA gene, complete cds.	0.007	3882275	(AB018320) KIAA0777 protein [Homo sapiens]	1.1

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
890	D83329	Mus musculus DNA for prostaglandin D2 synthase, complete cds	0.007	1001741	(D64004) hypothetical protein	0.97
891	AB012106	Brassica rapa mRNA for SRK45, complete cds	0.007	1723928	HYPOTHETICAL 11.6 KD PROTEIN IN NUT1-ARO2 INTERGENIC REGION PRECURSOR YGL149w - yeast (Saccharomyces	0.94
892	U76524	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	0.007	121452	GLUTENIN, HIGH MOLECULAR WEIGHT SUBUNIT 12 PRECURSOR >gi 82606 pir A24266 glutenin high molecular weight chain 12 precursor - wheat >gi 21779	0.79
893	AF027173	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-A) mRNA, complete cds	0.007	927287	(U30294) ORF2 [Prevotella ruminicola]	0.35
894	Y11918	H.sapiens IMAGE cDNA clone 26881	0.007	1055188	(U40061) contains similarity to transmembrane domains like those found in sugar transporter proteins	0.26
895	L36827	Mus Musculus alphaA-crystallin-binding protein I	0.007	4063019	(AF083061) ABC transporter TliF [Pseudomonas fluorescens]	0.21
896	L36827	Mus Musculus alphaA-crystallin-binding protein I	0.007	4063019	(AF083061) ABC transporter TliF [Pseudomonas fluorescens]	0.20
897	Z65719	H.sapiens CpG DNA, clone 54c10, reverse read cpg54c10.rtl.a	0.007	1097307	HIC-1 gene [Homo sapiens]	0.20
898	AF064029	Helianthus tuberosus lectin 1 mRNA, complete cds	0.007	1174915	UTROPHIN (DYSTROPHIN-RELATED PROTEIN 1) (DRP1) (DRP) >gi 284488 pir S28381 utrophin protein) [Homo sapiens]	0.002
899	AF051730	Mus musculus cathepsin S (CatS) gene, exon 6	0.007	1707017	(U78721) RNA helicase isolog [Arabidopsis thaliana]	0.001

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Oryctolagus				
900	U62398	cuniculus gp42/basigin/OX-47/HT7 mRNA, complete cds.	0.007	2370494	(Z98944) hypothetical protein	2e-04
901	X76341	M.musculus glutathione reductase mRNA.	0.007	3513303	(AC005594) R26984_1 [Homo sapiens]	8e-07
902	M26215	Rat (lambda 20B0.5) M-type 6-phosphofructo-2-kinase/fructose-2, 6-bisphosphatase	0.007	3036809	(AL022373) putative protein	6e-15
903	AB007902	Homo sapiens KIAA0442 mRNA, partial cds	0.007	2662165	(AB007902) HH0712 cDNA clone for KIAA0442 has a 574-bp insertion at position 1474 of the sequence of KIAA0442. [Homo sapiens]	2e-17
904	U93364	Lactococcus lactis cremoris plasmid pNZ4000 insertion sequence IS982 putative transposase gene and eps gene cluster (epsRXABCDEFGH IJKL), complete cds	0.007	2731377	(U28739) similar to alcohol dehydrogenase/ribitol dehydrogenase [Caenorhabditis elegans]	1e-31
905	AF093268	Rattus norvegicus homer-1c mRNA, complete cds	0.006	<NONE>	<NONE>	<NONE>
906	AF100694	Mus musculus Pontin52 mRNA, complete cds	0.006	<NONE>	<NONE>	<NONE>
907	AF074386	Sambucus nigra hevein-like protein mRNA, complete cds	0.006	<NONE>	<NONE>	<NONE>
908	AF027174	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-B) mRNA, complete cds	0.006	<NONE>	<NONE>	<NONE>
909	AJ005813	Arabidopsis thaliana mRNA for neoxanthin cleavage enzyme	0.006	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
910	AF027174	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-B) mRNA, complete cds	0.006	<NONE>	<NONE>	<NONE>
911	AF093268	Rattus norvegicus homer-1c mRNA, complete cds	0.006	<NONE>	<NONE>	<NONE>
912	AF093268	Rattus norvegicus homer-1c mRNA, complete cds	0.006	<NONE>	<NONE>	<NONE>
913	AB012106	Brassica rapa mRNA for SRK45, complete cds	0.006	<NONE>	<NONE>	<NONE>
914	AF064029	Helianthus tuberosus lectin 1 mRNA, complete cds	0.006	<NONE>	<NONE>	<NONE>
915	AF100694	Mus musculus Pontin52 mRNA, complete cds	0.006	<NONE>	<NONE>	<NONE>
916	AF093268	Rattus norvegicus homer-1c mRNA, complete cds	0.006	4049856	(AF063866) ORF MSV064 hypothetical protein [Melanoplus sanguinipes entomopoxvirus]	9.6
917	AF100694	Mus musculus Pontin52 mRNA, complete cds	0.006	3880536	(Z82070) predicted using Genefinder; similar to Lectin C-type domain short and long forms (2 domains); cDNA EST EMBL:C10633 comes from this gene; cDNA EST EMBL:C12424 comes from this gene; cDNA EST yk191e7.3 comes from this ...	7.9
918	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	0.006	3877761	(Z81552) F56G4.1 [Caenorhabditis elegans] >gi 3878615 gnl PID e1348240 (Z83118) F56G4.1	7.5
919	X80289	H.sapiens PTPL1 mRNA for protein tyrosine phosphatase	0.006	1168791	CATHEPSIN E PRECURSOR precursor - rabbit >gi 402729 (L08418) procathepsin E	7.4

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
920	AF074386	Sambucus nigra hevein-like protein mRNA, complete cds	0.006	1346371	DIACYLGLYCEROL KINASE, BETA DIACYLGLYCEROL KINASE). >gi 477059 pir A47744 diacylglycerol kinase (EC 2.7.1.107) beta - rat 90kDa-diacylglycerol kinase [Rattus	5.5
921	U72396	Lycopersicon esculentum class II small heat shock protein Le-HSP17.6 mRNA, complete cds	0.006	2196567	(D88588) lipoprotein [Escherichia coli]	4.3
922	AF074387	Sambucus nigra hevein-like protein mRNA, complete cds	0.006	2113798	(Z83259) AmphiBrf38 [Branchiostoma floridae]	4.3
923	AB012106	Brassica rapa mRNA for SRK45, complete cds	0.006	1388166	(U58282) Bowel [Drosophila melanogaster]	4.3
924	AF074386	Sambucus nigra hevein-like protein mRNA, complete cds	0.006	2496785	HYPOTHETICAL 20.1 KD PROTEIN Y4YS	4.2
925	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	0.006	416592	A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR >gi 101170 pir A41258 a-agglutinin core protein AGA1 - yeast (Saccharomyces cerevisiae)	2.7
926	AF064029	Helianthus tuberosus lectin 1 mRNA, complete cds	0.006	416592	A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR >gi 101170 pir A41258 a-agglutinin core protein AGA1 - yeast (Saccharomyces cerevisiae)	2.5
927	AJ005813	Arabidopsis thaliana mRNA for neoxanthin cleavage enzyme	0.006	3258584	(U41263) The 3' UTR of this gene overlaps the 3' UTR of T19D12.6(confirmed by EST hits) [Caenorhabditis elegans]	2.0
928	U33949	Human Down Syndrome region of chromosome 21. genomic sequence. clone A12H1-1A6.	0.006	3850997	(AF067150) beta-hydroxyacyl-ACP dehydratase precursor	1.9

242

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1175	AF027173	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-A) mRNA, complete cds	2e-04	<NONE>	<NONE>	<NONE>
1176	Y09232	H.sapiens fertilin alpha pseudogene	2e-04	<NONE>	<NONE>	<NONE>
1177	AJ005813	Arabidopsis thaliana mRNA for neoxanthin cleavage enzyme	2e-04	<NONE>	<NONE>	<NONE>
1178	AF100694	Mus musculus Pontin52 mRNA, complete cds	2e-04	<NONE>	<NONE>	<NONE>
1179	AF072847	Homo sapiens putative swelling-activated chloride channel (CLNS1A) gene, intron 6	2e-04	<NONE>	<NONE>	<NONE>
1180	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	2e-04	<NONE>	<NONE>	<NONE>
1181	U76524	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	2e-04	<NONE>	<NONE>	<NONE>
1182	AF027173	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-A) mRNA, complete cds	2e-04	1213557	(U50199) coded for by C. elegans cDNA yk89e9.5; coded for by C. elegans cDNA cm7g5; coded for by C. elegans cDNA cm14b9; coded for by C. elegans cDNA yk52g5.5; coded for by C. elegans cDNA yk76e5.5; coded for by C. elegans cDNA yk131f11.5; c...	8.4

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1183	AF090115	Lycopersicon esculentum cytosolic class II small heat shock protein HCT2 (HSP17.4) mRNA, complete cds	2e-04	729008	EPITHELIAL DISCOIDIN DOMAIN RECEPTOR 1 PRECURSOR (TYROSINE-PROTEIN KINASE CAK) (CELL ADHESION KINASE) (TYROSINE KINASE DDR) (DISCOIDIN RECEPTOR TYROSINE KINASE) (TRK E) (PROTEIN-TYROSINE KINASE RTK 6) sapiens]	8.3
1184	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	2e-04	2507582	HYPOTHETICAL 138.1 KD PROTEIN IN MOLR-BGLX INTERGENIC REGION >gi 1788436 (AE000300) putative regulator [Escherichia coli]	7.8
1185	AF074386	Sambucus nigra hevein-like protein mRNA, complete cds	2e-04	1085500	collagen alpha 1(IX) chain - mouse musculus] >gi 744962 prf 2015346A collagen: SUBUNIT=alpha1:ISO TYPE=EX [Mus musculus]	7.8
1186	AF027173	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-A) mRNA, complete cds	2e-04	2623967	(Y13942) GTN Reductase [Agrobacterium radiobacter]	7.4
1187	AJ005813	Arabidopsis thaliana mRNA for neoxanthin cleavage enzyme	2e-04	2497316	ADVANCED GLYCOSYLATION END PRODUCT-SPECIFIC RECEPTOR PRECURSOR (RECEPTOR FOR ADVANCED GLYCOSYLATION END PRODUCTS) products receptor precursor - bovine >gi 163651 (M91212) receptor for advanced glycosylation end products [Bos taurus]	5.3
1188	AF027174	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-B) mRNA, complete cds	2e-04	1001710	(D64004) hypothetical protein	3.5

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1189	AJ005813	Arabidopsis thaliana mRNA for neoxanthin cleavage enzyme	2e-04	3258584	(U41263) The 3' UTR of this gene overlaps the 3' UTR of T19D12.6(confirmed by EST hits) [Caenorhabditis elegans]	2.1
1190	AF027173	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-A) mRNA, complete cds	2e-04	2736338	(AF038623) contains similarity to RNA recognition motifs	0.89
1191	U72396	Lycopersicon esculentum class II small heat shock protein Le-HSP17.6 mRNA, complete cds	2e-04	2196567	(D88588) lipoprotein [Escherichia coli]	0.69
1192	AF090115	Lycopersicon esculentum cytosolic class II small heat shock protein HCT2 (HSP17.4) mRNA, complete cds	2e-04	3319874	(AJ006096) F-spondin [Branchiostoma floridae]	5e-04
1193	L26049	Chlamydomonas reinhardtii dynein heavy chain alpha (ODA11) gene, exons 2-15, and partial cds.	2e-04	3876775	(Z81077) predicted using Genefinder: Similarity to Yeast protein 8248 (TR:G587531)	2e-09
1194	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-04	<NONE>	<NONE>	<NONE>
1195	AF064029	Helianthus tuberosus lectin I mRNA, complete cds	1e-04	<NONE>	<NONE>	<NONE>
1196	L34219	Homo sapiens retinaldehyde-binding protein (CRALBP) gene, complete cds.	1e-04	<NONE>	<NONE>	<NONE>
1197	X51890	Rhesus monkey interleukin-3 gene	1e-04	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Plasmodium				
1198	AE001421	falciparum chromosome 2, section 58 of 73 of the complete sequence	1e-04	<NONE>	<NONE>	<NONE>
1199	AF090115	Lycopersicon esculentum cytosolic class II small heat shock protein HCT2 (HSP17.4) mRNA, complete cds	1e-04	<NONE>	<NONE>	<NONE>
1200	AF027174	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-B) mRNA, complete cds	1e-04	2576287	(Y15086) HepC protein [Cylindrotheca fusiformis]	4.7
1201	AJ005813	Arabidopsis thaliana mRNA for neoxanthin cleavage enzyme	1e-04	3395673	(AB016623) RWC-3 [Oryza sativa]	0.14
1202	AF038035	Homo sapiens BRCA1-associated RING domain protein (BARD1) gene, exons 2 and 3	9e-05	<NONE>	<NONE>	<NONE>
1203	AJ005813	Arabidopsis thaliana mRNA for neoxanthin cleavage enzyme	9e-05	<NONE>	<NONE>	<NONE>
1204	AB012106	Brassica rapa mRNA for SRK45, complete cds	9e-05	<NONE>	<NONE>	<NONE>
1205	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	9e-05	<NONE>	<NONE>	<NONE>
1206	AF034099	Laccaria bicolor glyoxal malate synthase protein mRNA, complete cds	9e-05	1351553	HYPOTHETICAL LIPOPROTEIN MG348 PRECURSOR >gi 1361668 pir E64238 hypothetical protein MG348 - Mycoplasma genitalium (SGC3) >gi 3844931	8.8

246

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1207	D50006	Human DNA for alpha-platelet-derived growth factor receptor, exon 6-10	9e-05	3063639	(AF056494) NADH dehydrogenase subunit 5 [Panorpa japonica]	5.1
1208	U50423	Human Down Syndrome region of chromosome 21, clone A41B8-1B7.	9e-05	124273	INHIBIN ALPHA CHAIN PRECURSOR bovine >gi163195 (M13273) inhibin A subunit [Bos taurus]	3.0
1209	AJ005813	Arabidopsis thaliana mRNA for neoxanthin cleavage enzyme	9e-05	4007782	(X72850) 2,4-dihydroxybenzoate monooxygenase [Sphingomonas sp.]	2.3
1210	AC005276	Homo sapiens clone fragment UWGC:gap3 from 7q31.3, complete sequence [Homo sapiens]	9e-05	1492075	(U60315) MC132L [Molluscum contagiosum virus subtype 1]	1.0
1211	AF100694	Mus musculus Pontin52 mRNA, complete cds	9e-05	2887423	(AB007884) KIAA0424 [Homo sapiens]	2e-10
1212	X77772	C.fuscus gamma-M2-1 crystallin mRNA.	9e-05	2072425	(U83115) non-lens beta gamma-crystallin like protein [Homo sapiens]	7e-25
1213	AB012106	Brassica rapa mRNA for SRK45, complete cds	8e-05	<NONE>	<NONE>	<NONE>
1214	L06178	Apis mellifera ligustica complete mitochondrial genome	8e-05	<NONE>	<NONE>	<NONE>
1215	AB012106	Brassica rapa mRNA for SRK45, complete cds	8e-05	<NONE>	<NONE>	<NONE>
1216	U76524	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	8e-05	<NONE>	<NONE>	<NONE>
1217	L06178	Apis mellifera ligustica complete mitochondrial genome	8e-05	<NONE>	<NONE>	<NONE>
1218	AB012106	Brassica rapa mRNA for SRK45, complete cds	8e-05	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Mus musculus				
1219	AF100694	Pontin52 mRNA, complete cds	8e-05	<NONE>	<NONE>	<NONE>
1220	AB012106	Brassica rapa mRNA for SRK45, complete cds	8e-05	<NONE>	<NONE>	<NONE>
1221	AB012106	Brassica rapa mRNA for SRK45, complete cds	8e-05	1722841	WNT-11 PROTEIN PRECURSOR (XWNT-11) clawed frog >gi 439108 (L23542) maternal protein	9.9
1222	AF027174	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-B) mRNA, complete cds	8e-05	1205991	(U35637) nebulin [Homo sapiens]	9.6
1223	AF024605	Homo sapiens serine protease-like protease Sequence 2 from patent US 5736377	8e-05	3242783	(AF055354) respiratory burst oxidase protein B	8.6
1224	Y13148	Rattus norvegicus mRNA for PAC608 gene	8e-05	2314243	(AE000616) alpha-ketoglutarate permease (kgtP)	8.1
1225	AJ005813	Arabidopsis thaliana mRNA for neoxanthin cleavage enzyme	8e-05	1170586	RAS GTPASE-ACTIVATING-LIKE PROTEIN IQGAP1 (P195) (K1AA0051) >gi 627594 pir A54854 Ras GTPase activating-related protein - human sapiens] >gi 536844 (L33075) ras GTPase-activating-like protein [Homo sapiens]	7.8
1226	AF027173	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-A) mRNA, complete cds	8e-05	464239	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4 >gi 1085185 pir S52968 NADH dehydrogenase chain 4 - honeybee mitochondrion (SGC4) >gi 552446 (L06178) NADH dehydrogenase subunit 4 [Apis mellifera ligustica]	3.5
1227	AF100694	Mus musculus Pontin52 mRNA, complete cds	8e-05	544353	F-SPONDIN PRECURSOR	3.5

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1228	U76524	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	8e-05	483243	apolipoprotein B-100 - chicken (fragment)	3.4
1229	AF093268	Rattus norvegicus homer-1c mRNA, complete cds	8e-05	91207	proline-rich protein - mouse (fragment) [musculus]	2.2
1230	AF027173	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-A) mRNA, complete cds	8e-05	2499181	ZONADHESIN PRECURSOR >gil1066466	2.2
1231	AF027173	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-A) mRNA, complete cds	8e-05	2499181	ZONADHESIN PRECURSOR >gil1066466	1.9
1232	AB012106	Brassica rapa mRNA for SRK45, complete cds	8e-05	2833647	(AF027972) flagelliform silk protein [Nephila clavipes]	1.6
1233	AF093268	Rattus norvegicus homer-1c mRNA, complete cds	8e-05	1163063	(Z49821) MYO2 [Saccharomyces cerevisiae]	0.90
1234	AF027174	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-B) mRNA, complete cds	8e-05	1653488	(D90914) hypothetical protein	0.30
1235	M26510	Chicken nonmuscle myosin heavy chain (MHC) gene, complete cds.	8e-05	112159	plectin - rat	0.003
1236	U56402	Human chromatin structural protein homolog	8e-05	2088823	(AF003384) weak similarity to the peptidase family A2	1e-13
1237	AF100694	Mus musculus Pontin52 mRNA, complete cds	8e-05	437181	(U02289) GTPase-activating protein [Caenorhabditis elegans]	2e-17
1238	AF100694	Mus musculus Pontin52 mRNA, complete cds	8e-05	465983	HYPOTHETICAL 80.8 KD PROTEIN ZC21.4 IN CHROMOSOME III	8e-27

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1239	AF090115	Lycopersicon esculentum cytosolic class II small heat shock protein HCT2 (HSP17.4) mRNA, complete cds	7e-05	<NONE>	<NONE>	<NONE>
1240	U83656	Rattus norvegicus NF-KB gene, promotor region	7e-05	3880858	(AL031633) predicted using Genefinder; cDNA EST yk304f12.5 comes from this gene [Caenorhabditis elegans]	9.3
1241	AF074387	Sambucus nigra hevein-like protein mRNA, complete cds	7e-05	3080538	(AL022600) hypothetical protein	9.2
1242	X89398	H.sapiens ung gene for uracil DNA-glycosylase	7e-05	549700	HYPOTHETICAL 23.7 KD PROTEIN IN MDH1-VMA5 INTERGENIC REGION >gi 539182 pir S37908 hypothetical protein YKL083w - yeast (Saccharomyces cerevisiae) >gi 486120 (Z280S2) ORF YKL083w	1.8
1243	M83753	Bovine follicle stimulating hormone-beta subunit gene, complete cds.	7e-05	2398621	(AJ000342) DMBT1 protein, 5.8 kb transcript [Homo sapiens]	1.8
1244	M80829	Rat troponin T cardiac isoform gene, complete cds	5e-05	854065	(X83413) U88 [Human herpesvirus 6]	2e-08
1245	AF074387	Sambucus nigra hevein-like protein mRNA, complete cds	4e-05	120240	FLAGELLIN B2 PRECURSOR Methanococcus voltae >gi 150063 (M72148) flagellin	5.2
1246	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	3e-05	<NONE>	<NONE>	<NONE>
1247	U76524	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	3e-05	<NONE>	<NONE>	<NONE>
1248	AF074386	Sambucus nigra hevein-like protein mRNA, complete cds	3e-05	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		<i>Rattus norvegicus</i>				
1249	AF093268	homer-1c mRNA, complete cds	3e-05	<NONE>	<NONE>	<NONE>
1250	AB012106	<i>Brassica rapa</i> mRNA for SRK45, complete cds	3e-05	2773226	(AF039716) Similar to protein kinase [<i>Caenorhabditis elegans</i>]	6.7
1251	AF100694	<i>Mus musculus</i> Pontin52 mRNA, complete cds	3e-05	2072961	(U93568) putative p150 [<i>Homo sapiens</i>]	5.6
1252	U72396	<i>Lycopersicon esculentum</i> class II small heat shock protein Le-HSP17.6 mRNA, complete cds	3e-05	121855	EXOGLUCANASE II PRECURSOR cellulose 1,4-beta cellobiosidase (EC 3.2.1.91) II precursor - fungus (<i>Trichoderma reesei</i>) 1,4-beta-cellobiosidase (EC 3.2.1.91) II - fungus cellobiohydrolase II [<i>Trichoderma reesei</i>]	4.6
1253	U76524	<i>Sambucus nigra</i> ribosome inactivating protein precursor mRNA, complete cds	3e-05	3880516	(AL021572) similar to CTP SYNTHASE (EC 6.3.4.2) (UTP-AMMONIA LIGASE) (CTP SYNTHETASE)	3.3
1254	M88299	Mouse brain-1 POU-domain protein, complete cds	3e-05	1947048	(U66102) intimin [<i>Escherichia coli</i>]	3.0
1255	U95098	<i>Xenopus laevis</i> mitotic phosphoprotein 44 mRNA, partial cds	3e-05	3122872	CELL-CYCLE NUCLEAR AUTOANTIGEN SG2NA (S/G2 NUCLEAR ANTIGEN) >gi 1082650 pir JC2522 nuclear autoantigen - human >gi 805095 (U17989) GS2NA	2.8
1256	U76524	<i>Sambucus nigra</i> ribosome inactivating protein precursor mRNA, complete cds	3e-05	1352145	CYTOCHROME C OXIDASE POLYPEPTIDE I chain I - <i>Thermus aquaticus</i> >gi 155083 (M84341) cytochrome c oxidase subunits precursor [<i>Thermus thermophilus</i>]	2.6
1257	U72396	<i>Lycopersicon esculentum</i> class II small heat shock protein Le-HSP17.6 mRNA, complete cds	3e-05	2811015	SEGMENTATION POLARITY PROTEIN ENGRAILED >gi 2076747 (U42429) engrailed [<i>Anopheles gambiae</i>] >gi 2148918 (U42214) engrailed [<i>Anopheles gambiae</i>]	2.0

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1258	AF027174	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-B) mRNA, complete cds	3e-05	1657752	(U62325) FE65-like protein [Homo sapiens]	1.7
1259	AF100694	Mus musculus Pontin52 mRNA, complete cds	3e-05	2072961	(U93568) putative p150 [Homo sapiens]	1.5
1260	U76523	Sambucus nigra lectin precursor mRNA, complete cds	3e-05	1352145	CYTOCHROME C OXIDASE POLYPEPTIDE I chain I - Thermus aquaticus >gi 155083 (M84341) cytochrome c oxidase subunits precursor [Thermus thermophilus]	1.1
1261	X91890	H.sapiens regulatory region of HOXA7 gene	3e-05	111013	Sxr (Bkm-homolog) sex-determining region protein - mouse	1.0
1262	L36936	Homo sapiens metase gene, partial cds.	3e-05	1944352	(D84239) IgG Fc binding protein [Homo sapiens]	0.99
1263	AB012105	Brassica rapa mRNA for SLG45, complete cds	3e-05	417782	SMP2 PROTEIN >gi 320853 pir S30911 SMP2 protein - yeast (Saccharomyces cerevisiae) gene [Saccharomyces cerevisiae]	0.89
1264	U76524	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	3e-05	1708501	INTEGRIN ALPHA CHAIN-LIKE PROTEIN alpha Int1p [Candida albicans]	0.39
1265	AF090115	Lycopersicon esculentum cytosolic class II small heat shock protein HCT2 (HSP17.4) mRNA, complete cds	3e-05	1587031	cis-Golgi matrix protein GM130 [Rattus norvegicus]	0.20
1266	Z81014	Human DNA sequence from cosmid U65A4, between markers DXS366 and DXS87 on chromosome X	3e-05	2072964	(U93569) putative p150 [Homo sapiens]	0.049

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1267	Z96668	H.sapiens telomeric DNA sequence, clone 7PTEL001, read 7PTELOO001.seq	3e-05	542429	glycosylated and myristilated smaller surface antigen - Plasmodium falciparum >gi 836640 (X76298) glycosylated and myristilated smaller surface antigen gallus] >gi 1092178 prf 2023165B surface antigen	0.029
1268	AB012105	Brassica rapa mRNA for SLG45, complete cds	3e-05	3879121	(Z70310) predicted using Genefinder; Similarity to Mouse ankyrin (PIR Acc. No. S37771); cDNA EST EMBL:T01923 comes from this gene; cDNA EST EMBL:D32335 comes from this gene; cDNA EST EMBL:D32723 comes from this gene; cDNA ES... Genefinder; Similarity to Mouse ankyrin (PIR Acc. No. S37771); cDNA EST EMBL:T01923 comes from this gene; cDNA EST EMBL:D32335 comes from this gene; cDNA EST EMBL:D32723 comes from this gene; cDNA ES...	2e-13
1269	AF074385	Sambucus nigra hevein-like protein mRNA, complete cds	3e-05	2497677	ZYXIN (ZYXIN 2) sapiens] >gi 1545954 gnl PID e223417 (X95735) zyxin	2e-23
1270	AF027174	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-B) mRNA, complete cds	1e-05	<NONE>	<NONE>	<NONE>
1271	X16318	Canine mRNA for signal recognition particle 54k protein	1e-05	3122612	PITUITARY HOMEODOMAIN 3 (HOMEODOMAIN PROTEIN PITX3) >gi 2645427 (AF005772) homeobox protein Pitx3 [Mus musculus]	4.4
1272	AB012105	Brassica rapa mRNA for SLG45, complete cds	1e-05	1652458	(D90905) DNA mismatch repair protein MutL [Synechocystis sp.]	0.62

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1273	U57843	Human phosphatidylinositol 3-kinase delta catalytic subunit mRNA, complete cds	1e-05	475909	(X67098) ORF1A [Homo sapiens]	0.22
1274	Z96569	H.sapiens telomeric DNA sequence, clone 2QTELO54, read 2QTELOO054.seq	1e-05	2137043	unknown protein - rabbit (fragment) cuniculus]	0.005
1275	AE000810	Methanobacterium thermoautotrophicum from bases 172512 to 182957 (section 16 of 148) of the complete genome	1e-05	3877579	(Z62217) similarity to mouse kinensin-like protein KIF4 (SW:P33174); cDNA EST EMBL:D27320 comes from this gene; cDNA EST EMBL:D27322 comes from this gene; cDNA EST EMBL:D27321 comes from this gene; cDNA EST EMBL:D35764 comes... Mouse kinensin-like protein KIF4 (SW:P33174); cDNA EST EMBL:D27320 comes from this gene; cDNA EST EMBL:D27322 comes from this gene; cDNA EST EMBL:D27321 comes from this gene; cDNA EST EMBL:D35764 comes...	6e-27
1276	AB012113	Homo sapiens gene for CC chemokine PARC precursor, complete cds	9e-06	<NONE>	<NONE>	<NONE>
1277	AC005830	Homo sapiens Xp22-154-155 BAC GSHB-52411 (Genome Systems Human BAC Library), complete sequence [Homo sapiens]	9e-06	<NONE>	<NONE>	<NONE>
1278	D86245	Human MHC (HLA) DRB intron 1 DNA, partial sequence	9e-06	1051253	(U37531) mucin apoprotein [Mus musculus]	1.3
1279	D79998	Human mRNA for KIAA0176 gene, partial cds	9e-06	2833253	HYPOTHETICAL PROTEIN KIAA0176 sapiens]	4e-06

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					(Z69635) Similarity to Yeast	
1280	U10246	Toxoplasma gondii RH uracil phosphoribosyl transferase gene. complete cds.	9e-06	3876090	uridine kinase (SW:URK1_YEAST); cDNA EST EMBL:Z14695 comes from this gene; cDNA EST CEMSE17F comes from this gene; cDNA EST EMBL:D67355 comes from this gene; cDNA EST yk209h1.5 comes from this ge...	7e-33
1281	U10246	Toxoplasma gondii RH uracil phosphoribosyl transferase gene. complete cds.	9e-06	3876090	(Z69635) Similarity to Yeast uridine kinase (SW:URK1_YEAST); cDNA EST EMBL:Z14695 comes from this gene; cDNA EST CEMSE17F comes from this gene; cDNA EST EMBL:D67355 comes from this gene; cDNA EST yk209h1.5 comes from this ge...	7e-34
1282	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	8e-06	<NONE>	<NONE>	<NONE>
1283	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	8e-06	<NONE>	<NONE>	<NONE>
1284	U66340	Human Rh blood group C antigen (RHCE) gene, exon 2, partial cds	8e-06	1707155	(U80837) F07E5.6 gene product [Caenorhabditis elegans]	9.6
1285	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	7e-06	<NONE>	<NONE>	<NONE>
1286	M29930	Human insulin receptor (allele 2) gene, exons 14, 15, 16 and 17.	4e-06	<NONE>	<NONE>	<NONE>
1287	L42103	Homo sapiens (subclone 5_d3 from P1 H25) DNA sequence.	3e-06	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Mus musculus				
1288	AF012244	cerberus-like (Cer-1) gene, complete cds	3e-06	<NONE>	<NONE>	<NONE>
1289	Z69366	Human DNA sequence from cosmid L96F8, Huntington's Disease Region, chromosome 4p16.3 contains EST.	3e-06	<NONE>	<NONE>	<NONE>
1290	Z69366	Human DNA sequence from cosmid L96F8, Huntington's Disease Region, chromosome 4p16.3 contains EST.	3e-06	<NONE>	<NONE>	<NONE>
1291	X85232	H.sapiens chromosome 3 sequences	3e-06	<NONE>	<NONE>	<NONE>
1292	M32674	Human platelet glycoprotein IIIa, exons 7, 8 and 9.	3e-06	<NONE>	<NONE>	<NONE>
1293	D16879	Human HepG2 3' region cDNA, clone hmd2a01	3e-06	998296	(U33484) ependymin [Hemiodus sp.]	5.6
1294	U18614	Lagothrix lagotricha interphotoreceptor retinoid-binding protein (IRBP) gene, intron 1, complete sequence	3e-06	1613846	(U71440) polyprotein [Rice tungro spherical virus]	5.0
1295	AF090115	Lycopersicon esculentum cytosolic class II small heat shock protein HCT2 (HSP17.4) mRNA, complete cds	3e-06	1477646	(U53204) plectin [Homo sapiens] >gi 1477651 (U63610) plectin [Homo sapiens]	4.0
1296	AF016898	Homo sapiens B-ATF gene, complete cds	3e-06	1085177	reverse transcriptase - fruit fly reverse transcriptase [Drosophila yakuba]	3.0
1297	AB018490	Homo sapiens DNA, trinucleotide repeats region	3e-06	3876572	(Z81522) predicted using Genefinder; similar to RNA recognition motif. (aka RRM, RBD, or RNP domain) [Caenorhabditis elegans]	3.0

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1298	AF027174	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-B) mRNA, complete cds	3e-06	4240137	(AB020631) KIAA0824 protein [Homo sapiens]	2.7
1299	M37929	Homo sapiens adenosine monophosphate deaminase 1 (AMPD1) gene, exons 11-12.	3e-06	1653775	(D90916) thiol:disulfide interchange protein DsbD [Synechocystis sp.]	1.7
1300	M37929	Homo sapiens adenosine monophosphate deaminase 1 (AMPD1) gene, exons 11-12.	3e-06	1653775	(D90916) thiol:disulfide interchange protein DsbD [Synechocystis sp.]	1.7
1301	U60496	Glycine max actin (Soy86) gene, partial cds	3e-06	1730738	ACTIN-LIKE PROTEIN ARP5 Ynl2430p [Saccharomyces cerevisiae]	2e-05
1302	X14363	Yersinia pseudotuberculosis rplC, rplD, rplW, rplB and rpsS genes for ribosomal proteins L3, L4, L23, L2 and S19	3e-06	585879	50S RIBOSOMAL PROTEIN L2 maritima >gi437926 (Z21677) ribosomal protein L2	2e-12
1303	Z34969	H.sapiens DNA for microsatellite polymorphism	2e-06	<NONE>	<NONE>	<NONE>
1304	X64707	H.sapiens BBC1 mRNA	1e-06	<NONE>	<NONE>	<NONE>
1305	AC005830	Homo sapiens Xp22-154-155 BAC GSHB-52411 (Genome Systems Human BAC Library), complete sequence [Homo sapiens]	1e-06	<NONE>	<NONE>	<NONE>
1306	J04058	Human electron transfer flavoprotein alpha-subunit mRNA, complete cds.	1e-06	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1307	L25647	Homo sapiens fibroblast growth factor receptor gene (located in the central MHC) signal peptide and consecutive exon	1e-06	1586734	mxoQ gene [Methylobacterium organophilum]	5.4
1308	L26261	Human MHC class III HLA-RP1 gene.	1e-06	1684985	(U20633) NADH dehydrogenase subunit [Neuwiedia veratrifolia]	1.8
1309	AF002283	Mus musculus alpha-actinin-2 associated LIM protein mRNA, alternatively spliced product, complete cds	1e-06	2996196	(AF053367) carboxyl terminal LIM domain protein [Mus musculus]	4e-17
1310	M10935	Human haptoglobin gene (alpha-2 allele), complete cds and haptoglobin-related gene, exon 1 and three Alu repeats.	6e-07	<NONE>	<NONE>	<NONE>
1311	AC002251	Homo sapiens (subclone 1_g6 from BAC H76) DNA sequence	4e-07	2144491	coagulation factor Xa (EC 3.4.21.6) precursor norvegicus]	4.2
1312	AF047717	Streptomyces chrysomallus actinomycin synthetase II (acmB) gene, complete cds	4e-07	699196	(U15181) 4-coumarate-coA ligase [Mycobacterium leprae]	1e-06
1313	U14417	Human Ral guanine nucleotide dissociation stimulator mRNA, partial cds.	4e-07	544402	GUANINE NUCLEOTIDE DISSOCIATION STIMULATOR RALGDS FORM A (RALGEF) >gi 321257 pir S28415 guanine nucleotide dissociation stimulator ralGDS - mouse >gi 193573 L07924) guanine nucleotide dissociation stimulator [Mus musculus]	8e-08
1314	Z79027	H.sapiens flow-sorted chromosome 6 HindIII fragment. SC6pA20G8	3e-07	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Homo sapiens				
1315	U67167	intestinal mucin (MUC2) gene. promoter region and partial cds	3e-07	<NONE>	<NONE>	<NONE>
1316	AF086256	Homo sapiens full length insert cDNA clone ZD41C11	3e-07	<NONE>	<NONE>	<NONE>
1317	U67228	Human clone HS4.61 Alu-Ya5 sequence	3e-07	1938437	(U97003) contains similarity to C4-type zinc fingers and a ligand-binding domain of nuclear hormone receptors	2.3
1318	U94346	Human calpain-like protease (htra-3) mRNA. complete cds	3e-07	2911858	(AF047659) No definition line found [Caenorhabditis elegans]	0.39
1319	Y15724	Homo sapiens SERCA3 gene. exons 1-7 (and joined CDS)	1e-07	<NONE>	<NONE>	<NONE>
1320	X13596	Bean DNA for glycine-rich cell wall protein GRP 1.8	1e-07	<NONE>	<NONE>	<NONE>
1321	M83094	Homo sapiens cytosolic selenium-dependent glutathione peroxidase gene, complete cds, and rhoh12 gene. 3' end.	1e-07	1326385	(U58751) C07G1.7 gene product [Caenorhabditis elegans]	8.0
1322	Z55905	H.sapiens CpG DNA, clone 71f4, forward read cpg71f4.ft1a.	1e-07	1076802	extensin-like protein - maize >gi600118 mays]	0.61
1323	X03541	Human mRNA of trk oncogene > :: gb I96186 I96186 Sequence 23 from patent US 5734039	1e-07	325465	(M74509) [Human endogenous retrovirus type C oncovirus sequence.], gene product [Homo sapiens]	3e-04
1324	AF027766	Canis familiaris Y-linked zinc finger protein	1e-07	220643	(D10628) zinc finger protein [Mus musculus]	7e-08
1325	D13613	Bovine mRNA for rabphilin-3A, complete cds > :: dbj E07809 E07809 cDNA encoding rabphilin-3A	1e-07	2822161	(AC004082) rab3 effector-like; 35% Similarity to AF007836 (PID:g2317778) [Homo sapiens]	6e-11

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Human mRNA for c-			(J04169) gag-onc fusion protein	
1326	X57110	cbl proto-oncogene	1e-07	323270	[Cas NS1 retrovirus]	3e-14
1327	X57110	Human mRNA for c-	1e-07	115855	PROTO-ONCOGENE C-CBL human >gi 29731 (X57110) c-	4e-19
		cbl proto-oncogene			cbl protein [Homo sapiens]	
1328	AC001178	Homo sapiens (subclone 2_g12 from BAC H94) DNA sequence	4e-08	<NONE>	<NONE>	<NONE>
1329	U11866	Human interleukin-8 receptor type B (IL8RB) gene, promoter and exons 1- 6	4e-08	<NONE>	<NONE>	<NONE>
1330	AC001225	Homo sapiens (subclone 2_e6 from BAC H94) DNA sequence	4e-08	478184	histone H1 II-1 (clone L95) - midge	6.5
1331	M73837	Human modulator recognition factor 2 (MRF-2) mRNA, complete cds.	4e-08	141448	HYPOTHETICAL 32.6 KD PROTEIN IN TRANSPOSON TN4556 >gi 80758 pir JQ0428 hypothetical 32.6K protein - Streptomyces fradiae transposon Tn4556	4.7
1332	AC006164	Homo sapiens clone UWGC:y28gap from 6p21, complete sequence [Homo sapiens]	4e-08	2580578	(AF000996) ubiquitous TPR motif, Y isoform [Homo sapiens]	1.2
1333	X01060	Human mRNA for transferrin receptor	4e-08	135514	T-CELL RECEPTOR BETA CHAIN PRECURSOR precursor (ANA 11) - rabbit	0.61
1334	Y10697	H.sapiens INE2 mRNA	4e-08	124909	INSULIN RECEPTOR- RELATED PROTEIN PRECURSOR (IRR) (IR- RELATED RECEPTOR) >gi 186555 sapiens]	0.14
1335	U60416	Rattus norvegicus myr 6 myosin heavy chain mRNA, complete cds	4e-08	102189	myosin I, high molecular weight - Acanthamoeba sp	3e-08

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					HYPOTHETICAL 55.2 KD	
1336	U23804	Drosophila melanogaster putative GTP-binding regulatory protein beta chain (GPB) mRNA, partial cds.	4e-08	2494916	TRP-ASP REPEATS CONTAINING PROTEIN T10F2.4 IN CHROMOSOME III protein; similar to G-Beta repeat region (Trp-Asp domains) of guanine nucleotide binding protein	1e-28
1337	AE000213	Escherichia coli K-12 MG1655 section 103 of 400 of the complete genome	4e-08	3294172	(AL022325) tF27C3.1.1 (protein similar to C. elegans protein B0035.16) (isoform 1) [Homo sapiens]	2e-67
1338	D89821	Mus musculus mRNA for RhoM, complete cds	2e-08	3024539	RHO-RELATED GTP-BINDING PROTEIN RHOD (RHO-RELATED RHOD HP1) (RHOHP1) sapiens]	1e-04
1339	U74382	Human telomeric repeat DNA-binding protein (PIN2) mRNA, complete cds	1e-08	<NONE>	<NONE>	<NONE>
1340	L35657	Homo sapiens (subclone H8 5_a10 from P1 35 H5 C8) DNA sequence.	1e-08	<NONE>	<NONE>	<NONE>
1341	L21936	Human succinate dehydrogenase flavoprotein subunit	1e-08	3201678	(AF060886) adenine phosphoribosyltransferase [Leishmania tarentolae]	4.0
1342	AB009777	Homo sapiens gene for osteonidogen, promoter region	1e-08	479388	tritin - wheat >gi 391929 gnl PID d1003454	2.2
1343	M58600	Human heparin cofactor II (HCF2) gene, exons 1 through 5.	1e-08	1730173	GLUCOSE-6-PHOSPHATE ISOMERASE, CYTOSOLIC 2 (GPI) (PHOSPHOGLUCOSE ISOMERASE) (PGI) isomerase [Clarkia concinna]	1.9
1344	M58600	Human heparin cofactor II (HCF2) gene, exons 1 through 5.	1e-08	1730173	GLUCOSE-6-PHOSPHATE ISOMERASE, CYTOSOLIC 2 (GPI) (PHOSPHOGLUCOSE ISOMERASE) (PGI) isomerase [Clarkia concinna]	1.7
1345	AC000980	Homo sapiens (subclone 1_g2 from P1 H31) DNA sequence	1e-08	439877	(L27428) reverse transcriptase [Homo sapiens]	1.1

261

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1346	U48734	Human non-muscle alpha-actinin mRNA, complete cds	1e-08	168237	(M76546) hydroxyproline-rich protein [<i>Helianthus annuus</i>]	0.19
1347	M76724	Human leukocyte adhesion receptor alpha subunit	1e-08	1177607	(X92485) pva1 [<i>Plasmodium vivax</i>]	0.19
1348	AF067959	Gallus gallus homeodomain protein HOXD-3 mRNA, complete cds	1e-08	3165574	(AF067942) No definition line found [<i>Caenorhabditis elegans</i>]	0.15
1349	Z81014	Human DNA sequence from cosmid U65A4, between markers DXS366 and DXS87 on chromosome X *	1e-08	2072964	(U93569) putative p150 [<i>Homo sapiens</i>]	0.001
1350	X57103	Human h-lys gene for lysozyme (upstream region)	7e-09	<NONE>	<NONE>	<NONE>
1351	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	7e-09	231629	BILE-SALT-ACTIVATED LIPASE PRECURSOR ESTER LIPASE) (STEROL ESTERASE) (CHOLESTEROL ESTERASE) salt-activated lipase [<i>Homo sapiens</i>] sapiens]	0.22
1352	L34741	Aplysia californica prohormone convertase (PC2) mRNA, complete cds.	5e-09	322054	cytochrome-c oxidase (EC 1.9.3.1) chain II precursor - <i>Synechocystis</i> sp. (PCC 6803) >gi 581739 sp.]	5.0
1353	AF052959	Homo sapiens type XV collagen (COL15A1) gene, exon 6	4e-09	131269	PHOTOSYSTEM II P680 CHLOROPHYLL A APOPROTEIN (CP-47 PROTEIN) >gi 72708 pir QJLV6A photosystem II chlorophyll a-binding protein psbB - liverwort (<i>Marchantia polymorpha</i>) chloroplast >gi 11700	1.8

267

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1354	L15470	Streptomyces clavuligerus (NRRL 3585) clavulanic acid biosynthesis protein (cla) gene, complete cds and clavamate synthase 2 (cs2) gene, partial cds.	4e-09	586028	POSSIBLE AROMATINASE (AOMATINASE) (UREOHYDROLASE) (AUH) (PROCLAVAMINIC ACID AMIDINO HYDROLASE) >gi 1361423 pir S57669 Proclavaminic acid amidino hydrolase - Streptomyces clavuligerus >gi 295171 Proclavaminic acid amidino hydrolase [Streptomyces clavuligerus] >gi 1586122 prf 2203286B proclavaminic acid amidino hydrolase [Streptomyces clavuligerus]	4e-13
1355	AB002302	Human mRNA for KIAA0304 gene, complete cds	2e-09	131600	GENERAL SECRETION PATHWAY PROTEIN L product [Klebsiella pneumoniae] >gi 149311 (M32613) pull	2.5
1356	L34219	Homo sapiens retinaldehyde-binding protein (CRALBP) gene, complete cds.	1e-09	<NONE>	<NONE>	<NONE>
1357	AB002302	Human mRNA for KIAA0304 gene, complete cds	1e-09	2224549	(AB002302) KIAA0304 [Homo sapiens]	5.0
1358	D85731	Homo sapiens HSPA1L gene for Heat shock protein 70 testis variant, 5'UTR, partial sequence	1e-09	1389766	(U58658) unknown [Homo sapiens]	1.3
1359	AF064483	Homo sapiens natural resistance-associated macrophage protein 2 (NRAMP2) gene, exon 17, alternatively spliced non-IRE form, complete cds	8e-10	113671	!!!! ALU CLASS F WARNING ENTRY !!!!	0.72

263

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1360	AF002283	Mus musculus alpha-actinin-2 associated LIM protein mRNA, alternatively spliced product, complete cds	6e-10	2996196	(AF053367) carboxyl terminal LIM domain protein [Mus musculus]	4e-21
1361	M26220	African green monkey origin of replication	5e-10	2143455	gene DMR-N9 protein - mouse (fragment)	8.8
1362	Z78006	H.sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA7F10	4e-10	2072977	(U93574) putative p150 [Homo sapiens]	0.005
1363	U82303	Homo sapiens unknown protein mRNA, partial cds	2e-10	1825711	(U88183) similar to the immunoglobulin superfamily, most similar to neural cell adhesion proteins [Caenorhabditis elegans]	0.031
1364	AF079764	Drosophila melanogaster enhancer of polycomb	2e-10	3757890	(AF079764) enhancer of polycomb [Drosophila melanogaster]	1e-10
1365	L24123	Homo sapiens NRF1 protein (NRF1) mRNA.	2e-10	3004573	(AC004520) similar to NFE2-related transcription factors; similar to I48694 (PID:g2137676) [Homo sapiens]	4e-53
1366	M91454	Orangutan alpha-globin gene duplicate region.	1e-10	464239	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4 >gi 1085185 pir S52968 NADH dehydrogenase chain 4 - honeybee mitochondrion (SGC4) >gi 552446 (L06178) NADH dehydrogenase subunit 4 [Apis mellifera ligustica]	6.0
1367	D87117	House mouse; Musculus domesticus brain mRNA for SAP102, complete cds	6e-11	473912	(L31961) phosphoprotein [Mus cookii]	2.2
1368	AC001002	Homo sapiens (subclone 2_h9 from P1 H39) DNA sequence	5e-11	<NONE>	<NONE>	<NONE>

264

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1369	AC001002	Homo sapiens (subclone 2_h9 from P1 H39) DNA sequence	5e-11	<NONE>	<NONE>	<NONE>
1370	AB007874	Homo sapiens KIAA0414 mRNA, partial cds	5e-11	<NONE>	<NONE>	<NONE>
1371	AC001002	Homo sapiens (subclone 2_h9 from P1 H39) DNA sequence	5e-11	<NONE>	<NONE>	<NONE>
1372	AC001002	Homo sapiens (subclone 2_h9 from P1 H39) DNA sequence	5e-11	<NONE>	<NONE>	<NONE>
1373	AC001002	Homo sapiens (subclone 2_h9 from P1 H39) DNA sequence	5e-11	<NONE>	<NONE>	<NONE>
1374	AC001002	Homo sapiens (subclone 2_h9 from P1 H39) DNA sequence	5e-11	<NONE>	<NONE>	<NONE>
1375	Z21852	H.sapiens mRNA for HERV-K long terminal repeat	5e-11	419481	gag polyprotein - human endogenous virus S71	4.6
1376	AB007928	Homo sapiens mRNA for KIAA0459 protein, partial cds	5e-11	2947238	(AF051782) diaphanous 1 [Homo sapiens]	2.8
1377	D87117	House mouse: Musculus domesticus brain mRNA for SAPI02, complete cds	5e-11	473912	(L31961) phosphoprotein [Mus cookii]	1.8
1378	AJ131501	Homo Sapiens DNA sequence between two AML1 gene promoters, 6423 BP	5e-11	728831	!!!! ALU SUBFAMILY J WARNING ENTRY	0.20
1379	M27826	Human endogenous retroviral protease mRNA, complete cds.	5e-11	88558	retroviral proteinase-like protein - human	0.002

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					HYPOTHETICAL 55.2 KD	
1380	U23804	Drosophila melanogaster putative GTP-binding regulatory protein beta chain (GPB) mRNA, partial cds.	5e-11	2494916	TRP-ASP REPEATS CONTAINING PROTEIN T10F2.4 IN CHROMOSOME III protein; similar to G-Beta repeat region (Trp-Asp domains) of guanine nucleotide binding protein	1e-30
1381	Z22784	M.musculus troponin I gene.	3e-11	3892202	(AF072889) transcription repressor brain factor 2	0.053
1382	AB007880	Homo sapiens KIAA0420 mRNA, complete cds	2e-11	<NONE>	<NONE>	<NONE>
1383	AF020361	9 Homo sapiens BAX gene, exon 6, partial sequence	2e-11	<NONE>	<NONE>	<NONE>
1384	L35600	Homo sapiens DNA sequence.	2e-11	1174952	GLYCOPROTEIN D PRECURSOR gD [Bovine herpesvirus 1]	0.25
1385	U21943	Human organic anion transporting polypeptide	2e-11	2738223	(U95011) brain-specific organic anion transporter	9e-19
1386	U90878	Homo sapiens carboxyl terminal LIM domain protein	2e-11	2996196	(AF053367) carboxyl terminal LIM domain protein [Mus musculus]	4e-23
1387	U31929	Human orphan nuclear receptor (DAX1) gene, complete cds	6e-12	<NONE>	<NONE>	<NONE>
1388	M25828	Human von Willebrand factor gene, exon 1, 2, and 3, and three Alu repetitive elements.	6e-12	<NONE>	<NONE>	<NONE>
1389	AB020648	Homo sapiens mRNA for KIAA0841 protein, partial cds	3e-12	<NONE>	<NONE>	<NONE>
1390	Z15026	H.sapiens genes for tumor necrosis factor (Tnfa) and lymphotoxine (Tnfb)	2e-12	<NONE>	<NONE>	<NONE>
1391	L28101	Homo sapiens kallistatin (PI4) gene, exons 1-4, complete cds	2e-12	<NONE>	<NONE>	<NONE>
1392	Z47046	Human cosmid QLL2C9 from Xq28	2e-12	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		H.sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA20E2	2e-12	106322	hypothetical protein (L1H 3' region) - human	1.5
1393	Z79007					
1394	U34377	Human tyrosine kinase TXK (txk) gene, exon 13.	1e-12	151484	(M55524) ORF 4; putative [Pseudomonas aeruginosa]	4.3
1395	D70845	Mus musculus apg-1 gene for novel member of heat shock protein 110, promoter region	1e-12	113658	ALKALINE PROTEINASE PRECURSOR (ALP) precursor - fungus (Acremonium chrysogenum)	3.5
1396	M63978	Human vascular endothelial growth factor gene, exon 8.	1e-12	3982737	(AF069731) calmodulin-dependent protein kinase II beta M isoform [Rattus norvegicus]	0.083
1397	U60266	Homo sapiens lysosomal alpha-mannosidase (manB) mRNA, complete cds	8e-13	<NONE>	<NONE>	<NONE>
1398	Z68297	Caenorhabditis elegans cosmid F11A10, complete sequence [Caenorhabditis elegans]	7e-13	2393734	(AC002542) similar to C. elegans F11A10.5; 80% similarity to Z68297 (PID:g1130619) [Homo sapiens]	5e-34
1399	Z68297	Caenorhabditis elegans cosmid F11A10, complete sequence [Caenorhabditis elegans]	7e-13	2393734	(AC002542) similar to C. elegans F11A10.5; 80% similarity to Z68297 (PID:g1130619) [Homo sapiens]	3e-38
1400	Z68885	Human DNA sequence from cosmid L21F12B, Huntington's Disease Region, chromosome 4p16.3, contains EST.	6e-13	<NONE>	<NONE>	<NONE>
1401	X76104	H.sapiens DAP-kinase mRNA	6e-13	2911154	(AB007143) ZIP-kinase [Mus musculus]	0.007
1402	Z78668	H.sapiens flow-sorted chromosome 6 TaqI fragment, SC6pA13G4	5e-13	106322	hypothetical protein (L1H 3' region) - human	2e-06
1403	L35600	Homo sapiens DNA sequence.	3e-13	3184290	(AC004136) hypothetical protein [Arabidopsis thaliana]	1.7

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Cloning vector				
1404	AF090452	pKODT complete sequence	2e-13	3876730	(Z49966) F35C11.4 [Caenorhabditis elegans]	7.8
1405	D28126	Human gene for ATP synthase alpha subunit, complete cds (exon 1 to 12)	2e-13	419481	gag polyprotein - human endogenous virus S71	3.4
1406	AF005219	Homo sapiens transcription factor HOXD13	2e-13	2822166	(AC004080) transcription factor HOXA13 [Homo sapiens]	5e-09
1407	AB018301	Homo sapiens mRNA for KIAA0758 protein, partial cds	2e-13	3882237	(AB018301) KIAA0758 protein [Homo sapiens]	1e-23
1408	D70845	Mus musculus apg-1 gene for novel member of heat shock protein 110, promoter region	1e-13	113658	ALKALINE PROTEINASE PRECURSOR (ALP) precursor - fungus (Acremonium chrysogenum)	3.1
1409	AG000691	Homo sapiens genomic DNA, 21q region, clone: T171BG33	8e-14	930045	(X15332) alpha-1 (III) collagen [Homo sapiens]	3e-04
1410	D30785	Mouse mRNA for neuropsin, complete cds	8e-14	3559978	(AJ005641) serine protease [Rattus rattus]	2e-12
1411	U32710	Haemophilus influenzae Rd section 25 of 163 of the complete genome	8e-14	4106673	(AL035064) queuine trna-ribosyltransferase [Schizosaccharomyces pombe]	2e-38
1412	AG000836	Homo sapiens genomic DNA, 21q region, clone: 64E11X19	7e-14	1363925	hypothetical protein 2 - North American opossum (fragment) >gi897721 (Z48955) ORF-2, putative RT [Didelphis virginiana]	1.1
1413	Z62664	H.sapiens CpG DNA, clone 71d11, forward read cpg71d11.ft1a	7e-14	3953461	(AC002328) F20N2.6 [Arabidopsis thaliana]	0.085
1414	AB014532	Homo sapiens mRNA for KIAA0632 protein, partial cds	7e-14	113668	!!!! ALU CLASS C WARNING ENTRY !!!!	0.040

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1415	Z96478	H.sapiens telomeric DNA sequence, clone 20PTEL004, read 20PTELOO004.seq	7e-14	2981631	(AB012223) ORF2 [Canis familiaris]	2e-04
1416	AF100694	Mus musculus Pontin52 mRNA, complete cds	4e-14	<NONE>	<NONE>	<NONE>
1417	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	4e-14	<NONE>	<NONE>	<NONE>
1418	AF033349	Homo sapiens MLL gene breakpoint cluster region, intron 1, partial sequence	3e-14	728831	!!!! ALU SUBFAMILY J WARNING ENTRY	9.3
1419	AC001526	Homo sapiens (subclone 4_f6 from P1 H54) DNA sequence	3e-14	99861	extensin - almond >gi 20420 (X65718) extensin	9.2
1420	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	3e-14	728832	!!!! ALU SUBFAMILY SB WARNING ENTRY	0.15
1421	AF100694	Mus musculus Pontin52 mRNA, complete cds	2e-14	3913573	EPHRIN-A2 PRECURSOR (EPH-RELATED RECEPTOR TYROSINE KINASE LIGAND 6) (LERK-6) sapiens] >gi 2924761 (AC004258) EPL6_HUMAN [Homo sapiens]	8.7
1422	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	9e-15	119040	E1B PROTEIN, SMALL 1-ANTIGEN (E1B 19K) >gi 74142 pir Q1AD25 early E1B 21K protein II - human adenovirus 5 >gi 58489 (X02996) mRNA 5 first reading frame [Human adenovirus type 5] adenovirus type 5] >gi 209797 (J01969) 21 kD protein	1.5

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					transcription factor GATA-4.	
1423	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	8e-15	477102	retinoic acid-inducible - mouse >gi 293345 (M98339) GATA-binding transcription factor [Mus musculus]	0.57
1424	AB012223	Canis familiaris LINE 1 element ORF2 mRNA, complete cds	8e-15	92385	hypothetical protein - rat (fragment)	0.003
1425	AF100694	Mus musculus Pontin52 mRNA, complete cds	3e-15	<NONE>	<NONE>	<NONE>
1426	X12433	Human pHS1-2 mRNA with ORF homologous to membrane receptor proteins	3e-15	422532	collagen alpha 3(IV) chain - sea urchin	8.9
1427	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	3e-15	1353143	PROBABLE NUCLEAR HORMONE RECEPTOR E02H1.7 >gi 3875431 gnl PID e1344980 (Z47075) similar to Zinc finger, C4 type (two domains) [Caenorhabditis elegans]	5.0
1428	Z69651	Human DNA sequence from cosmid L75B9. Huntington's Disease Region, chromosome 4p16.3	3e-15	403460	(L24521) transformation-related protein [Homo sapiens]	0.60
1429	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	2e-15	108750	Ig heavy chain precursor (B/MT.4A.17.H5.A5) - bovine >gi 440 (X62916) anti-testosterone antibody [Bos taurus]	1.1
1430	X83299	H.sapiens SMA3 mRNA	2e-15	671530	(X83299) SMA3 gene product [Homo sapiens]	0.32
1431	U01877	Human p300 protein mRNA, complete cds. > :: gb 162297 162297 Sequence 1 from patent US 5658784	2e-15	3024341	E1A-ASSOCIATED PROTEIN P300	0.019

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					HYPOTHETICAL 45.1 KD	
1432	X16516	Mouse MHC (Qa) Q2k gene for class I antigen, exons 4-8	1e-15	2496897	PROTEIN CT6CT0.6 IN CHROMOSOME III >gi 3874384 gnl PID e1344078 EST EMBL:C08256 comes from this gene; cDNA EST EMBL:C09941 comes from this gene; cDNA EST yk340a10.3 comes from this gene; cDNA EST yk340a10.5 comes from this gene [Ca...	7e-08
1433	M74165	Chicken tensin mRNA, complete cds.	1e-15	283920	tensin - chicken >gi 212752 (M74165) tensin	2e-19
1434	X71893	H.sapiens gene for immunoglobulin kappa light chain variable region O4 and O5	9e-16	<NONE>	<NONE>	<NONE>
1435	U05227	Human Rar protein mRNA, complete cds.	9e-16	3036779	(284479) match: multiple proteins; match: O00407 Q12829 P22127 P36861 Q40219; match: P70550 Q41022 P22125 Q08155 P35286; match: P51148 P51147 P35293 P36861 P35289; match: P35284 Q40217 P51152 P51157 P51158; match: Q41022	3e-06
1436	M23404	Chicken erythrocyte anion transport protein (band3) mRNA, complete cds.	9e-16	726403	(U23175) similar to anion exchange protein [Caenorhabditis elegans]	1e-28
1437	X16145	Rat mRNA for liver alpha-L-Fucosidase (EC 3.2.1.51)	9e-16	67502	alpha-L-fucosidase (EC 3.2.1.51) 1 precursor, tissue - human >gi 178409 (M29877) alpha-L-fucosidase precursor (EC 3.2.1.5) [Homo sapiens]	2e-29
1438	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	8e-16	<NONE>	<NONE>	<NONE>
1439	AF076981	Mus musculus brain mitochondrial carrier protein BMCP1 (Bmcp1) mRNA, complete cds	8e-16	3851540	(AF078544) brain mitochondrial carrier protein-1 [Homo sapiens]	2e-13

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		H.sapiens MN/CA9			!!!! ALU SUBFAMILY J	
1440	Z54349	GENE	5e-16	728831	WARNING ENTRY	0.002
1441	AF077003	Mus musculus SH3 domain-containing adapter protein mRNA, complete cds	3e-16	309123	(M35526) complement component C5D [Mus musculus]	3.1
1442	X64587	M.musculus mRNA for splicing factor U2AF (65 kD)	3e-16	2143767	glycoprotein - rat >gi 986943 (L08134) glycoprotein [Rattus norvegicus] norvegicus]	0.003
1443	AB014561	Homo sapiens mRNA for KIAA0661 protein, complete cds	3e-16	3327136	(AB014561) KIAA0661 protein [Homo sapiens]	1e-20
1444	Z73987	Human DNA sequence from cosmid N120B6 on chromosome 22 Contains ESTs, complete sequence [Homo sapiens]	1e-16	<NONE>	<NONE>	<NONE>
1445	M58318	Homo sapiens ala gene.	1e-16	<NONE>	<NONE>	<NONE>
1446	U44103	Human small GTP binding protein Rab9 mRNA, complete cds	1e-16	1552584	(Z80233) hypothetical protein - Rv0029	1.3
1447	AB014561	Homo sapiens mRNA for KIAA0661 protein, complete cds	9e-17	3327136	(AB014561) KIAA0661 protein [Homo sapiens]	2e-20
1448	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-17	<NONE>	<NONE>	<NONE>
1449	M76762	Mus musculus ribosomal protein (Kc 3) gene, exons 1 to 5, and complete cds.	1e-17	1073048	pupR protein - Pseudomonas putida >gi 525260	0.36
1450	D50561	Human DNA, replication enhancing element (REE1)	4e-18	126295	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG	0.78
1451	D16431	Human mRNA for hepatoma-derived growth factor, complete cds	4e-18	3242079	(AJ006984) proline-rich protein	0.018

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1452	AF088983	Mus musculus heat shock protein hsp40-3 mRNA. complete cds	4e-18	3873707	(Z73102) Similarity to B.subtilis DNAJ protein (SW:DNAJ_BACSU); cDNA EST yk437a1.5 comes from this gene [Caenorhabditis elegans]	9e-25
1453	U60205	Human methyl sterol oxidase (ERG25) mRNA. complete cds	3e-18	<NONE>	<NONE>	<NONE>
1454	AF038177	Homo sapiens clone 23899 mRNA sequence	1e-18	1360775	G protein-coupled receptor 74 - equine herpesvirus 2 >gi 695246 (U20824) G protein-coupled receptor [Equine herpesvirus 2]	5.1
1455	AB014561	Homo sapiens mRNA for KIAA0661 protein. complete cds	1e-18	3327136	(AB014561) KIAA0661 protein [Homo sapiens]	1e-21
1456	AB014561	Homo sapiens mRNA for KIAA0661 protein. complete cds	1e-18	3327136	(AB014561) KIAA0661 protein [Homo sapiens]	1e-22
1457	U34374	Human tyrosine kinase TXK (txk) gene. exons 9 and 10.	1e-19	<NONE>	<NONE>	<NONE>
1458	AB006969	Homo sapiens hGAA1 mRNA. complete cds	1e-19	4151809	(AF102855) synaptic SAPAP-interacting protein Synamon	0.19
1459	AB002293	Human mRNA for KIAA0295 gene. partial cds	1e-19	2224531	(AB002293) KIAA0295 [Homo sapiens]	6e-17
1460	Z59664	H.sapiens CpG DNA. clone 168f9. reverse read cpg168f9.r1a.	5e-20	3880251	(Z82055) predicted using Genefinder	6.5
1461	M73837	Human modulator recognition factor 2 (MRF-2) mRNA. complete cds.	5e-20	284313	modulator recognition factor 2 - human factor 2 [Homo sapiens]	0.019

273

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1462	U24267	Human pyrroline-5-carboxylate dehydrogenase	5e-20	2506350	DELTA-1-PYRROLINE-5-CARBOXYLATE DEHYDROGENASE PRECURSOR (P5C DEHYDROGENASE) >gi 1353248 sapiens] >gi 1353250 (U24267) pyrroline 5-carboxylate dehydrogenase [Homo sapiens] >gi 1589585 prf 2211355A Delta1-pyrroline-5-carboxylate dehydrogenase [Homo sapiens]	5e-04
1463	U13262	Mus musculus myelin gene expression factor	4e-20	536926	(U13262) myelin gene expression factor [Mus musculus]	3e-07
1464	U13262	Mus musculus myelin gene expression factor	4e-20	3126878	(AF061832) M4 protein deletion mutant [Homo sapiens]	1e-08
1465	Z61239	H.sapiens CpG DNA, clone 48f10, forward read cpg48f10.ft1a.	4e-20	1669601	(D88747) AR401 [Arabidopsis thaliana]	8e-19
1466	U89915	Mus musculus junctional adhesion molecule (Jam) mRNA, complete cds	1e-20	3462455	(U89915) junctional adhesion molecule [Mus musculus]	7e-11
1467	AF029071	Gallus gallus p52 pro-apototic protein mRNA, complete cds	7e-22	2599492	(AF029071) p52 pro-apototic protein [Gallus gallus]	1e-15
1468	M25636	Figure 4. Nucleotide sequence of the pKS36 1.797 kb insert.	6e-22	1196398	(M21305) unknown protein [Homo sapiens]	0.65
1469	AB020655	Homo sapiens mRNA for KIAA0848 protein, complete cds	6e-22	4240325	(AB020725) KIAA0918 protein [Homo sapiens]	1e-19

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					PROCOLLAGEN ALPHA	
1470	S80935	chorionic gonadotropin beta 1 (CG beta 1) subunit	5e-22	115310	I(IV) CHAIN PRECURSOR >gi 84917 pir A31893 collagen alpha 1(IV) chain precursor - fruit fly (Drosophila melanogaster) melanogaster] >gi 157078 (M96575) type IV collagen pro-collagen [Drosophila melanogaster]	0.027
1471	AF053066	Homo sapiens microsatellite D5S2926 sequence	2e-22	728831	!!!! ALU SUBFAMILY J WARNING ENTRY	3e-04
1472	U55177	Danio rerio carbonic anhydrase homolog CAH-Z mRNA, complete cds	2e-22	3123190	CARBONIC ANHYDRASE (CARBONATE DEHYDRATASE) >gi 2576335 (U55177) CAH-Z [Danio rerio]	5e-14
1473	AF064250	Gallus gallus ubiquitin specific protease 66	2e-22	2736064	(AF016107) ubiquitin specific protease 41 [Gallus gallus]	7e-37
1474	AF030880	Homo sapiens pendrin (PDS) mRNA, complete cds	2e-22	729367	DRA PROTEIN (DOWN-REGULATED IN ADENOMA) >gi 2135020 pir A47456 down-regulated in adenoma (DRA) - human >gi 291964 (L02785) Nuclear localization signal at AA 569-573, 576-580, 579-583; acidic transcr. activ. domain 620-640; homeobox motif 653-676 [Homo sapiens]	4e-53
1475	AF100694	Mus musculus Pontin52 mRNA, complete cds	6e-23	<NONE>	<NONE>	<NONE>
1476	X57398	Human mRNA for pM5 protein	3e-23	107350	Pm5 protein - human >gi 1335273 gnl PID e36241	1e-04
1477	AB010998	Rattus norvegicus PAD-R11 mRNA for Peptidylarginine deiminase type I, complete cds	2e-23	<NONE>	<NONE>	<NONE>
1478	D10871	Human h NAT allele 2-2 gene for arylamine N-acetyltransferase	2e-23	171200	(J04734) CDC6 protein [Saccharomyces cerevisiae]	9.8
1479	D10871	Human h NAT allele 2-2 gene for arylamine N-acetyltransferase	2e-23	171200	(J04734) CDC6 protein [Saccharomyces cerevisiae]	8.3

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Homo sapiens MLL-				
1480	AF024541	AF4 fusion protein mRNA, partial cds	2e-23	2136142	serine/proline-rich FEL protein, splice form 1 - human	1e-20
1481	L13773	Human AF-4 mRNA, complete cds.	2e-23	3063962	(AF031404) MLL-AF4 fusion protein [Homo sapiens]	1e-20
1482	AF100694	Mus musculus Pontin52 mRNA, complete cds	8e-24	<NONE>	<NONE>	<NONE>
1483	U75467	Drosophila melanogaster Rga and Atu genes, complete cds	8e-24	1658503	(U75467) Atu [Drosophila melanogaster]	2e-37
1484	D17076	Human HepG2 partial cDNA, clone hmd5a09m5	7e-24	<NONE>	<NONE>	<NONE>
1485	AF100694	Mus musculus Pontin52 mRNA, complete cds	7e-24	1169643	FMRFAMIDE-RELATED NEUROPEPTIDES PRECURSOR >gil416208 (U03137) neuropeptide precursor FMRFamide-related peptide [Lymnaea stagnalis]	7e-10
1486	M11167	Human 28S ribosomal RNA gene.	2e-24	3875481	(Z81054) predicted using Genefinder; Similarity to UDP-glucuronosyltransferases	5.1
1487	AF100694	Mus musculus Pontin52 mRNA, complete cds	2e-24	549173	USPI PROTEIN PRECURSOR >gil169623	1.2
1488	AB003468	Cloning vector pAP3neo DNA, complete sequence	2e-24	987050	(X65335) lacZ gene product [unidentified cloning vector]	0.058
1489	X03541	Human mRNA of trk oncogene >:: gb I96186 I96186 Sequence 23 from patent US 5734039	2e-24	325465	(M74509) [Human endogenous retrovirus type C oncovirus sequence.], gene product [Homo sapiens]	3e-04
1490	L81652	Homo sapiens (subclone 2_g11 from P1 H43) DNA sequence	2e-24	225047	reverse transcriptase related protein [Homo sapiens]	4e-12
1491	U95760	Drosophila melanogaster strawberry notch (sno) mRNA, complete cds	2e-24	2078282	(U95760) Sno [Drosophila melanogaster]	2e-11
1492	AF100694	Mus musculus Pontin52 mRNA, complete cds	8e-25	2623773	(AF004835) tyrocidine synthetase 3 [Brevibacillus brevis]	8.6

276

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1493	AB002405	Homo sapiens mRNA for LAK-4p. complete cds	8e-25	2496822	HYPOTHETICAL 127.3 KD PROTEIN B0416.1 IN CHROMOSOME X >gi 746502 (U23516) B0416.1 gene product [Caenorhabditis elegans]	9e-11
1494	K03002	Human mRNA from chromosome 15 gene with homology to MHC-HLA-SB-1 intron A.	8e-25	1514614	(X92842) nuclear protein [Mus musculus]	1e-13
1495	U61232	Human tubulin-folding cofactor E mRNA, complete cds	7e-25	1465772	(U61232) cofactor E [Homo sapiens]	2e-05
1496	U10245	Arabidopsis thaliana Col-O putative RNA helicase A mRNA, complete cds.	5e-25	1353239	(U10245) putative RNA helicase A [Arabidopsis thaliana]	1e-37
1497	X89211	H.sapiens DNA for endogenous retroviral like element	3e-25	2065210	(Y12713) Pro-Pol-dUTPase polyprotein	5e-06
1498	L81652	Homo sapiens (subclone 2_g11 from P1 H43) DNA sequence	3e-25	2072961	(U93568) putative p150 [Homo sapiens]	5e-16
1499	X82895	H.sapiens mRNA for DLG2	2e-25	2497511	MAGUK P55 SUBFAMILY MEMBER 2 (MPP2 PROTEIN) (DISCS, LARGE HOMOLOG 2)	1e-34
1500	M36654	Mouse homeo box 2.6 (Hox-2.6) mRNA, complete cds.	9e-26	3323169	(AE001255) T. pallidum predicted coding region TP0854	1.9
1501	L36315	Mus musculus (clone pMLZ-1) zinc finger protein	9e-26	1806134	(Z67747) zinc finger protein [Mus musculus]	4e-05
1502	AB018281	Homo sapiens mRNA for KIAA0738 protein, complete cds	9e-26	728831	!!! ALU SUBFAMILY J. WARNING ENTRY	1e-07
1503	AF017433	Homo sapiens putative transcription factor CR53	9e-26	3219985	ZINC FINGER PROTEIN ZFP-29	1e-17

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Homo sapiens				
1504	AC001225	(subclone 2_e6 from BAC H94) DNA sequence	8e-26	2653713	(U91823) small S protein [Hepatitis B virus]	4.3
1505	AF100694	Mus musculus Pontin52 mRNA, complete cds	8e-26	283446	cyteine-rich surface antigen 72, CRP72 - Giardia lamblia (fragment)	3.4
1506	X94912	H.sapiens Pr22 gene	3e-26	728837	!!!! ALU SUBFAMILY SQ WARNING ENTRY	4e-09
1507	AF100694	Mus musculus Pontin52 mRNA, complete cds	2e-26	<NONE>	<NONE>	<NONE>
1508	U44103	Human small GTP binding protein Rab9 mRNA, complete cds	1e-26	3327038	(AB014512) KIAA0612 protein [Homo sapiens]	8.7
1509	AF100694	Mus musculus Pontin52 mRNA, complete cds	9e-27	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	0.14
1510	AG001212	Homo sapiens genomic DNA, 21q region, clone: 9H11N46	9e-27	126296	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG protein [Nycticebus coucang]	0.012
1511	AF027131	Mus musculus mucin glycoprotein MUC3 mRNA, partial cds	9e-27	2589172	(U76551) mucin Muc3 [Rattus norvegicus]	2e-14
1512	U49057	Rattus norvegicus CTD-binding SR-like protein rA9 mRNA, complete cds	5e-27	1438534	(U49057) rA9 [Rattus norvegicus]	1e-04
1513	J03764	Human, plasminogen activator inhibitor-1 gene, exons 2 to 9.	3e-27	<NONE>	<NONE>	<NONE>
1514	Z78160	M.musculus partial cochlear mRNA (clone 28D2)	3e-27	1490362	(Z78160) unknown [Mus musculus]	2e-05
1515	Z64210	H.sapiens CpG DNA, clone 99b4, reverse read cpg99b4.r1a.	3e-27	2257538	(AB004538) LIPOIC ACID SYNTHETASE PRECURSOR(LIP-SYN) [Schizosaccharomyces pombe]	1e-06

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Homo sapiens				
1516	L35659	(subclone H8 6_h6 from P1 35 H5 C8) DNA sequence.	1e-27	<NONE>	<NONE>	<NONE>
1517	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-27	1644471	(U72686) odorant receptor 4 [Danio rerio]	7.5
1518	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-27	2738388	(AF003534) hypothetical protein 004L [Chilo iridescent virus]	6.7
1519	AB009271	Homo sapiens gene for BCNT, partial cds	1e-27	3880909	(AL032636) Y40B1B.3 [Caenorhabditis elegans]	4.6
1520	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-27	2133579	spermatophorin Sp23 - yellow mealworm molitor]	0.85
1521	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-27	121805	ENDOGLUCANASE A PRECURSOR	0.58
1522	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-27	3722000	(AF035323) survival motor neuron protein [Bos taurus]	0.10
1523	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-27	3328188	(AF074902) laminin alpha chain [Caenorhabditis elegans]	0.083
1524	AF074382	Homo sapiens Ikb kinase gamma subunit	1e-27	3641280	(AF074382) Ikb kinase gamma subunit [Homo sapiens]	0.041
1525	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-27	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	6e-04
1526	L78778	Homo sapiens (subclone 2_e10 from P1 H49) DNA sequence	1e-27	225047	reverse transcriptase related protein [Homo sapiens]	2e-09
1527	L03427	Human zinc finger protein basonuclin mRNA, complete cds.	1e-27	1488275	(U59694) zinc finger protein basonuclin [Homo sapiens]	9e-22
1528	U09954	Human ribosomal protein L9 gene, 5' region and complete cds.	4e-28	2257538	(AB004538) LIPOIC ACID SYNTHETASE PRECURSOR(LIP-SYN) [Schizosaccharomyces pombe]	2e-04

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1529	Z64210	H.sapiens CpG DNA, clone 99b4, reverse read cpg99b4.rt1a.	4e-28	3878570	(Z46381) similar to lipoic acid synthase; cDNA EST yk283b6.3 comes from this gene; cDNA EST yk283b6.5 comes from this gene; cDNA EST yk472f5.3 comes from this gene; cDNA EST yk472f5.5 comes from this gene; cDNA EST yk476e7.3...	7e-11
1530	U55177	Danio rerio carbonic anhydrase homolog CAH-Z mRNA, complete cds	4e-28	3123190	CARBONIC ANHYDRASE (CARBONATE DEHYDRATASE) >gi 2576335 (U55177) CAH-Z [Danio rerio]	5e-21
1531	D43682	Human mRNA for very-long-chain acyl-CoA dehydrogenase (VLCAD), complete cds	4e-28	1351839	ACYL-COA DEHYDROGENASE, VERY-LONG-CHAIN SPECIFIC PRECURSOR (VLCAD) >gi 930358 taurus]	3e-27
1532	AF016591	Homo sapiens survival motor neuron pseudogene, complete sequence	3e-28	728831	!!!! ALU SUBFAMILY J WARNING ENTRY	3e-08
1533	AF100694	Mus musculus Pontin52 mRNA, complete cds	2e-28	728832	!!!! ALU SUBFAMILY SB WARNING ENTRY	2.5
1534	AF100694	Mus musculus Pontin52 mRNA, complete cds	2e-28	118588	DEHYDRIN DHN3 >gi 100035 pir S18139 dehydrin DHN3 - garden pea >gi 20709 (X63063) pea dehydrin DHN3 [Pisum sativum]	0.004
1535	AF100694	Mus musculus Pontin52 mRNA, complete cds	2e-28	1169643	FMRFAMIDE-RELATED NEUROPEPTIDES PRECURSOR >gi 416208 (U03137) neuropeptide precursor FMRFamide-related peptide [Lymnaea stagnalis] (AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	6e-04
1536	AF100694	Mus musculus Pontin52 mRNA, complete cds	2e-28	4056454		9e-05

280

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	
1537	AF100694	Mus musculus Pontin52 mRNA, complete cds	2e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	2e-06
1538	AF100694	Mus musculus Pontin52 mRNA, complete cds	2e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	2e-09
1539	AF100694	Mus musculus Pontin52 mRNA, complete cds	2e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	1e-09
1540	AF100694	Mus musculus Pontin52 mRNA, complete cds	2e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	5e-10
1541	AF100694	Mus musculus Pontin52 mRNA, complete cds	2e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	1e-11
1542	AF100694	Mus musculus Pontin52 mRNA, complete cds	2e-28	3157926	(AC002131) Strong similarity to extensin-like protein gb Z34465 from Zea mays. [Arabidopsis thaliana]	8e-12
1543	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	<NONE>	<NONE>	<NONE>
1544	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	<NONE>	<NONE>	<NONE>
1545	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Mus musculus				
1546	AF100694	Pontin52 mRNA, complete cds	1e-28	<NONE>	<NONE>	<NONE>
1547	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	<NONE>	<NONE>	<NONE>
1548	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	<NONE>	<NONE>	<NONE>
1549	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	<NONE>	<NONE>	<NONE>
1550	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	<NONE>	<NONE>	<NONE>
1551	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	<NONE>	<NONE>	<NONE>
1552	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	<NONE>	<NONE>	<NONE>
1553	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	<NONE>	<NONE>	<NONE>
1554	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	<NONE>	<NONE>	<NONE>
1555	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	<NONE>	<NONE>	<NONE>
1556	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	<NONE>	<NONE>	<NONE>
1557	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	<NONE>	<NONE>	<NONE>
1558	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	<NONE>	<NONE>	<NONE>
1559	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	<NONE>	<NONE>	<NONE>
1560	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	<NONE>	<NONE>	<NONE>
1561	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Mus musculus				
1562	AF100694	Pontin52 mRNA, complete cds	1e-28	<NONE>	<NONE>	<NONE>
1563	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	<NONE>	<NONE>	<NONE>
1564	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	<NONE>	<NONE>	<NONE>
1565	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	<NONE>	<NONE>	<NONE>
1566	M87708	Human simple repeat polymorphism.	1e-28	<NONE>	<NONE>	<NONE>
1567	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	<NONE>	<NONE>	<NONE>
1568	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	3924779	(AF100694) similar to human B; cDNA EST yk450d8.5 comes from this gene; cDNA EST yk249a6.5 comes from this gene; cDNA EST yk219a2.5 comes from this gene; cDNA EST yk355e4.5 comes from this gene; cDNA EST yk224f4.5 comes fr... >gi 3924881 gnl PID e1354569 from this gene; cDNA EST yk249a6.5 comes from this gene; cDNA EST yk219a2.5 comes from this gene; cDNA EST yk355e4.5 comes from this gene; cDNA EST yk224f4.5 comes from...	3.0
1569	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	1169643	FMRFAMIDE-RELATED NEUROPEPTIDES PRECURSOR >gi 416208 (U03137) neuropeptide precursor FMRFamide-related peptide [Lymnaea stagnalis]	0.66

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1570	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	3924779	(U60315) similar to B. cDNA EST yk450d8.5 comes from this gene; cDNA EST yk249a6.5 comes from this gene; cDNA EST yk219a2.5 comes from this gene; cDNA EST yk355e4.5 comes from this gene; cDNA EST yk224f4.5 comes fr... >gi 3924881 gnl PID e1354569 from this gene; cDNA EST yk249a6.5 comes from this gene; cDNA EST yk219a2.5 comes from this gene; cDNA EST yk355e4.5 comes from this gene; cDNA EST yk224f4.5 comes from...	0.65
1571	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	2133579	spermatophorin Sp23 - yellow mealworm molitor]	0.49
1572	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	2133579	spermatophorin Sp23 - yellow mealworm molitor]	0.49
1573	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	283446	cyteine-rich surface antigen 72, CRP72 - Giardia lamblia (fragment)	0.45
1574	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	2498937	SPERMATOPHORIN SP23 PRECURSOR mealworm >gi 161725 (M92928) structural protein	0.33
1575	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	1492050	(U60315) MC107L [Molluscum contagiosum virus subtype 1]	0.18
1576	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	2133579	spermatophorin Sp23 - yellow mealworm molitor]	0.088
1577	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	118588	DEHYDRIN DHN3 >gi 100035 pir S18139 dehydrin DHN3 - garden pea >gi 20709 (X63063) pea dehydrin DHN3 [Pisum sativum]	0.018
1578	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	118588	DEHYDRIN DHN3 >gi 100035 pir S18139 dehydrin DHN3 - garden pea >gi 20709 (X63063) pea dehydrin DHN3 [Pisum sativum]	0.016

284

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1579	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	118588	DEHYDRIN DHN3 >gi 100035 pir S18139 dehydrin DHN3 - garden pea >gi 20709 (X63063) pea dehydrin DHN3 [Pisum sativum]	0.012
1580	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	0.010
1581	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	118588	DEHYDRIN DHN3 >gi 100035 pir S18139 dehydrin DHN3 - garden pea >gi 20709 (X63063) pea dehydrin DHN3 [Pisum sativum]	0.002
1582	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	1169643	FMRFAMIDE-RELATED NEUROPEPTIDES PRECURSOR >gi 416208 (U03137) neuropeptide precursor FMRFamide-related peptide [Lymnaea stagnalis]	0.002
1583	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	0.002
1584	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	118588	DEHYDRIN DHN3 >gi 100035 pir S18139 dehydrin DHN3 - garden pea >gi 20709 (X63063) pea dehydrin DHN3 [Pisum sativum]	0.002
1585	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	0.002
1586	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	118588	DEHYDRIN DHN3 >gi 100035 pir S18139 dehydrin DHN3 - garden pea >gi 20709 (X63063) pea dehydrin DHN3 [Pisum sativum]	0.001

225

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1587	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	0.001
1588	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	6e-04
1589	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	5e-04
1590	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	5e-04
1591	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	118588	DEHYDRIN DHN3 >gi 100035 pir S18139 dehydrin DHN3 - garden pea >gi 20709 (X63063) pea dehydrin DHN3 [Pisum sativum]	2e-04
1592	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	2e-04
1593	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	5e-05

256

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1594	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	5e-05
1595	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	1e-05
1596	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	1e-05
1597	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	9e-06
1598	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	6e-06
1599	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	5e-06
1600	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	544357	RNA-BINDING PROTEIN FUS/TLS protein [human. Peptide, 526 aa] [Homo sapiens]	4e-06

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1601	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	2e-06
1602	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	2e-06
1603	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	9e-07
1604	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	8e-07
1605	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	1169643	FMRFAMIDE-RELATED NEUROPEPTIDES PRECURSOR >gi 416208 (U03137) neuropeptide precursor FMRFamide-related peptide [Lymnaea stagnalis]	7e-07
1606	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	6e-07
1607	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	5e-07

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1608	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	3e-07
1609	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	1e-07
1610	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	1e-07
1611	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	7e-08
1612	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	2e-08
1613	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	6e-09

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1614	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	5e-09
1615	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	4e-09
1616	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	7e-10
1617	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	6e-10
1618	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	5e-10
1619	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	4e-10

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1620	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	2e-10
1621	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	5e-11
1622	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	2e-12
1623	AF032896	Petromyzon marinus polyadenylate binding protein	1e-28	1082703	polyadenylate binding protein II human	2e-27
1624	AF100694	Mus musculus Pontin52 mRNA, complete cds	9e-29	118588	DEHYDRIN DHN3 >gi 100035 pir S18139 dehydrin DHN3 - garden pea >gi 20709 (X63063) pea dehydrin DHN3 [Pisum sativum]	0.013
1625	AF100694	Mus musculus Pontin52 mRNA, complete cds	9e-29	2133579	spermatophorin Sp23 - yellow mealworm molitor]	6e-04
1626	AF100694	Mus musculus Pontin52 mRNA, complete cds	9e-29	3876465	(Z81071) predicted using Genefinder; Similarity to Human small nuclear ribonucleoprotein E cDNA EST yk375g7.5 comes from this gene; cDNA EST yk435f5.3 comes from this gen...	9e-06
1627	AF100694	Mus musculus Pontin52 mRNA, complete cds	8e-29	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	2e-06

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					ADP-RIBOSYLATION	
1628	AF100694	Mus musculus Pontin52 mRNA, complete cds	4e-29	728883	FACTOR 3 fruit fly (Drosophila melanogaster) >gi 507234 (L25063) ADP ribosylation factor 3 [Drosophila melanogaster]	0.016
1629	AF100694	Mus musculus Pontin52 mRNA, complete cds	4e-29	544357	RNA-BINDING PROTEIN FUS/TLS protein [human, Peptide, 526 aa] [Homo sapiens] (AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	2e-07
1630	AF100694	Mus musculus Pontin52 mRNA, complete cds	4e-29	4056454	ACYL-COA DEHYDROGENASE, VERY-LONG-CHAIN SPECIFIC PRECURSOR (VLCAD) dehydrogenase precursor - rat Acyl-CoA dehydrogenase [Rattus norvegicus] (Z95556) accD1 [Mycobacterium tuberculosis]	1e-08
1631	D43682	Human mRNA for very-long-chain acyl-CoA dehydrogenase (VLCAD), complete cds	4e-29	1168287	ACYL-COA DEHYDROGENASE, VERY-LONG-CHAIN SPECIFIC PRECURSOR (VLCAD) dehydrogenase precursor - rat Acyl-CoA dehydrogenase [Rattus norvegicus]	6e-37
1632	Y07660	M.tuberculosis accBC gene	4e-29	2113935	(Z95556) accD1 [Mycobacterium tuberculosis]	3e-47
1633	X55367	Human alpha-satellite DNA from clone pTRA-2.	1e-29	<NONE>	<NONE>	<NONE>
1634	L81866	Homo sapiens (subclone 1_f1 from PI H54) DNA sequence	1e-29	<NONE>	<NONE>	<NONE>
1635	S75940	[Alu repeats, clone 52H10] [human, colonic mucosa, Genomic, 943 nt]	1e-29	728831	!!!! ALU SUBFAMILY J WARNING ENTRY	1e-07
1636	AB001907	Homo sapiens PACE4 gene, exon 13	1e-29	728831	!!!! ALU SUBFAMILY J WARNING ENTRY	2e-09
1637	AF077003	Mus musculus SH3 domain-containing adapter protein mRNA, complete cds	5e-30	<NONE>	<NONE>	<NONE>

292

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1638	AF100694	Mus musculus Pontin52 mRNA, complete cds	4e-30	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	3e-10
1639	M27072	Xenopus laevis poly(A)-binding protein (ABP-EF) mRNA, complete cds.	4e-30	1352709	POLYADENYLATE-BINDING PROTEIN polyadenylate-binding protein - African clawed frog laevis]	5e-21
1640	X58386	B.taurus mRNA for bovine vacuolar ATPase subunit A	2e-30	2773154	(AF039573) abscisic acid- and stress-inducible protein	4.3
1641	Y07660	M.tuberculosis accBC gene	1e-30	2113935	(Z95556) accD1 [Mycobacterium tuberculosis]	4e-47
1642	AJ236940	Sus scrofa mRNA for hypothetical protein (5' clone 7C4)	4e-31	4102021	(AF007561) delta 6-desaturase [Borago officinalis]	7.4
1643	AF039400	Homo sapiens calcium-dependent chloride channel-1 (hCLCA1) mRNA, complete cds	2e-31	3721912	(AB017156) gob-5 [Mus musculus]	7e-08
1644	L77036	Homo sapiens (subclone 5_d9 from P1 H19) DNA sequence.	1e-31	461663	BOMBYXIN B-2 HOMOLOG PRECURSOR silkworm >gil217385 gnl PID d1003528 (D13924) Samia bombyxin homolog B-2 [Samia cynthia]	1.1
1645	X61971	H.sapiens mRNA for macropain subunit delta	1e-31	296734	(X61971) macropain subunit delta [Homo sapiens]	3e-06
1646	L00016	human mitochondrial trnas and partial proteins 4 & 5; histidyl-, seryl-, leucyl-trna genes: urf4 and urf5 (partial).	5e-32	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	0.002
1647	M17887	Human acidic ribosomal phosphoprotein P2 mRNA, complete cds.	5e-32	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	1e-05

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1659	U53446	Human mitogen-responsive phosphoprotein DOC-2 mRNA, complete cds.	6e-34	3395443	(AC004683) putative ammonium transporter. 3' partial	4.7
1660	AF013988	Homo sapiens serine protease mRNA, complete cds	4e-34	2507226	PROTEIN-TYROSINE PHOSPHATASE EPSILON PRECURSOR (R-PTP-EPSILON) >gil1439605 (U62387) protein tyrosine phosphatase-e [Mus musculus]	3.2
1661	U53446	Human mitogen-responsive phosphoprotein DOC-2 mRNA, complete cds.	2e-34	104757	LEP100 protein precursor - chicken >gil212254 gallus]	1.6
1662	AJ233632	Homo sapiens endogenous retroviral sequence ERV-L pol gene, clone ERV-L Human6	2e-34	3860513	(AJ233597) reverse transcriptase [Mus famulus]	4e-10
1663	AF086310	Homo sapiens full length insert cDNA clone ZD51F08	8e-35	2947070	(AC002521) putative Ser/Thr protein kinase [Arabidopsis thaliana]	2.3
1664	X17206	Human mRNA for LLRep3	3e-35	730652	40S RIBOSOMAL PROTEIN S2 (STRINGS OF PEARLS PROTEIN) >gil1085158 pir S50325 ribosomal protein S2 - fruit fly (Drosophila melanogaster) melanogaster] >gil515972 (U01335) ribosomal protein S2	2e-10
1665	AB011137	Homo sapiens mRNA for KIAA0565 protein, complete cds	3e-35	3043654	(AB011137) KIAA0565 protein [Homo sapiens]	2e-16
1666	U62801	Human protease M mRNA, complete cds	2e-35	3929231	(AF091247) potassium channel [Rattus norvegicus]	1.0
1667	AF020760	Homo sapiens serine protease (Omi) mRNA, complete cds	1e-35	2738915	(AF020760) serine protease [Homo sapiens]	9e-14

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Human DNA				
1668	Z93943	sequence from cosmid U235H3 on chromosome X	8e-36	1196432	(M22333) unknown protein [Homo sapiens]	3e-10
1669	X06778	Rabbit 18S rRNA	7e-36	118588	DEHYDRIN DHN3 >gi100035 pir S18139 dehydrin DHN3 - garden pea >gi20709 (X63063) pea dehydrin DHN3 [Pisum sativum]	0.011
1670	AB007962	Homo sapiens mRNA. chromosome 1 specific transcript KIAA0493	3e-36	3329243	(AE001350) hypothetical protein [Chlamydia trachomatis]	3.1
1671	Z81014	Human DNA sequence from cosmid U65A4, between markers DXS366 and DXS87 on chromosome X *	3e-36	141103	HYPOTHETICAL PROTEIN ORF-1137 mouse	0.038
1672	Z81014	Human DNA sequence from cosmid U65A4, between markers DXS366 and DXS87 on chromosome X *	3e-36	198651	(M29325) ORF1 [Mus musculus]	0.006
1673	U49082	Human transporter protein (g17) mRNA. complete cds	3e-36	1840045	(U49082) transporter protein [Homo sapiens]	2e-15
1674	J03133	Human transcription factor SP1 mRNA. 3' end.	3e-36	477133	HF-1 regulatory element binding protein - rat	2e-31
1675	AB007934	Homo sapiens mRNA for KIAA0465 protein. partial cds	1e-36	3413892	(AB007934) KIAA0465 protein [Homo sapiens]	4e-37
1676	M34857	Mouse Hox-2.5 mRNA.	9e-37	106296	homeotic protein Hox B9 - human (fragment)	0.15
1677	L35657	Homo sapiens (subclone H8 5_a10 from P1 35 H5 C8) DNA sequence.	9e-37	2072960	(U93568) p40 [Homo sapiens]	3e-05
1678	X80240	H.sapiens endogenous retrovirus HERV-KC4 DNA	8e-37	4185944	(Y17833) env protein [Human endogenous retrovirus K]	1e-15

225

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Human DNA				
1679	Z93943	sequence from cosmid U235H3 on chromosome X	9e-38	106322	hypothetical protein (LIH 3' region) - human	4e-13
1680	X97303	H.sapiens mRNA for Ptg-12 protein	4e-38	466044	HYPOTHETICAL ZINC FINGER PROTEIN ZK686.4 IN CHROMOSOME III >gi 630780 pir S44909 ZK686.4 protein - Caenorhabditis elegans >gi 304346 (L17337) coded for by C. elegans cDNAs GenBank:M88869 and T01933; putative [Caenorhabditis elegans]	3e-37
1681	Y08999	H.sapiens mRNA for Sop2p-like protein	3e-38	3334339	SOP2-LIKE PROTEIN	5e-06
1682	Z62887	H.sapiens CpG DNA, clone 74g6, forward read cpg74g6.ft1a	2e-38	1245686	(U53181) F36D4.2 gene product [Caenorhabditis elegans]	0.19
1683	U35032	Human endogenous retrovirus clone c5.11, HERV-H multiply spliced subgenomic leader, protease and integrase region mRNA, partial cds	1e-38	59977	(Z14310) tripartite fusion transcript PLA2L [Human endogenous retrovirus]	1e-06
1684	D86974	Human mRNA for KIAA0220 gene, partial cds	1e-38	3337386	(AC002544) Unknown gene product splice form-2 [Homo sapiens]	8e-11
1685	M31013	Human nonmuscle myosin heavy chain (NMHC) mRNA, 3' end.	1e-38	4115748	(AB022023) nonmuscle myosin heavy chain B	2e-11
1686	AF006087	Homo sapiens Arp2/3 protein complex subunit p20-Arc (ARC20) mRNA, complete cds	4e-39	<NONE>	<NONE>	<NONE>
1687	X58374	D.melanogaster crn mRNA	4e-39	2655888	(AL009171) 62D9.a [Drosophila melanogaster]	4e-12
1688	D85815	Human DNA for rhoHP1, complete cds	1e-39	134080	GTP-BINDING PROTEIN TC10 ras-like protein [Homo sapiens]	3e-26

206

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1689	U49057	Rattus norvegicus CTD-binding SR-like protein rA9 mRNA, complete cds	4e-40	1438534	(U49057) rA9 [Rattus norvegicus]	5e-05
1690	Y08999	H.sapiens mRNA for Sop2p-like protein	4e-40	3334339	SOP2-LIKE PROTEIN	9e-08
1691	AB002293	Human mRNA for KIAA0295 gene, partial cds	4e-40	2224531	(AB002293) KIAA0295 [Homo sapiens]	1e-30
1692	AF086222	Homo sapiens full length insert cDNA, clone ZC66E08	1e-40	2829669	DOUBLE-STRANDED RNA-SPECIFIC EDITASE 1 (DSRNA ADENOSINE DEAMINASE) (RNA EDITING ENZYME 1) >gi 1707502 gnl PID e254627 (X99227) double-stranded RNA-specific editase [Homo sapiens] editase 1 hRED1-L [Homo sapiens] >gi 2039300 (U76421) dsRNA adenosine deaminase DRADA2b [Homo sapiens]	0.61
1693	AF044127	Homo sapiens peroxisomal short-chain alcohol dehydrogenase (SCAD-SRL) mRNA, complete cds	1e-40	4105190	(AF044127) peroxisomal short-chain alcohol dehydrogenase	2e-06
1694	U36778	Mus musculus Sil mRNA, complete cds	1e-40	88608	SIL protein - human >gi 338088 (M74558) SIL	6e-23
1695	U36778	Mus musculus Sil mRNA, complete cds	1e-40	88608	SIL protein - human >gi 338088 (M74558) SIL	6e-23
1696	U36778	Mus musculus Sil mRNA, complete cds	1e-40	88608	SIL protein - human >gi 338088 (M74558) SIL	5e-23
1697	U36778	Mus musculus Sil mRNA, complete cds	1e-40	88608	SIL protein - human >gi 338088 (M74558) SIL	5e-23
1698	AB018285	Homo sapiens mRNA for KIAA0742 protein, partial cds	1e-40	3882205	(AB018285) KIAA0742 protein [Homo sapiens]	6e-31

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					ATP-BINDING CASSETTE	
1699	X75927	M.musculus abc2 mRNA	1e-40	728773	TRANSPORTER 1 ABC1 - human >gi 495257 (X75926) abc1 [Mus musculus]	3e-37
1700	AF038200	Homo sapiens clone 23954 mRNA sequence	5e-41	3211975	(AF068195) putative glioblastoma cell differentiation-related protein [Homo sapiens]	5e-14
1701	U20521	Human estrogen sulfotransferase (STE) gene, exon 8 and complete cds	4e-41	<NONE>	<NONE>	<NONE>
1702	AF026548	Homo sapiens branched chain alpha-ketoacid dehydrogenase kinase precursor, mRNA, nuclear gene encoding mitochondrial protein, complete cds	2e-41	3182923	[3-METHYL-2-OXOBUTANOATE DEHYDROGENASE (LIPOAMIDE)] KINASE PRECURSOR alpha-ketoacid dehydrogenase kinase precursor [Homo sapiens]	2e-09
1703	Y07660	M.tuberculosis accBC gene	2e-41	465847	HYPOTHETICAL 66.5 KD PROTEIN F02A9.5 IN CHROMOSOME III >gi 280542 pir S28313 hypothetical protein F02A9.5 - Caenorhabditis elegans GeneFinder: similar to Propionyl-CoA carboxylase beta chain; cDNA EST EMBL:M89018 comes from this gene; cDNA EST EMBL:D28069 comes from this gene; cDNA EST EMBL:D28068 comes from this gene; cDNA EST ...	3e-38
1704	AG001237	Homo sapiens genomic DNA, 21q region, clone: 9H11N46	1e-41	106322	hypothetical protein (L1H 3' region) - human	5e-09
1705	AB007934	Homo sapiens mRNA for KIAA0465 protein, partial cds	1e-41	3413892	(AB007934) KIAA0465 protein [Homo sapiens]	3e-12
1706	AF055029	Homo sapiens clone 24711 mRNA sequence	5e-42	3250681	(AL024486) putative protein	2.2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1707	Z49747	O.cuniculus mRNA for phospholipase C	5e-42	130227	PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE DELTA 1 (PLC-DELTA-1) (PHOSPHOLIPASE C-DELTA-1) (PLC-III) >gi 163538 (M20638) phospholipase C-III [Bos taurus]	5e-36
1708	M93651	Human set gene, complete cds.	2e-42	<NONE>	<NONE>	<NONE>
1709	AJ236940	Sus scrofa mRNA for hypothetical protein (5' clone 7C4)	2e-42	2062403	(U79010) delta 6 desaturase [Borago officinalis]	8.5
1710	J03634	Human erythroid differentiation protein mRNA	2e-42	1708436	INHIBIN BETA A CHAIN PRECURSOR	2e-10
1711	AJ223777	Mus musculus mRNA for striatin	6e-43	2494917	STRIATIN >gi 1495773 gnl PID e254158	2e-32
1712	AF016411	Homo sapiens potassium channel subunit KCNA3.1B	2e-43	2708514	(AF016411) KCNA3.1B [Homo sapiens]	3e-13
1713	AC001443	Homo sapiens (subclone 2_f10 from BAC 2913	1e-43	111814	hypothetical protein 3 - rat >gi 56589	2e-06
1714	X82895	H.sapiens mRNA for DLG2	6e-44	2497511	MAGUK P55 SUBFAMILY MEMBER 2 (MPP2 PROTEIN) (DISCS. LARGE HOMOLOG 2)	6e-52
1715	U17077	Human BENE mRNA, partial cds.	3e-44	53912	(X57960) ribosomal protein L7 [Mus musculus] >gi 55489	8e-30
1716	AJ222700	Homo sapiens mRNA for TSC-22 protein	2e-44	<NONE>	<NONE>	<NONE>
1717	J03634	Human erythroid differentiation protein mRNA	2e-44	124279	INHIBIN BETA A CHAIN PRECURSOR PROTEIN) (EDF) >gi 87936 pir B24248 inhibin beta-A chain precursor - human >gi 181947 (J03634) erythroid differentiation protein precursor [Homo sapiens] sapiens] >gi 226350 prf 1608260B inhibin beta.A [Homo sapiens]	0.73

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1718	AB014518	Homo sapiens mRNA for KIAA0618 protein, complete cds	7e-45	1911548	(S80864) cytochrome c-like polypeptide sapiens]	1.6
1719	X76808	H.sapiens genomic DNA clone d2	7e-45	868201	(U29380) similar to adenylate cyclase [Caenorhabditis elegans]	2e-09
1720	AB021288	Homo sapiens mRNA for beta 2-microglobulin, complete cds	2e-45	2465521	(U95995) RNA-dependent RNA polymerase [Cryptosporidium parvum]	0.15
1721	X63468	H.sapiens mRNA for transcription factor TFIIIE alpha	8e-46	<NONE>	<NONE>	<NONE>
1722	AF019226	Homo sapiens D2-2 mRNA, 3'UTR	7e-46	<NONE>	<NONE>	<NONE>
1723	D31764	Human mRNA for KIAA0064 gene, complete cds	2e-46	3123050	HYPOTHETICAL PROTEIN KIAA0064	1e-15
1724	K02774	Human MHC class II HLA-DR-beta-psi (DW4/DR4) pseudogene, exons 3,4, 5,6, clones cosII-3301 and cosII-801.	1e-46	4185946	(Y17834) gag protein [Human endogenous retrovirus K]	2e-14
1725	X92109	H.sapiens hcgIX gene	9e-47	2498185	BRIDE OF SEVENLESS PROTEIN PRECURSOR >gi 1079166 pir A47530 bride of sevenless precursor - fruit fly (Drosophila virilis) >gi 290216 virilis]	1.4
1726	X93334	H.sapiens mitochondrial DNA, complete genome	8e-47	128753	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4 >gi 86696 pir A00435 NADH dehydrogenase (ubiquinone)	4e-15
1727	M85145	Human tumor necrosis factor receptor, 3' flank.	3e-47	<NONE>	<NONE>	<NONE>
1728	X80240	H.sapiens endogenous retrovirus HERV-KC4 DNA	3e-47	4185944	(Y17833) env protein [Human endogenous retrovirus K]	7e-18
1729	Z63594	H.sapiens CpG DNA, clone 8719, forward read cpg8719.frla.	1e-47	3322743	(AE001222) T. pallidum predicted coding region TP0454	2.4

Nearest Neighbor (BlastN vs. Genbank)				Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1730	X62295	R.rattus mRNA for vascular type-1 angiotensin II receptor	4e-48	1209756	(U43629) integral membrane protein [Beta vulgaris]	1e-07
1731	M85145	Human tumor necrosis factor receptor, 3' flank.	3e-48	<NONE>	<NONE>	<NONE>
1732	AB020712	Homo sapiens mRNA for KIAA0905 protein, complete cds	4e-49	4240299	(AB020712) KIAA0905 protein [Homo sapiens]	2e-20
1733	AB020712	Homo sapiens mRNA for KIAA0905 protein, complete cds	3e-49	4240299	(AB020712) KIAA0905 protein [Homo sapiens]	2e-20
1734	X62295	R.rattus mRNA for vascular type-1 angiotensin II receptor	1e-49	1209756	(U43629) integral membrane protein [Beta vulgaris]	7e-12
1735	AJ007509	Homo sapiens mRNA for E1B-55kDa-associated protein	1e-49	3319956	(AJ007509) E1B-55kDa-associated protein	4e-24
1736	X97303	H.sapiens mRNA for Ptg-12 protein	1e-49	466044	HYPOTHETICAL ZINC FINGER PROTEIN ZK686.4 IN CHROMOSOME III >gi 630780 pir S44909 ZK686.4 protein - Caenorhabditis elegans >gi 304346 (L17337) coded for by C. elegans cDNAs GenBank:MS8869 and T01933; putative [Caenorhabditis elegans]	8e-31
1737	AF038404	Homo sapiens homolog of Nedd5 (hNedd5) mRNA, complete cds	4e-50	<NONE>	<NONE>	<NONE>
1738	L43618	Homo sapiens polycystic kidney disease (PKD1) gene, exons 35-42	4e-50	903758	(L43619) polycystic kidney disease 1 protein [Homo sapiens]	3e-1
1739	AF009424	Homo sapiens clone 22 mRNA, alternative splice variant alpha-1, complete cds	4e-50	2271473	(AF009426) clone 22 [Homo sapiens]	5e

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					monosaccharid transport protein	
1740	L77040	Homo sapiens (subclone 8_c11 from P1 H22) DNA sequence.	2e-50	99758	STP4 - Arabidopsis thaliana >gi 16524 (X66857) sugar transport protein [Arabidopsis thaliana]	6.4
1741	L35657	Homo sapiens (subclone H8 5_a10 from P1 35 H5 C8) DNA sequence.	2e-50	2072960	(U93568) p40 [Homo sapiens]	2e-05
1742	U80745	Homo sapiens CTG7a mRNA, partial cds	1e-50	<NONE>	<NONE>	<NONE>
1743	D84514	Bovine mRNA for p97, partial cds	1e-50	3978527	(AF103728) structural polyprotein [Sindbis virus]	9.9
1744	M22960	Human protective protein mRNA, complete cds.	1e-50	131081	LYSOSOMAL PROTECTIVE PROTEIN PRECURSOR (CATHEPSIN A) (CARBOXYPEPTIDASE C) human >gi 190233 (M22960) protective protein precursor	1e-12
1745	X86018	H.sapiens mRNA for MUF1 protein	1e-50	1082610	muf1 protein - human >gi 762953 (X86018) muf1 [Homo sapiens]	1e-21
1746	U03495	Human transcription factor LSF-ID mRNA, complete cds.	7e-51	2136296	transcription factor LSF - human >gi 476099	1e-21
1747	AB015344	Homo sapiens HRIHFB2157 mRNA, partial cds	5e-51	3970874	(AB015344) HRIHFB2157 [Homo sapiens]	2e-35
1748	M93339	Human zinc finger protein mRNA.	4e-51	3024110	MYC-ASSOCIATED ZINC FINGER PROTEIN sapiens]	2e-06
1749	U71363	Human zinc finger protein zfp6 (ZF6) mRNA, partial cds	4e-51	2689441	(AC003682) FIS547_1 [Homo sapiens]	2e-11
1750	X56932	H.sapiens mRNA for 23 kD highly basic protein	4e-51	730451	60S RIBOSOMAL PROTEIN L13A (23 KD HIGHLY BASIC PROTEIN) >gi 345897 pir S29539 basic protein. 23K - human >gi 23691 (X56932) 23 kD highly basic protein [Homo sapiens]	1e-11
1751	Z79054	H.sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA21E11	2e-51	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Homo sapiens				
1752	AF068245	BAF60b gene. partial sequence	5e-52	<NONE>	<NONE>	<NONE>
1753	AJ236932	Sus scrofa mRNA for hypothetical protein (5' clone 4B8)	5e-52	400927	RIBONUCLEOPROTEIN RB97D ribonucleoprotein [Drosophila melanogaster]	4.7
1754	AF003693	Mus musculus scaffold protein Pbp1 homolog mRNA, complete cds	6e-53	2197106	(AF003693) scaffold protein Pbp1 homolog [Mus musculus]	2e-54
1755	M27319	Human calmodulin mRNA, complete cds.	5e-53	115528	CALMODULIN >gi 102408 pir JC1309 calmodulin - Stylyonchia lemnae (SGC5) >gi 161195	0.002
1756	M74555	Mouse house-keeping protein mRNA, complete cds.	5e-53	284775	house-keeping protein - mouse >gi 193871	5e-30
1757	X92720	H.sapiens mRNA for phosphoenolpyruvate carboxykinase	6e-54	2135915	phosphoenolpyruvate carboxykinase (GTP) (EC 4.1.1.32) precursor, mitochondrial - human carboxykinase (GTP) [Homo sapiens]	6e-21
1758	AF007872	Homo sapiens torsinB (DQ1) mRNA, partial cds	2e-54	2760121	(AB002405) LAK-4p [Homo sapiens]	0.27
1759	U49507	Mus musculus B6CBA Lisch7 mRNA, partial cds.	2e-54	1236083	(U49507) Lisch7 [Mus musculus]	3e-27
1760	Z73360	Human DNA sequence from cosmid 92M18. BRCA2 gene region chromosome 13q12-13.	1e-55	2370371	(Y14657) hydrophobin [Pleurotus ostreatus] >gi 2982620 gnl PID e1283986 (AJ225061) POH2 hydrophobin [Pleurotus ostreatus]	2.0
1761	U83702	Human cytochrome c oxidase subunit VIa gene, exon 3 and complete cds	8e-56	2982994	(AE000682) hypothetical protein [Aquifex aeolicus]	7.0
1762	Y12781	Homo sapiens mRNA for transducin (beta) like 1 protein	7e-56	3021409	(Y12781) transducin (beta) like 1 protein [Homo sapiens]	7e-59

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1763	AB020673	Homo sapiens mRNA for KIAA0866 protein, complete cds	8e-57	2104553	(AF001548) Myosin heavy chain (MHY11) (5'partial) [Homo sapiens]	4e-04
1764	AJ236932	Sus scrofa mRNA for hypothetical protein (5' clone 4B8)	3e-57	400927	RIBONUCLEOPROTEIN RB97D ribonucleoprotein [Drosophila melanogaster]	4.7
1765	L06900	Human dystrophin gene, intron 1 containing pseudo exon.	1e-58	4185129	(AC005724) unknown protein [Arabidopsis thaliana] thaliana]	7.0
1766	X93334	H.sapiens mitochondrial DNA, complete genome	9e-59	1492050	(U60315) MC107L [Molluscum contagiosum virus subtype 1]	0.17
1767	AF064856	Rattus sp. 7acomp protein mRNA, complete cds	3e-59	3169626	(AF064856) 7acomp protein [Rattus sp.]	2e-31
1768	AF081484	Homo sapiens alpha-tubulin isoform 1 mRNA, complete cds	2e-59	32015	(X06956) alpha-tubulin [Homo sapiens]	4e-22
1769	X71427	Homo sapiens mRNA for FUS-CHOP protein fusion	1e-60	746557	(U23523) histidine-rich [Caenorhabditis elegans]	0.45
1770	AF013988	Homo sapiens serine protease mRNA, complete cds	1e-60	2564316	(AB006622) No similarities to any reported proteins [Homo sapiens]	0.26
1771	U25691	Mus musculus lymphocyte specific helicase mRNA, complete cds	7e-61	2137490	lymphocyte specific helicase - mouse musculus]	3e-25
1772	X93334	H.sapiens mitochondrial DNA, complete genome	4e-61	70656	ubiquitin / ribosomal protein S27a - human extension protein, HUBCEP80 [human, Peptide, 156 aa] ubiquitin extention protein [Cavia porcellus]	9e-08
1773	D38255	Homo sapiens mRNA for CAB1, complete cds	4e-61	2135214	gene MLN 64 protein - human	4e-23
1774	U25691	Mus musculus lymphocyte specific helicase mRNA, complete cds	8e-62	2137490	lymphocyte specific helicase - mouse musculus]	8e-26

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1775	M21731	Human lipocortin-V mRNA. complete cds.	6e-62	3212603	Human Annexin V With Proline Substitution By Thioproline	2e-20
1776	AF021936	Rattus norvegicus myotonic dystrophy kinase-related Cdc42-binding kinase MRCK-beta (MRCK-beta) mRNA. complete cds	2e-62	2736153	(AF021936) myotonic dystrophy kinase-related Cdc42-binding kinase MRCK-beta [Rattus norvegicus]	3e-27
1777	Y12059	H.sapiens HUNKI mRNA	1e-62	3184498	(AC004798) R31546_1 [Homo sapiens]	3e-09
1778	L37368	Human (clone E5.1) RNA-binding protein mRNA. complete cds.	6e-63	477578	sialidase - Actinomyces viscosus >gi 141852	7.8
1779	M27877	Figure 2. Nucleotide and translated protein sequences of HPF1, -2, and -9.	5e-63	1731443	ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1) >gi 106023 pir A32891 finger protein 1, placental - human	3e-33
1780	AF095448	Homo sapiens putative G protein-coupled receptor	2e-63	3116131	(AL023288) hypothetical protein	4.6
1781	L19437	Human transaldolase mRNA containing transposable element. complete cds	2e-63	1553119	(U63159) transaldolase [Mus musculus]	4e-18
1782	L41351	Homo sapiens prostatic mRNA. complete cds	1e-63	2833277	PROSTASIN PRECURSOR precursor - human >gi 862305 (L41351) prostatic [Homo sapiens] >gi 1143194 (U33446) prostatic [Homo sapiens]	6e-14
1783	AF053470	Homo sapiens 10kD protein (BC10) mRNA. complete cds	6e-64	482237	hypothetical protein K03H1.9 - Caenorhabditis elegans	0.029

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1784	D37791	Mouse mRNA for beta-1,4-galactosyltransferase	6e-64	3880102	(Z95590) similar to FYVE zinc finger; cDNA EST yk265b4.5 comes from this gene; cDNA EST yk359g9.5 comes from this gene; cDNA EST yk319c2.5 comes from this gene [Caenorhabditis elegans] zinc finger; cDNA EST yk265b4.5 comes from this gene; cDNA EST yk359g9.5 comes from this gene; cDNA EST yk319c2.5 comes from this gene [Caenorhabditis elegans]	3e-16
1785	AF015770	Mus musculus radical fringe (radical-fringe) mRNA, complete cds	6e-64	2204355	(U94350) radical fringe precursor [Mus musculus]	1e-36
1786	Z79054	H.sapiens flow-sorted chromosome 6 HindIII fragment. SC6pA21E11	2e-64	<NONE>	<NONE>	<NONE>
1787	M83094	Homo sapiens cytosolic selenium-dependent glutathione peroxidase gene, complete cds, and rhoh12 gene, 3' end.	1e-64	2447063	(U42580) A565R [Paramecium bursaria Chlorella virus 1]	8.8
1788	Y10211	H.sapiens LAG-3 gene, promoter region	7e-65	1944540	(X14112) tegument protein [human herpesvirus 1]	2.3
1789	M19045	Human lysozyme mRNA, complete cds.	2e-65	<NONE>	<NONE>	<NONE>
1790	U01882	Homo sapiens SS-A/Ro autoantigen 52 kda component gene, complete cds	2e-65	585401	LIPASE MODULATOR PRECURSOR (LIPASE HELPER PROTEIN) >gi 480045 pir S36249 lipB protein - Pseudomonas glumae >gi 49207 (X70354) helper protein	4.2
1791	AF069517	Homo sapiens RNA binding protein DEF-3 mRNA, complete cds	2e-65	3212101	(AF069517) RNA binding protein DEF-3 [Homo sapiens]	1e-25

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Homo sapiens jerky gene product homolog mRNA, complete cds				
1792	AF004715		2e-65	2314829	(AF004715) jerky gene product homolog [Homo sapiens]	2e-45
1793	X59652	C. longicaudatus hprt mRNA for hypoxanthine	3e-66	631625	hypoxanthine (guanine) phosphoribosyltransferase - long-tailed hamster phosphoribosyltransferase [Cricetus longicaudatus]	6e-54
1794	U94350	Mus musculus radical fringe precursor mRNA, complete cds	3e-67	2204355	(U94350) radical fringe precursor [Mus musculus]	2e-33
1795	AF015811	Mus musculus putative lysophosphatidic acid acyltransferase mRNA, complete cds	3e-68	2317725	(AF015811) putative lysophosphatidic acid acyltransferase [Mus musculus]	7e-51
1796	J03137	Cow phosphoinositide-specific phospholipase C	3e-69	226908	phospholipase C 154 [Bos taurus]	3e-25
1797	AF044574	Rattus norvegicus putative peroxisomal 2,4-dienoyl-CoA reductase (DCR-AKL) mRNA, complete cds	1e-69	4105269	(AF044574) putative peroxisomal 2,4-dienoyl-CoA reductase [Rattus norvegicus]	2e-33
1798	AF015811	Mus musculus putative lysophosphatidic acid acyltransferase mRNA, complete cds	4e-70	2317725	(AF015811) putative lysophosphatidic acid acyltransferase [Mus musculus]	3e-19
1799	X65157	M.musculus mRNA for desmoyokin, partial	5e-74	109781	desmoyokin - mouse (fragment) >gi50675	9e-37
1800	Z97207	Mus musculus mRNA for B-IND1 protein	2e-74	2231019	(Z97207) B-IND1 protein [Mus musculus]	6e-21
1801	U27196	Gallus gallus zinc finger protein (Fzf-1) mRNA, complete cds.	6e-75	984814	(U27196) zinc finger protein [Gallus gallus] gallus]	2e-44

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					70 KD WD-REPEAT TUMOR-SPECIFIC ANTIGEN >gi 2505957 gnl PID e353992 (Y15054) 70 kD tumor-specific antigen [Rattus norvegicus]	
1802	Y15054	Rattus norvegicus mRNA for 70 kDa tumor specific antigen, partial	3e-77	3123027		4e-42
1803	X65157	M.musculus mRNA for desmoyokin, partial	3e-79	109781	desmoyokin - mouse (fragment) >gi 50675	9e-33
1804	U50736	Rattus norvegicus cardiac adriamycin responsive protein mRNA, complete cds	2e-84	1362781	cytokine inducible nuclear protein C193 - human >gi 793841 (X83703) nuclear protein [Homo sapiens]	7e-30
1805	AF072865	Rattus norvegicus thioredoxin reductase (TrxR2) mRNA, nuclear gene encoding mitochondrial protein, complete cds	2e-84	3757888	(AF072865) thioredoxin reductase [Rattus norvegicus]	6e-43
1806	AF044574	Rattus norvegicus putative peroxisomal 2,4-dienoyl-CoA reductase (DCR-AKL) mRNA, complete cds	6e-85	4105269	(AF044574) putative peroxisomal 2,4-dienoyl-CoA reductase [Rattus norvegicus]	1e-41
1807	U19181	Rattus norvegicus Rabin3 mRNA, complete cds	2e-87	624225	(U19181) Rabin3 [Rattus norvegicus]	2e-41
1808	U40342	Mus musculus ninein mRNA, complete cds	1e-91	1113865	(U40342) ninein [Mus musculus]	2e-36
1809	X67877	R.norvegicus mRNA for cytosolic resiniferatoxin-binding protein	4e-92	136077	TROPOMYOSIN BETA 3, FIBROBLAST chicken >gi 515694 (M23082) tropomyosin [Gallus gallus]	0.56
1810	AF044574	Rattus norvegicus putative peroxisomal 2,4-dienoyl-CoA reductase (DCR-AKL) mRNA, complete cds	5e-93	4105269	(AF044574) putative peroxisomal 2,4-dienoyl-CoA reductase [Rattus norvegicus]	1e-50
1811	AF035527	Mus musculus EHF (Ehf) mRNA, complete cds	2e-95	3138930	(AF035527) EHF [Mus musculus]	2e-47

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1812	AB016930	Cricetus griseus mRNA for Phosphatidylglycerophosphate synthase, complete cds	6e-96	4159682	(AB016930) Phosphatidylglycerophosphate synthase [Cricetus griseus]	7e-41
1813	AB005549	Rattus norvegicus mRNA for atypical PKC specific binding protein, complete cds	7e-97	3868778	(AB005549) atypical PKC specific binding protein [Rattus norvegicus]	3e-41
1814	X90849	G.gallus PB1 gene	2e-97	2134381	polybromo 1 protein - chicken chicken >gi 951231 (X90849) polybromo 1 protein [Gallus gallus]	1e-34
1815	S79873	h-lamp-2=lysosome-associated membrane protein-2 protein-2b (LAMP2) mRNA, alternatively spliced form h-lamp-2b, complete cds.	3e-98	<NONE>	<NONE>	<NONE>
1816	U67203	Mus musculus ACF7 neural isoform 1 (mACF7) mRNA, partial cds	2e-98	1675224	(U67204) ACF7 neural isoform 2 [Mus musculus]	9e-39
1817	L14684	Rattus norvegicus nuclear-encoded mitochondrial elongation factor G mRNA, complete cds.	e-100	585084	ELONGATION FACTOR G, MITOCHONDRIAL PRECURSOR (MEF-G) >gi 543383 pir S40780 translation elongation factor G, mitochondrial - rat >gi 310102	2e-30
1818	X84692	M.musculus Spnr mRNA for RNA binding protein	e-133	1363238	spermatid perinuclear RNA-binding protein Spnr - mouse >gi 673454 (X84692) spermatid perinuclear RNA binding protein [Mus musculus]	5e-35
1819	U50736	Rattus norvegicus cardiac adriamycin responsive protein mRNA, complete cds	e-113	1362781	cytokine inducible nuclear protein C193 - human >gi 793841 (X83703) nuclear protein [Homo sapiens]	2e-36
1820	S66855	HoxB9=Hox-2.5 [mice, embryos, mRNA Partial, 786 nt]	e-107	1708355	HOMEODOMAIN PROTEIN HOX-B9 (HOX-2.5)	8e-37

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		HoxB9=Hox-2.5				
1821	S66855	[mice, embryos, mRNA Partial, 786 nt]	e-108	1708355	HOMEBOX PROTEIN HOX-B9 (HOX-2.5)	4e-37
1822	U92072	Rattus norvegicus m-tomosyn mRNA, complete cds	e-102	3790389	(U92072) m-tomosyn [Rattus norvegicus]	2e-38
1823	D17577	Mouse mRNA for kinesin-like protein (Kif1b), complete cds	e-129	2497524	KINESIN-LIKE PROTEIN KIF1B mouse >gi 407339 gnl PID d1005029 (D17577) Kif1b [Mus musculus]	2e-39
1824	AF062484	Mus musculus SDP8 mRNA, complete cds	e-122	3126981	(AF062484) SDP8 [Mus musculus]	5e-40
1825	X73683	R.norvegicus mRNA for histone H3.3	e-109	122075	(H3.3Q) histone H3.3 - fruit fly (Drosophila melanogaster) histone H3.3B - chicken >gi 2119023 pir S61218 histone H3.3 - fruit fly (Drosophila hydei) 1-136 [Oryctolagus cuniculus] >gi 8046 (X55822) Histone H3.3Q gene product [Drosophila melanogaster] >gi 51198 gallus] >gi 161190 (M17876) histone H3 [Spisula solidissima] >gi 211853 (M11393) histone 3.3 [Gallus gallus] >gi 306848 (M11354) H3.3 histone [Homo sapiens melanogaster] >gi 963031 (X81205) histone H3.3 H3.3A variant [Drosophila melanogaster] musculus]	2e-40
1826	U67203	Mus musculus ACF7 neural isoform 1 (mACF7) mRNA, partial cds	e-102	1675224	(U67204) ACF7 neural isoform 2 [Mus musculus]	2e-40
1827	D17577	Mouse mRNA for kinesin-like protein (Kif1b), complete cds	e-131	2497524	KINESIN-LIKE PROTEIN KIF1B mouse >gi 407339 gnl PID d1005029 (D17577) Kif1b [Mus musculus]	7e-42

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1828	AB016930	Cricetulus griseus mRNA for Phosphatidylglycerophosphate synthase, complete cds	e-131	4159682	(AB016930) Phosphatidylglycerophosphate synthase [Cricetulus griseus]	3e-43
1829	U09874	Mus musculus SKD3 mRNA, complete cds.	e-122	2493735	SKD3 PROTEIN SKD3 [Mus musculus]	7e-48
1830	X99145	C.familiaris mRNA for C3VS protein	e-110	1429314	(X99145) overexpressed in thyroid tissue after TSH stimulation [Canis familiaris]	2e-49
1831	X99836	P.walti mRNA for rnp associated protein 55	e-106	4200286	(X99836) rap55 [Pleurodeles walti]	2e-50
1832	AF077003	Mus musculus SH3 domain-containing adapter protein mRNA, complete cds	e-121	3550240	(AF077003) SH3 domain-containing adapter protein; CD2AP	3e-51
1833	AF060246	Mus musculus strain C57BL/6 zinc finger protein 106 (Zfp106) mRNA, H3a-a allele, complete cds	e-118	3372657	(AF060246) zinc finger protein 106 [Mus musculus]	1e-52
1834	Z14030	R.norvegicus mRNA for TRAP-complex gamma subunit.	e-120	1174453	TRANSLUCON-ASSOCIATED PROTEIN, GAMMA SUBUNIT (TRAP-GAMMA) (SIGNAL SEQUENCE RECEPTOR GAMMA SUBUNIT) (SSR-GAMMA) >gi 423185 pir S33294 translocon-associated protein gamma chain - rat norvegicus]	7e-54
1835	AF077003	Mus musculus SH3 domain-containing adapter protein mRNA, complete cds	e-132	3550240	(AF077003) SH3 domain-containing adapter protein; CD2AP	5e-54
1836	L20427	Rattus norvegicus dihydroxypolyprenylbenzoate methyltransferase mRNA, complete cds	e-116	457372	(L20427) dihydroxypolyprenylbenzoate methyltransferase dihydroxypolyprenylbenzoate methyltransferase [Rattus norvegicus]	4e-56

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1837	X80169	M.musculus mRNA for 200 kD protein	e-122	1717793	PROTEIN TSG24 (MEIOTIC CHECK POINT REGULATOR) >gi 1083553 pir A55117 tsg24	2e-56
1838	AF080568	Rattus norvegicus CTP:phosphoethanolamine cytidyltransferase mRNA. complete cds	e-119	3396102	(AF080568) CTP:phosphoethanolamine cytidyltransferase	6e-58
1839	X99145	C.familiaris mRNA for C3VS protein	e-121	1429314	(X99145) overexpressed in thyroid tissue after TSH stimulation [Canis familiaris]	2e-58
1840	AF019075	Pan troglodytes breast and ovarian cancer susceptibility (BRCA1) gene. partial cds	e-145	2218154	(AF005068) breast and ovarian cancer susceptibility protein splice variant [Homo sapiens]	1e-55
1841	U55042	Bos taurus myosin X. complete cds	e-122	1755049	(U55042) myosin X [Bos taurus]	1e-61
1842	AJ007780	Mus musculus mRNA for poly(ADP-ribose) polymerase-2	e-119	3283975	(AF072521) poly-(ADPribosyl)-transferase homolog PARP	4e-62
1843	AF072865	Rattus norvegicus thioredoxin reductase (TrxR2) mRNA. nuclear gene encoding mitochondrial protein. complete cds	e-105	3757888	(AF072865) thioredoxin reductase [Rattus norvegicus]	3e-62
1844	U55042	Bos taurus myosin X. complete cds	e-121	1755049	(U55042) myosin X [Bos taurus]	1e-62
1845	X61506	Mouse E46 mRNA for E46 protein	e-139	114909	BRAIN PROTEIN E46	9e-67
1846	D90335	Bovine mRNA for GTP-binding protein alpha-subunit	e-148	585174	GUANINE NUCLEOTIDE-BINDING PROTEIN, ALPHA-14 SUBUNIT (GLI) >gi 108711 pir A40891 GTP-binding protein GLI alpha chain - bovine protein, alpha-subunit [Bos taurus]	2e-69
1847	U49507	Mus musculus B6CBA Lisch7 mRNA. partial cds.	e-140	2121326	(AC002128) Lisch7 [Homo sapiens]	2e-74

Table 4

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
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22	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
23	<NONE>	<NONE>	<NONE>	1079469	tMDC I protein - crab-eating macaque	9.3
24	<NONE>	<NONE>	<NONE>	3043656	(AB011138) KIAA0566 protein [Homo sapiens]	9.3
25	<NONE>	<NONE>	<NONE>	112175	potassium channel protein RK5 - rat protein [Rattus norvegicus]	8.6
26	<NONE>	<NONE>	<NONE>	3769624	(AF091565) olfactory receptor [Rattus norvegicus]	7.2
27	<NONE>	<NONE>	<NONE>	3876443	(Z81517) F23B1.6 [Caenorhabditis elegans]	7.1
28	<NONE>	<NONE>	<NONE>	2224464	(AB001684) ORF249 [Chlorella vulgaris]	6.9
29	<NONE>	<NONE>	<NONE>	1519707	(U67940) ORFveg106: random cDNA sequence [Dictyostelium discoideum]	6.7
30	<NONE>	<NONE>	<NONE>	227491	protein kinase C II [Xenopus laevis]	6.7
31	<NONE>	<NONE>	<NONE>	630575	C50C3.4 protein - Caenorhabditis elegans	6.0
32	<NONE>	<NONE>	<NONE>	137290	35 KD PROTEIN IN RNA2 clover necrotic mosaic virus >gi 61466 (X08021) ORF for 35 kDa polypeptide (AA 1-317) [Red clover necrotic mosaic virus]	6.0

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
33	<NONE>	<NONE>	<NONE>	30041	(X16711) pid:g30041 [Homo sapiens]	5.9
34	<NONE>	<NONE>	<NONE>	2493585	CELL DIVISION PROTEIN FTSW	5.7
35	<NONE>	<NONE>	<NONE>	1001450	(D63999) hypothetical protein	5.7
36	<NONE>	<NONE>	<NONE>	3182918	NITROGEN REGULATORY PROTEIN AREA	5.2
37	<NONE>	<NONE>	<NONE>	140011	MITOCHONDRIAL RIBOSOMAL PROTEIN S5 Emericella nidulans mitochondrion (SGC3) >gi 12709 nidulans> >gi 472822 (J01390) unknown protein (AL034393) predicted using Genefinder; similar to WD domain, G-beta repeat; cDNA EST yk362f7.5 comes from this gene; cDNA EST yk362f7.3 comes from this gene [Caenorhabditis elegans]	4.3
38	<NONE>	<NONE>	<NONE>	3979943	(U31329) polyketide synthase [Aspergillus terreus]	4.0
39	<NONE>	<NONE>	<NONE>	950203	(AL031530) hypothetical zinc finger protein [Schizosaccharomyces pombe]	3.3
40	<NONE>	<NONE>	<NONE>	3560232	AXONEME-ASSOCIATED PROTEIN MST101(1) product [Drosophila hydei]	3.0
41	<NONE>	<NONE>	<NONE>	730071	HYPOTHETICAL 21.7 KD PROTEIN IN INTE-PIN INTERGENIC REGION >gi 1787402 (AE000214) orf, hypothetical protein [Escherichia coli]	2.6
42	<NONE>	<NONE>	<NONE>	2506641	(AF071556) anthranilate dioxygenase large subunit	2.5
43	<NONE>	<NONE>	<NONE>	3511232	(U43139) envelope glycoprotein gp120 [Human immunodeficiency virus type 1]	2.4
44	<NONE>	<NONE>	<NONE>	1150900	(Z75536) similar to dynein heavy chain; cDNA EST EMBL:D27549 comes from this gene; cDNA EST EMBL:D34859 comes from this gene [Caenorhabditis elegans]	1.9
45	<NONE>	<NONE>	<NONE>	3876099		1.4

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
46	<NONE>	<NONE>	<NONE>	3881150	(AL032647) predicted using Genefinder	1.4
47	<NONE>	<NONE>	<NONE>	132200	COLANIC ACID CAPSULAR BIOSYNTHESIS ACTIVATION PROTEIN A >gi 95605 pir S17701 rcsA protein	1.1
48	<NONE>	<NONE>	<NONE>	2204286	(U61380) germination protein [Bacillus megaterium]	1.0
49	<NONE>	<NONE>	<NONE>	1723955	HYPOTHETICAL 11.4 KD PROTEIN IN FOX1-KEX1 INTERGENIC REGION >gi 2132566 pir S64222 probable membrane protein YGL204c - yeast (Saccharomyces cerevisiae) >gi 1322838 gnl PID e243803 (Z72726) ORF YGL204c [Saccharomyces cerevisiae]	0.84
50	<NONE>	<NONE>	<NONE>	3201564	(AJ006514) prolipoprotein diacylglycerol transferase [Vibrio cholerae]	0.31
51	<NONE>	<NONE>	<NONE>	2808721	(AL021428) hypothetical protein Rv0064	0.27
52	<NONE>	<NONE>	<NONE>	602434	(U17986) GABA/noradrenaline transporter [Homo sapiens]	0.13
53	<NONE>	<NONE>	<NONE>	3347955	(AF076184) cytosolic sorting protein PACS-1b [Rattus norvegicus]	0.12
54	<NONE>	<NONE>	<NONE>	1255887	(U55544) coded for by C. elegans cDNA yk92b4.5; coded for by C. elegans cDNA yk73a1.5; coded for by C. elegans cDNA yk102e9.5; coded for by C. elegans cDNA yk71c8.5; coded for by C. elegans cDNA yk66d11.5; coded for by C. elegans cDNA yk66c3...	0.074
55	<NONE>	<NONE>	<NONE>	103076	Bkm-like sex-determining region hypothetical protein CS314 - fruit fly (Drosophila melanogaster)	0.003
56	<NONE>	<NONE>	<NONE>	107560	Ras inhibitor (clone JC265) - human sapiens]	0.002

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					Bkm-like sex-determining	
57	<NONE>	<NONE>	<NONE>	103076	region hypothetical protein CS314 - fruit fly (<i>Drosophila melanogaster</i>)	2e-04
58	<NONE>	<NONE>	<NONE>	2702370	(AF038604) contains similarity to <i>Drosophila</i> ovarian tumor locus protein (GB:X13693) [<i>Caenorhabditis elegans</i>]	6e-05
59	<NONE>	<NONE>	<NONE>	3859713	(AL033501) phox domain protein [<i>Candida albicans</i>]	3e-05
60	<NONE>	<NONE>	<NONE>	2088839	(AF003386) F59E12.5 gene product [<i>Caenorhabditis elegans</i>]	2e-08
61	<NONE>	<NONE>	<NONE>	121059	GC-RICH SEQUENCE DNA-BINDING FACTOR GCF - human >gi179412 (M29204) DNA-binding factor [<i>Homo sapiens</i>]	4e-09
62	<NONE>	<NONE>	<NONE>	3875246	(Z81490) similar to WD domain, G-beta repeats (2 domains); cDNA EST EMBL:T00482 comes from this gene; cDNA EST EMBL:T00923 comes from this gene; cDNA EST yk449d4.3 comes from this gene; cDNA EST yk449d4.5 comes from this gen...	9e-24
63	<NONE>	<NONE>	<NONE>	1465834	(U64857) No definition line found [<i>Caenorhabditis elegans</i>]	9e-28
64	<NONE>	<NONE>	<NONE>	3327136	(AB014561) KIAA0661 protein [<i>Homo sapiens</i>]	1e-29
65	<NONE>	<NONE>	<NONE>	3880433	(Z66521) similar to mitochondrial RNA splicing MSR4 like protein; cDNA EST EMBL:C09217 comes from this gene [<i>Caenorhabditis elegans</i>]	8e-31
66	D42133	Rat annexin V gene, exon7 and exon8	5.0	<NONE>	<NONE>	<NONE>
67	L35679	Homo sapiens (subclone H8 2_d11 from P1 35 H5 C8) DNA sequence.	5.0	1086902	(U41278) coded for by <i>C. elegans</i> cDNA yk79g8.5; coded for by <i>C. elegans</i> cDNA cm10c8; coded for by <i>C. elegans</i> cDNA yk79g8.3; similar to leucine-rich repeats found in many proteins [<i>Caenorhabditis elegans</i>]	6.6

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		HIV-1 strain BX220				
68	U90184	from USA, envelope glycoprotein C2V3 region (env) gene, partial cds	5.0	1297070	(Z71986) convicilin precursor [Vicia narbonensis]	6.6
69	U61465	Human myosin VIIa (MYO7A) gene, 5' exon 37	5.0	2313225	(AE000535) L-lactate permease (lctP) [Helicobacter pylori 26695]	5.0
70	AF013717	Homo sapiens periplakin (PPL) mRNA, partial cds	5.0	3719238	(AF064869) brain-enriched guanylate kinase-associated protein 2; BEGA2 [Rattus norvegicus]	3.8
71	X58245	Soybean mRNA for HMG-1 like protein	5.0	2995363	(AL022245) biotin synthase	0.99
72	AF102425	Fraseria paniculata tRNA-Leu (tmL) gene, intron, chloroplast sequence	4.9	3522958	(AC004411) putative pectinesterase [Arabidopsis thaliana]	6.4
73	X82817	H.sapiens PTP1C/HCP-variant gene	4.9	3875514	(Z81494) cDNA EST EMBL:D27474 comes from this gene; cDNA EST EMBL:D27473 comes from this gene; cDNA EST EMBL:T00471 comes from this gene; cDNA EST EMBL:D34192 comes from this gene; cDNA EST EMBL:D37241 comes from this gene; ...	2.8
74	U04827	Mus musculus brain fatty acid-binding protein	4.9	3676132	(AL031765) 1-evidence=predicted by content; 1-method=genefinder;084; 1-method_score=31.96; 1-evidence_end; 2-evidence=predicted by match; 2-match_accession=SPTREMBL:Q93319; 2-match_description=HYPOTHETICAL PROTEIN C33A11.2;...	2e-09
75	AF038859	Neospora hughesi strain NE1 internal transcribed spacer 1, complete sequence	4.8	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		M.musculus MFH-1				
76	Y08222	gene	4.8	<NONE>	<NONE>	<NONE>
77	AJ224475	Borrelia burgdorferi left chromosomal subtelomeric region (pfpB gene)	4.8	4218141	(AJ236702) HMR1 protein [Antirrhinum majus]	8.3
78	U02486	Mus musculus LAF putative membrane protein (KRAG) gene, exon 3 and complete cds	4.8	3258103	(AP000006) 367aa long hypothetical protein [Pyrococcus horikoshii]	2.7
79	AB000280	Rat mRNA for peptide/histidine transporter, complete cds	4.8	806317	(M29067) unknown protein [Saccharomyces cerevisiae]	0.001
80	Z49771	A.cepa mitochondrial gene for NADH dehydrogenase subunit 3 and ribosomal protein S12	4.5	<NONE>	<NONE>	<NONE>
81	M63494	Mouse IgG receptor (beta-Fc-gamma-RII) gene, exons 6 and 7, clones lambda-Fc(3.2.93).	4.3	<NONE>	<NONE>	<NONE>
82	Z14035	S.pombe car1 gene	2.0	3790665	(AF099000) No definition line found [Caenorhabditis elegans]	1.2
83	U17129	Rhodococcus erythropolis ThcA (thcA) gene, complete cds; and unknown genes	2.0	2828280	(AL021687) putative protein [Arabidopsis thaliana] >gi 2832633 gnl PID e1249651 (AL021711) putative protein [Arabidopsis thaliana]	2e-26
84	AE001386	Plasmodium falciparum chromosome 2, section 23 of 73 of the complete sequence	2.0	4176500	(AL031177) dJ889M15.3 (novel protein)	9e-59
85	U79292	Human clone 23734 mRNA sequence	1.9	<NONE>	<NONE>	<NONE>
86	V00159	Chloroplast Euglena gracilis gene coding for the 5S and 16S rRNA.	1.9	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	1.9	<NONE>	<NONE>	<NONE>
87	U95094					
88	X93206	H. salinarium TATA box-binding protein genes and ORFs	1.9	<NONE>	<NONE>	<NONE>
89	U60979	Caenorhabditis elegans programmed cell death specifier (ces-2) gene, complete cds	1.9	<NONE>	<NONE>	<NONE>
90	X56272	C. tentans ORFs (A-E) for hemoglobin	1.9	<NONE>	<NONE>	<NONE>
91	L22383	Homo sapiens DNA sequence, repeat region.	1.9	<NONE>	<NONE>	<NONE>
92	U82814	Hirudo medicinalis neuron-specific protein mRNA, complete cds	1.9	3822533	(AF094531) immunoglobulin heavy chain precursor	2.0
93	U18504	Haplomitrium hookeri 18S rRNA gene, partial sequence.	1.9	1083969	hypothetical protein 6 - fowlpox virus virus]	2.0
94	X53676	Pseudomonas stutzeri nosDFY genes involved in copper processing	1.9	2980781	(AL022198) putative protein	0.70
95	U60086	Dictyostelium discoideum multidrug resistance transporter/Ser protease (tagC) mRNA, complete cds.	1.9	3879530	(Z49130) cDNA EST yk486b9.3 comes from this gene; cDNA EST yk486b9.5 comes from this gene	6e-05
96	U33447	Human putative G-protein-coupled receptor (GPR17) gene, complete cds	1.9	3880034	(Z75550) similar to cell division control protein [Caenorhabditis elegans]	7e-14
97	M81327	Sus scrofa lactoferrin mRNA, complete cds. > :: gb I28421 I28421 Sequence 5 from patent US 5571691	1.8	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		S.iniae lctP & lctO genes and ORF1				
98	Y07622		1.8	<NONE>	<NONE>	<NONE>
99	M60474	Mouse myristoylated alanine-rich C-kinase substrate (MARCKS) mRNA, complete cds.	1.8	<NONE>	<NONE>	<NONE>
100	Y13901	Homo sapiens FGFR-4 gene	1.8	<NONE>	<NONE>	<NONE>
101	U44400	Human Down Syndrome region of chromosome 21, clone A31D6-1D6.	1.8	<NONE>	<NONE>	<NONE>
102	U92808	Ruminococcus albus beta-glucosidase (gluA) mRNA, complete cds	1.8	<NONE>	<NONE>	<NONE>
103	L25051	Candida albicans argininosuccinate lyase (ARG4) gene, complete cds.	1.8	<NONE>	<NONE>	<NONE>
104	AE000546	Helicobacter pylori 26695 section 24 of 134 of the complete genome	1.8	<NONE>	<NONE>	<NONE>
105	J00978	Xenopus laevis major beta-globin gene, complete cds.	1.8	<NONE>	<NONE>	<NONE>
106	U41716	Human immunodeficiency virus type 1 isolate JW95-5, vpr gene, complete cds.	1.8	<NONE>	<NONE>	<NONE>
107	X66286	G.gallus mRNA for tensin	1.8	<NONE>	<NONE>	<NONE>
108	U76636	Xenopus calbindin D28k mRNA, complete cds	1.8	<NONE>	<NONE>	<NONE>
109	J00664	rabbit embryonic beta-4-globin gene.	1.8	<NONE>	<NONE>	<NONE>
110	M21535	Human erg protein (ets-related gene) mRNA, complete cds.	1.8	2983160	(AE000693) hypothetical protein [Aquifex aeolicus]	7.7

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Rat troponin T			(Z46595) incomplete interleukin	
111	M80829	cardiac isoform gene, complete cds	1.8	999450	11 receptor isoform [Homo sapiens]	7.3
					BRANCHED-CHAIN AMINO ACID TRANSPORT SYSTEM CARRIER PROTEIN (BRANCHED-CHAIN AMINO ACID UPTAKE CARRIER) >gi 1075007 pir D64056 membrane-associated component, branched amino acid transport system (brnQ) homolog - Haemophilus influenzae (strain Rd KW20) system II carrier protein (brnQ) [Haemophilus influenzae Rd]	
112	D37887	Cyprinus carpio c-myc gene for c-Myc, complete cds	1.8	3023408		7.2
		Homo sapiens G protein-coupled receptor kinase 1 and G protein-coupled receptor kinase 1b (GRK1) gene, alternatively spliced, alternative exon 6, exon 7, and partial cds				
113	AF019765		1.8	498643	(U10270) G-box binding factor 1 [Zea mays]	7.2
		Helicobacter pylori J166 virulence regulon transcriptional activator homolog gene, partial cds, strain-specific genomic sequence B2				
114	AF025967		1.8	3850108	(AL033388) putative calcium-transporting atpase [Schizosaccharomyces pombe]	5.7
					PROBABLE HYDROXYACYLGLUTATHIONE HYDROLASE (GLYOXALASE II) (GLX II) protein [Escherichia coli] >gi 1786406 (AE000130) probable hydroxyacylglutathione hydrolase [Escherichia coli]	
115	U13183	Xenopus laevis (Xwnt-4) mRNA, complete cds.	1.8	2494853		5.5

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
116	S68944	Na+/Cl(-)-dependent neurotransmitter transporter	1.8	2276316	(Z96810) GLYT-1 LIKE [Homo sapiens]	5.5
117	M92905	Rat calcium channel alpha-1 subunit (rbB-I) mRNA, complete cds.	1.8	3165522	(AF067607) Similar to cuticular collagen; C18H7.3	5.5
118	X12429	Xenopus laevis U1 70K gene exon 10	1.8	2735957	(AF015685) reverse transcriptase domain protein (Z81072) Similarity to human cyclin A/CDK2-associated protein P19 (RNA polymerase elongation factor)	3.3
119	D83333	Mouse hepatitis virus genomic RNA for spike protein, partial cds	1.8	3876559	(SW:SKP1_HUMAN); cDNA EST EMBL:T00114 comes from this gene; cDNA EST yk390f11.5 comes from this gene; cDNA EST yk402e11.5 co... >gi 3877216 gnl PID e1346850 protein P19 (RNA polymerase elongation factor) gene; cDNA EST yk390f11.5 comes from this gene; cDNA EST yk402e11.5 co...	3.3
120	AF016972	Cervus elaphus REDDEER mitochondrial D-loop, complete sequence	1.8	3878057	(Z99942) similar to von Willebrand factor type A domain; cDNA EST yk412d4.5 comes from this gene; cDNA EST yk412d4.3 comes from this gene	3.2
121	AB010741	Oncorhynchus mykiss mRNA for rtSox24, complete cds	1.8	1730805	HYPOTHETICAL 21.0 KD PROTEIN IN RPS3-PSD1 INTERGENIC REGION >gi 2132762 pir S63129 probable membrane protein YNL174w - yeast (Saccharomyces cerevisiae) >gi 1302152 gnl PID e239548 (Z71451) ORF YNL174w [Saccharomyces cerevisiae]	2.5
122	U32844	Haemophilus influenzae Rd section 159 of 163 of the complete genome	1.8	728910	A-TYPE INCLUSION PROTEIN (AT1) camelpox virus >gi 62381 (X69774) 84kDa A-type inclusion protein [unidentified]	1.9

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
123	U18321	Human ionizing radiation resistance conferring protein mRNA, complete cds.	1.8	2133273	ribosomal protein YS7 homolog <i>Emericella nidulans</i>	1.4
124	M28668	Human cystic fibrosis mRNA, encoding a presumed transmembrane conductance regulator (CFTR). > :: gb I11500 I11500 Sequence 1 from Patent US 5407796	1.8	90492	filaggrin precursor - mouse (fragment)	0.87
125	AF064553	Mus musculus NSD1 protein mRNA, complete cds	1.8	2501207	PROBABLE PROTEIN DISULFIDE ISOMERASE P5 PRECURSOR >gi 1065461 (U40411) Similar to protein disulfide-isomerase. [<i>Caenorhabditis elegans</i>]	0.87
126	AB002314	Human mRNA for KIAA0316 gene, complete cds	1.8	115131	REGULATORY PROTEIN BRLA (BRISTLE A PROTEIN) >gi 83718 pir A28913 regulatory protein brlA - <i>Emericella nidulans</i> >gi 168029 (M20631) brlA protein	0.84
127	L42096	Homo sapiens (subclone 10_d2 from P1 H21) DNA sequence.	1.8	2135624	metalloproteinase 1 (EC 3.4.24.-) - human	0.65
128	M37278	R.norvegicus renin gene, exons 1-9.	1.8	4050087	(AF109907) S164 [Homo sapiens]	0.58
129	X82879	Artificial sequences DNA for ART 2 consensus	1.8	310929	(L13442) cysteine-rich extensin-like protein-4 [<i>Nicotiana tabacum</i>]	0.52
130	D89729	Homo sapiens mRNA for CRM1 protein, complete cds	1.8	3559944	(AJ010792) Muc5AC protein [<i>Mus musculus</i>]	0.38
131	U78076	Mus musculus sepiapterin reductase gene, exons 1 and 2	1.8	2984225	(AE000766) enolase-phosphatase E-1 [<i>Aquifex aeolicus</i>]	0.095

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
132	X52133	Paramecium 168G gene for 168G surface protein	1.8	115316	COLLAGEN ALPHA 1(VIII) CHAIN PRECURSOR (ENDOTHELIAL COLLAGEN) >gi 105686 pir S15435 collagen alpha 1(VIII) chain precursor - (U61944) coded for by C. elegans cDNA yk112f3.5; coded for by C. elegans cDNA cm21d2; coded for by C. elegans cDNA CEESR07F; coded for by C. elegans cDNA yk112f3.3; coded for by C. elegans cDNA CEESR29F [Caenorhabditis elegans]	0.073
133	M77830	Human desmoplakin I mRNA, complete cds.	1.8	1397246	(U43192) myosin II heavy chain [Naegleria fowleri]	1e-04
134	AJ224150	Plasmodium berghei EF-1alpha A-gene	1.8	1353761	(U58748) similar to potential transmembrane domains in S. cerevisiae nuclear division RFT1 protein (SP:P38206)	2e-05
135	AJ005518	Mus musculus somatostatin receptor 2 gene, exon1 and 5' flanking region	1.8	1326350	(AL031174) hypothetical protein	2e-08
136	AF002217	Ralstonia eutropha megaplasmid pHG1 nitric oxide reductase (norB) gene, complete cds	1.8	3393018	(AL033388) 3-oxoacyl-[acyl-carrier-protein]-synthase	2e-08
137	AF039035	Caenorhabditis elegans cosmid C53A3	1.8	3850109	(AL022600) putative mannose-1 phosphate gaunyl transferase [Schizosaccharomyces pombe]	3e-11
138	M81769	S.domesticus immunoglobulin rearranged gamma chain mRNA, VJC region, complete cds.	1.8	3080527	HYPOTHETICAL 24.2 KD PROTEIN C13A11.03 IN CHROMOSOME I >gi 984224 (Z54096) unknown	3e-14
139	Y11106	P.pastoris PYC1 gene	1.8	1175412	(AL021687) putative protein [Arabidopsis thaliana] >gi 2832633 gnl PID e1249651 (AL021711) putative protein [Arabidopsis thaliana]	1e-15
140	U87803	Human putative Ca2+/calmodulin-dependent protein kinase kinase gene, 3' flanking region, partial sequence	1.8	2828280		3e-17

324

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Plasmodium				
141	AE001430	falciparum chromosome 2, section 67 of 73 of the complete sequence	1.8	1931647	(U95973) endomembrane protein EMP70 precursor isolog	2e-20
142	L19708	Rat N-methyl-D-aspartate receptor (NMDAR1) gene, first exon.	1.8	1731181	HYPOTHETICAL 75.5 KD PROTEIN C14A4.3 IN CHROMOSOME II >gi 3874230 gnl PID e1351618 protein (Swiss Prot accession number P38376); cDNA EST yk220e10.5 comes from this gene [Caenorhabditis elegans]	3e-21
143	Y10728	P.schwarzi mitochondrial cytb gene, partial	1.8	3878644	(Z81103) predicted using Genefinder; cDNA EST yk303g11.5 comes from this gene; cDNA EST yk303g11.3 comes from this gene [Caenorhabditis elegans]	1e-28
144	AB006631	Homo sapiens mRNA for KIAA0293 gene, partial cds	1.8	4176500	(AL031177) dJ889M15.3 (novel protein)	7e-45
145	AF106967	Mus musculus I3 protein mRNA, complete cds	1.7	<NONE>	<NONE>	<NONE>
146	AE001073	Archaeoglobus fulgidus section 34 of 172 of the complete genome	1.7	<NONE>	<NONE>	<NONE>
147	U12977	Pseudomonas lemoignei poly(3-hydroxybutyrate) depolymerase A precursor (phaZ5) gene, complete cds, and glycerol-3-phosphate-dehydrogenase homolog, complete cds.	1.7	<NONE>	<NONE>	<NONE>
148	M27038	Mus musculus (SK/CamRk) germline IgK chain gene, J1-5 region.	1.7	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		H.sapiens HBF-1				
149	X74142	mRNA for transcription factor	1.7	<NONE>	<NONE>	<NONE>
150	U40830	Streptococcus thermophilus DeoD gene, partial cds and EpsA, EpsB, EpsC, EpsD, EpsE, EpsF, EpsG, EpsH, EpsI, EpsJ, EpsK, EpsL, EpsM, Orf14.9 protein genes, complete cds	1.7	<NONE>	<NONE>	<NONE>
151	L29172	Rabbit Ig germline gamma H-chain (allotype d12,e15) C-region gene, 3' end.	1.7	<NONE>	<NONE>	<NONE>
152	M19045	Human lysozyme mRNA, complete cds.	1.7	<NONE>	<NONE>	<NONE>
153	AE001159	Borrelia burgdorferi (section 45 of 70) of the complete genome	1.7	<NONE>	<NONE>	<NONE>
154	L17027	Plasmid pFdA (from Fremyella diplosiphon) DNA sequence, including unidentified cds and stem loop.	1.7	<NONE>	<NONE>	<NONE>
155	U12232	Arabidopsis thaliana Columbia GTP binding protein beta subunit (AGB1) mRNA, complete cds.	1.7	<NONE>	<NONE>	<NONE>
156	D42056	Arabidopsis thaliana ATPK6 mRNA for ribosomal-protein S6 kinase homolog, complete cds	1.7	<NONE>	<NONE>	<NONE>
157	X98117	Rhizobium leguminosarum prsD, prsE, ORF3 genes	1.7	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
158	AF039084	Spinacia oleracea heat shock 70 protein protein, complete cds	1.7	<NONE>	<NONE>	<NONE>
159	Z12651	R.norvegicus gene for catechol methyltransferase	1.7	<NONE>	<NONE>	<NONE>
160	AF002968	Fringilla coelebs mitochondrial control region, partial sequence	1.7	<NONE>	<NONE>	<NONE>
161	AE001160	Borrelia burgdorferi (section 46 of 70) of the complete genome	1.7	<NONE>	<NONE>	<NONE>
162	U67553	Methanococcus jannaschii section 95 of 150 of the complete genome	1.7	<NONE>	<NONE>	<NONE>
163	M86247	S.ruminantium plasmid pS23 DNA.	1.7	<NONE>	<NONE>	<NONE>
164	S74436	oIL-8=interleukin-8 [sheep, spleen cells, mRNA, 1435 nt]	1.7	<NONE>	<NONE>	<NONE>
165	D12719	Candida maltosa ALK7 (CYP52A10) and ALK8 complete cds	1.7	<NONE>	<NONE>	<NONE>
166	U02625	Geotrichum candidum NRRL Y-553 lipase gene, partial cds.	1.7	321245	230k bullous pemphigoid antigen BPM1 - mouse	9.3
167	Z58881	H.sapiens CpG DNA, clone 114a4, reverse read cpgl114a4.r1a.	1.7	1854675	(U66298) bone morphogenetic protein-6 [Rattus norvegicus]	9.1
168	U43674	Agrobacterium tumefaciens conjugal transfer region 1 genes	1.7	1352066	LARGE PROLINE-RICH PROTEIN BAT2 MHC class III histocompatibility antigen HLA-B-associated transcript 2 - human >gi 179339 (M33509) HLA-B-associated transcript 2 (BAT2) [Homo sapiens] >gi 179345 (M33518) HLA-B-associated transcript 2 (BAT2) [Homo sapiens]	9.1

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
169	AL023827	Caenorhabditis elegans cosmid Y12A6A, complete sequence [Caenorhabditis elegans]	1.7	731440	PROTOPORPHYRINOGEN OXIDASE (PPO) yeast (Saccharomyces cerevisiae) >gi 603606 (U18778) Hem14p: protoporphyrinogen oxidase [Saccharomyces cerevisiae] >gi 1403536 gnl PID e249333 (Z71381) protoporphyrinogen oxidase [Saccharomyces cerevisiae]	8.9
170	X69662	X.laevis mRNA for glutathione synthetase, large subunit	1.7	4038057	(AC005897) hypothetical protein [Arabidopsis thaliana]	8.8
171	Z35824	S.cerevisiae chromosome II reading frame ORF YBL063w	1.7	3021450	(Y15515) prdl-a [Hydra vulgaris]	7.0
172	M65139	Cowpea chlorotic mottle virus (CCMV) 1a protein gene, complete cds.	1.7	2506307	COLLAGEN ALPHA 1(XII) CHAIN PRECURSOR 1(XII) chain - chicken >gi 222811 gnl PID d1001160 gallus] >gi 2326442 gnl PID e39435 (X61024) collagen-type XII alpha 1 chain [Gallus gallus]	7.0
173	X15065	Drosophila distal BX-C region (bithorax complex) pH189 5' region;	1.7	1723625	HYPOTHETICAL 10.0 KD PROTEIN IN ALPA-GABD INTERGENIC REGION (F87) >gi 1033124 (U36840) ORF_f87 [Escherichia coli] >gi 1788982 (AE000348) orf, hypothetical protein	6.9

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
174	Z46255	S.cerevisiae chromosome VI lambda clone.	1.7	3875228	(Z46792) similar to lethal(1) discs large-1 tumor suppressor protein-like repeats; cDNA EST EMBL:D33495 comes from this gene; cDNA EST EMBL:D35117 comes from this gene; cDNA EST EMBL:D36356 comes from this gene; cDNA EST EMB... >gi 3879984 gnl PID e1351767 suppressor protein-like repeats; cDNA EST EMBL:D33495 comes from this gene; cDNA EST EMBL:D35117 comes from this gene; cDNA EST EMBL:D36356 comes from this gene; cDNA EST EMB...	6.7
175	U01066	Human CD4 promoter, partial sequence.	1.7	125448	THYMIDINE KINASE saimiriine herpesvirus 1 (strain 11[Onc]) >gi 60341	6.7
176	U34743	Phalaenopsis sp. 'hybrid SM9108' homeobox protein mRNA, complete cds	1.7	1022918	(U38184) ATPase subunit 6 [Trypanosoma cruzi]	6.7
177	U14662	Baboon herpesvirus HVP2 gB glycoprotein (UL27) gene, complete cds.	1.7	3218378	(AL023862) hypothetical protein SC3F9.07 [Streptomyces coelicolor]	6.7
178	AB017006	Homo sapiens PMS2L15 mRNA, partial cds	1.7	1465855	(U64859) glutamine-rich protein [Caenorhabditis elegans]	6.7
179	U92651	Brassica oleracea var. botrytis tonoplast intrinsic protein bobTIP26-1 mRNA, complete cds	1.7	3023675	DYNEIN HEAVY CHAIN, CYTOSOLIC (DYHC) dynein heavy chain [Schizosaccharomyces pombe]	6.6
180	AF000634	Lytechinus variegatus notch homolog mRNA, complete cds	1.7	148574	(M58520) endo-1,4-beta-glucanase [Fibrobacter succinogenes]	6.6

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
181	M92354	Arabidopsis thaliana anthranilate synthase alpha subunit gene, complete cds.	1.7	738308	blue light photoreceptor [Arabidopsis thaliana]	6.5
182	AJ234856	Hordeum vulgare genomic DNA fragment; clone MWG2234.rev	1.7	3142302	(AC002411) Strong similarity to myosin heavy chain gb Z34293 from A. thaliana. [Arabidopsis thaliana]	6.5
183	U76827	Stercorarius parasiticus bird J33 cytochrome b protein, partial cds	1.7	3413810	(Y17034) Bassoon [Mus musculus]	5.4
184	U05211	Saccharomyces cerevisiae Ttp1p (TTP1) gene, complete cds.	1.7	403173	(L24492) lipoprotein [Rhodococcus erythropolis]	4.9
185	AF076974	Homo sapiens TRRAP protein (TRRAP) mRNA, complete cds	1.7	1170140	PUTATIVE ENDOGLUCANASE TYPE K PRECURSOR (ENDO-1,4-BETA-GLUCANASE) (CELLULASE)	4.1
186	AE000753	Aquifex aeolicus section 85 of 109 of the complete genome	1.7	1169357	DNA ADENINE METHYLASE site-specific DNA-methyltransferase (adenine-specific) dam methylase gene product [Vibrio cholerae]	4.0
187	AF005638	Tupaia glis apolipoprotein AI prepropeptide mRNA, complete cds	1.7	3355682	(AL031124) putative secreted lyase	4.0
188	M23090	Human germline IgK chain gene V3-region, clone Humkv328h5	1.7	2257483	(AB004534) pi003 [Schizosaccharomyces pombe]	4.0
189	M24001	Mink enteritis virus antigenic type 2 capsid protein genes VP1 and VP2, complete cds.	1.7	2143504	myotonic dystrophy kinase - mouse (fragment) kinase, DM-kinase (C-terminal, alternatively spliced, clone delta II,III,IV,V) [mice. brain. Peptide Partial, 474 aa] [Mus sp.]	3.9
190	X59964	H.sapiens CST4 gene for Cystatin D	1.7	1766075	(U37273) winged helix protein CWH-2 [Gallus gallus]	3.1

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
191	X95276	<i>P.falciparum</i> complete gene map of plastid-like DNA (IR-B)	1.7	3219951	HYPOTHETICAL 11.7 KD PROTEIN C6B12.13 IN CHROMOSOME I >gi 2330843 gnl PID e334047 pombe]	3.0
192	D84487	Rat PMSG-induced ovarian mRNA, 3' sequence, N10	1.7	173164	(J02719) valyl-tRNA synthetase [Saccharomyces cerevisiae]	2.3
193	L14851	<i>Rattus norvegicus</i> neurexin III-alpha gene, complete cds.	1.7	3323586	(AF060869) single-strand binding protein [Salmonella typhimurium]	2.3
194	M97002	<i>Xenopus laevis</i> /gilli hybrid pseudo-IgH chain gene, V region, clone LG7G342A.	1.7	2118407	MHC sex-limited protein - mouse (fragment) musculus]	2.3
195	L07025	<i>Bacillus thuringiensis</i> delta-endotoxin (CryA(a)) gene, 5' end. > :: gb I34520 I34520 Sequence 1 from patent US 5596071 > :: gb I39790 I39790 Sequence 1 from patent US 5616495 > :: gb AR008487 AR008487 Sequence 1 from patent US 5753492	1.7	2496940	HYPOTHETICAL 53.4 KD PROTEIN D1054.13 IN CHROMOSOME V >gi 3875316 gnl PID e1344967	1.8
196	S73149	insulin-like growth factor II {intron 7} [human, Genomic, 1702 nt]	1.7	3327038	(AB014512) KIAA0612 protein [Homo sapiens]	1.8
197	D86990	Human (lambda) DNA for immunoglobulin light chain	1.7	494367	Fv Fragment (Murine Se155-4) Complex With The Trisaccharide: Alpha-D-Galactose(1-2)[alpha-D-Abequose(1-3)]alpha-D-Mannose (P1-Ome) (Part Of The Cell-Surface Carbohydrate Of Pathogenic Salmonella)	1.8

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Plasmid pFdA (from				
198	L17027	Fremyella diplosiphon) DNA sequence, including unidentified cds and stem loop.	1.7	1082702	poliovirus receptor-related protein - human	1.4
199	AL022273	Caenorhabditis elegans cosmid H22D14, complete sequence [Caenorhabditis elegans]	1.7	3924605	(AF069442) putative inhibitor of apoptosis [Arabidopsis thaliana]	1.4
200	U89926	Drosophila melanogaster cut gene, partial sequence	1.7	2245100	(Z97343) DNA-binding protein homolog	1.3
201	Z25749	H.sapiens gene for ribosomal protein S7	1.7	2493459	PROTEIN KINASE C SUBSTRATE, 60.1 KD PROTEIN, HEAVY CHAIN (PKCSH) (80K-H PROTEIN) >gi 1215746	1.1
202	U59841	Fundulus heteroclitus lactate dehydrogenase B	1.7	3005587	(AF048977) Ser/Arg-related nuclear matrix protein [Homo sapiens]	0.82
203	X55763	Rabbit mRNA for smooth muscle calcium channel blocker (CaCB) receptor	1.7	3883128	(AF082302) arabinogalactan-protein [Arabidopsis thaliana]	0.82
204	Z75528	Caenorhabditis elegans cosmid C18B12A, complete sequence [Caenorhabditis elegans]	1.7	940397	(D10123) core [Hepatitis C virus]	0.80
205	U50912	Human XIST gene, poly purine-pyrimidine repeat region	1.7	2338027	(AF005370) large tegument protein [Alcelaphine herpesvirus 1]	0.59
206	X12817	Ovis aries beta-lactoglobulin gene	1.7	987050	(X65335) lacZ gene product [unidentified cloning vector]	0.45
207	AF004419	Homo sapiens troponin T (TNNT2) gene, exon 13	1.7	2996364	(AF053947) unknown [Yersinia pestis] >gi 3883090	0.22
208	L43643	Gallus domesticus DNA microsatellite marker MCW119	1.7	464896	TRANSDUCIN-LIKE ENHANCER PROTEIN 1 enhancer-of-split homolog TLE-1 - human >gi 307510	0.20

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
209	Z73278	<i>S.cerevisiae</i> chromosome XII reading frame ORF YLR106c	1.7	1351657	HYPOTHETICAL 123.9 KD PROTEIN C30D11.04C IN CHROMOSOME I >gi 2130411 pir S62562 hypothetical protein SPAC30D11.4c - fission yeast nuclear pore complex protein [Schizosaccharomyces pombe]	0.20
210	M22345	Mouse endogenous provirus gag, pol, and env region DNA.	1.7	2444455	(AF020765) hypothetical protein [Myxococcus xanthus]	0.12
211	AE000360	<i>Escherichia coli</i> K-12 MG1655 section 250 of 400 of the complete genome	1.7	2736361	(AF039038) No definition line found [Caenorhabditis elegans]	0.12
212	AB020692	Homo sapiens mRNA for KIAA0885 protein, complete cds	1.7	2605924	(AF029726) histidine kinase C [Dictyostelium discoideum]	0.094
213	S69429	testis-determining gene/SRY homolog [Sminthopsis macroura=striped-faced dunnarts, Genomic, 855 nt]	1.7	2499016	TONB PROTEIN >gi 1666536 (U23764) TonB [Pseudomonas aeruginosa]	0.092
214	S69429	testis-determining gene/SRY homolog [Sminthopsis macroura=striped-faced dunnarts, Genomic, 855 nt]	1.7	2499016	TONB PROTEIN >gi 1666536 (U23764) TonB [Pseudomonas aeruginosa]	0.088
215	U67205	Mus musculus ACF7 neural isoform 3 (mACF7) mRNA, partial cds	1.7	2047349	(AF000198) weak similarity to HSP90 [Caenorhabditis elegans]	0.052
216	X98188	Artificial DNA sequence for mammalian lambda-neo minichromosome, 1400 bp	1.7	2493779	PUTATIVE CUTICLE COLLAGEN C09G5.6 collagen; cDNA EST yk244c3.5 comes from this gene; cDNA EST yk244c3.3 comes from this gene [Caenorhabditis elegans]	0.042
217	U70139	Mus musculus putative CCR4 protein mRNA, partial cds	1.7	2252630	(U95973) hypothetical protein [Arabidopsis thaliana]	0.041

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
218	L38808	Homo sapiens alpha-1 type V collagen (COL5A1) gene, 5' flank and exon 1.	1.7	2895760	(AF045246) universal minicircle sequence binding protein minicircle sequence binding protein [Crithidia fasciculata]	0.039
219	Z72151	B.napus mRNA for AMP-binding protein	1.7	190475	(K02576) salivary proline-rich protein 1 [Homo sapiens]	0.011
220	X94152	R.norvegicus mRNA for cysteine sulfinate decarboxylase	1.7	2136212	synapsin IIb - human >gi1594277 (U40215) synapsin IIb [Homo sapiens]	0.008
221	L20255	Mouse stathmin gene sequence.	1.7	2317934	(U97553) unknown [murine herpesvirus 68]	0.006
222	L13600	Rattus norvegicus glycine transporter mRNA, complete cds.	1.7	726403	(U23175) similar to anion exchange protein [Caenorhabditis elegans]	0.003
223	AJ224150	Plasmodium berghei EF-1alpha A-gene	1.7	2072290	(U95094) XL-INCENP [Xenopus laevis]	0.001
224	S80642	butyrophilin [mice, lactating mammary gland, mRNA Partial, 3193 nt]	1.7	2695746	(AJ223010) Pmt2 [Schizosaccharomyces pombe]	9e-04
225	M22363	C.elegans unc-86 gene encoding two alternative proteins, complete cds.	1.7	2224683	(AB002369) KIAA0371 [Homo sapiens]	1e-04
226	X92123	M.musculus cgt gene exon 1	1.7	3874232	(Z49909) similar to Prokaryotic ribonuclease PH [Caenorhabditis elegans]	3e-05
227	AB016000	Ipomoea nil PKn2 (knotted-like gene) mRNA, complete cds	1.7	2183083	(AF000422) TTF-I interacting peptide 5 [Homo sapiens] (AL032643) similar to Uncharacterized protein family UPF0034, Double-stranded RNA binding motif; cDNA EST yk489b3.5 comes from this gene; cDNA EST yk439g7.5 comes from this gene [Caenorhabditis elegans]	1e-05
228	D14133	Bovine mRNA for synaptocanalin I	1.7	3925277		2e-06

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
229	L01991	Mus musculus TAFG-1-like neuronal glycoprotein (PCS) mRNA, complete cds.	1.7	3006139	(AL022299) hypothetical protein	4e-07
230	X63016	Tomato yellow leaf curl virus Thailand isolate complete genome (TYLCV-TH B-DNA)	1.7	3643608	(AC005395) hypothetical protein [Arabidopsis thaliana]	1e-07
231	Z22802	H.sapiens microsatellite repeat. > :: gb G34562 G34562 human STS SHGC-51834	1.7	100210	extensin precursor (clone Tom L 4) - tomato esculentum]	4e-09
232	K02765	Human complement component C3 mRNA, alpha and beta subunits, complete cds.	1.7	2984320	(AE000773) acetoin utilization protein [Aquifex aeolicus]	1e-09
233	Z74818	S.cerevisiae chromosome XV reading frame ORF YOL076w	1.7	3873700	(Z73102) predicted using Genefinder; Similarity to Bacillus subtilis DNAJ protein gene; cDNA EST EMBL:C12520 comes from this gene; cDNA EST EMBL:D71409 comes from this ge...	7e-11
234	D21871	Pig mRNA for thimet oligopeptidase	1.7	2632098	(Y15513) Prodos protein [Drosophila melanogaster]	8e-13
235	Y14344	Gallus gallus gene encoding neurofascin. exons 9,10,11 & 12	1.7	3876421	(Z81070) cDNA EST EMBL:C12730 comes from this gene; cDNA EST yk200b6.5 comes from this gene; cDNA EST yk349a12.5 comes from this gene [Caenorhabditis elegans]	3e-14
236	Z73608	S.cerevisiae chromosome XVI reading frame ORF YPL252c	1.7	1439663	(U64605) C05D9.6 gene product [Caenorhabditis elegans]	6e-18

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					OLIGOSACCHARYL	
237	AG000518	Homo sapiens genomic DNA, 21q region, clone: T171N23	1.7	1174468	TRANSFERASE STT3 SUBUNIT HOMOLOG >gi 529357 (U13019) No definition line found [Caenorhabditis elegans]	6e-18
238	D17716	Human mRNA for N-acetylglucosaminyltransferase V, complete cds	1.7	961446	(D63877) KIAA0157 gene product is novel.	5e-19
239	AF102512	Cheilodactylus vittatus country USA: Midway Island cytochrome c oxidase subunit I gene, mitochondrial gene encoding mitochondrial protein, partial cds	1.7	1572756	(U70848) C43G2.1 gene product [Caenorhabditis elegans]	5e-40
240	L30107	Rattus norvegicus liver-specific transporter gene, promoter region.	1.7	4176443	(AL022238) dJ1042K10.4 (novel protein)	3e-49
241	X91220	H.sapiens mRNA for Na-Cl electroneutral thiazide-sensitive cotransporter	1.7	3478637	(AC005546) R29425_1 [Homo sapiens]	6e-54
242	U97146	Rattus norvegicus calcium-independent phospholipase A2 mRNA, complete cds	1.6	<NONE>	<NONE>	<NONE>
243	Z48508	Pea seed-borne mosaic virus RNA for coat protein and polymerase (partial)	1.6	<NONE>	<NONE>	<NONE>
244	M18349	Rat leukocyte common antigen (L-CA) gene, exons 1 through 5.	1.6	<NONE>	<NONE>	<NONE>
245	M13158	Yeast (S.pombe) cdc25+ gene (mitosis initiation). complete cds.	1.6	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Mycoplasma genitalium section 34 of 51 of the complete genome	1.6	<NONE>	<NONE>	<NONE>
246	U39712					
247	M17922	Mouse Murine urokinase-type plasminogen activator protein gene, complete cds.	1.6	3875750	(Z81499) predicted using Genefinder; cDNA EST yk410e3.3 comes from this gene; cDNA EST yk410e3.5 comes from this gene [Caenorhabditis elegans]	8.0
248	M89986	Human polymorphic loci in Xq28.	1.6	3261710	(Z84724) psd [Mycobacterium tuberculosis]	6.4
249	M89986	Human polymorphic loci in Xq28.	1.6	2143805	inositol-polyphosphate 4-phosphatase - rat	6.2
250	U68725	Rattus norvegicus Deleted in colorectal Cancer	1.6	1256804	(U51449) RING3 protein [Xenopus laevis]	5.8
251	X95199	P.platessa GSTA, GSTA1, GSTA2, and PPTN genes	1.6	3915113	MALEYLACETATE REDUCTASE Pseudomonas cepacia >gi 643636 (U19883) maleylacetate reductase [Burkholderia cepacia]	4.9
252	Y09103	D.melanogaster RPA1 gene	1.6	3916021	HYPOTHETICAL 91 KD PROTEIN IN COB INTRON >gi 2654230 gnl PID e1192341 (X02819) unidentified reading frame [Schizosaccharomyces pombe]	4.8
253	Z14078	T.aestivum mitochondrion fMet, 18S, 5S repeat unit DNA	1.6	2501668	DYSTROPHIN-RELATED PROTEIN 2 sapiens]	3.6
254	AB002314	Human mRNA for KIAA0316 gene, complete cds	1.6	130997	REPETITIVE PROLINE-RICH CELL WALL PROTEIN 1 PRECURSOR >gi 81809 pir A29324 proline-rich protein precursor - soybean >gi 170049 (J02746) proline-rich protein [Glycine max]	2.8
255	M21488	Human muscle creatine kinase gene (CKMM), exon 2.	1.6	119399	ENV POLYPROTEIN PRECURSOR (COAT POLYPROTEIN) [CONTAINS: COAT PROTEIN GP62; COAT PROTEIN GP40]	2.2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
256	AE001164	<i>Borrelia burgdorferi</i> (section 50 of 70) of the complete genome	1.6	4050089	(AF109907) hypothetical protein [Homo sapiens]	1.5
257	X61757	<i>M.musculus</i> rearranged T-cell receptor beta variable region (Vb17a)	1.6	3377766	(AF080090) semaphorin IV isoform b [Mus musculus]	1.2
258	M15346	<i>T.cruzi</i> tandemly repeated gene encoding an 85 kDa antigen with homology to heat shock proteins.	1.6	2804437	(AF043695) similar to zinc metalloprotease family of peptidases [Caenorhabditis elegans]	0.41
259	L39018	<i>Rattus norvegicus</i> sodium channel protein 6 (SCP6) mRNA, complete cds	1.6	2920535	(AF018081) type XVIII collagen [Homo sapiens]	0.037
260	M29483	Human leukocyte adhesion protein p150.95 alpha subunit gene, exons 7 - 15.	1.6	1840045	(U49082) transporter protein [Homo sapiens]	2e-09
261	L06844	<i>Aspergillus niger</i> beta D-fructofuranosidase (suc1) gene, one exon.	1.6	4206210	(AF071527) putative calcium channel [Arabidopsis thaliana]	9e-10
262	M10946	Chicken aldolase B gene, complete cds, clones lambda-C(11.1.4).	1.6	2746775	(AF040640) similar to peptidase family C19 (ubiquitin carboxyl-terminal hydrolase) [Caenorhabditis elegans]	1e-31
263	X07881	Human gene PRB3L for proline-rich protein G1	1.5	<NONE>	<NONE>	<NONE>
264	U22260	<i>Nicotiana tabacum</i> UMP synthase (pyr5-6) mRNA, partial cds	1.5	3880923	(Z99271) similar to Reverse transcriptase comes from this gene [Caenorhabditis elegans]	0.50
265	U76759	<i>Mus musculus</i> nuclear protein NIP45 mRNA, complete cds	1.4	1330394	(U58761) C01F1.6 gene product [Caenorhabditis elegans]	8.9

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					POTASSIUM-	
266	AF076470	Rice tungro bacilliform virus Serdang strain, complete genome	1.4	1703461	TRANSPORTING ATPASE BETA CHAIN (PROTON PUMP) (GASTRIC H+/K+ ATPASE BETA SUBUNIT) 3.6.1.36) beta chain - human >gi 184105 (M75110) H,K-ATPase beta subunit [Homo sapiens]	8.9
267	X64659	C.jacchus interferon gene for interferon gamma	1.4	1486485	(U28832) US10 [Gallid herpesvirus 1] >gi 1486497	6.8
268	U11825	Schistosoma japonicum structural muscle protein paramyosin mRNA, complete cds.	0.88	<NONE>	<NONE>	<NONE>
269	D84278	Human DNA for CD38: exon 1	0.68	3766363	(AL031907) hypothetical serine rich protein [Schizosaccharomyces pombe]	3.0
270	M59755	Bovine lens aldose reductase pseudogene, 3' end.	0.67	<NONE>	<NONE>	<NONE>
271	M81758	Homo sapiens skeletal muscle voltage-dependent sodium channel alpha subunit (SkM1) mRNA, complete cds.	0.65	2437819	(Z86105) 1,4-beta-glucanase [Anaerocellum thermophilum]	3.6
272	L01965	Human type IV sodium channel alpha polypeptide	0.64	2437819	(Z86105) 1,4-beta-glucanase [Anaerocellum thermophilum]	3.5
273	U90122	Danio rerio bone morphogenetic protein-4 (bmp4) mRNA, partial cds	0.63	2983532	(AE000720) formate dehydrogenase alpha subunit [Aquifex aeolicus]	7.9
274	L41624	Hylobates lar mucin (MUC1) gene, exons 1-6.	0.63	1517808	(D79215) FGF-10 [Rattus norvegicus]	0.91

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					(U67956) coded for by C.	
275	AF030881	Fugu rubripes sushi retrotransposon gag polyprotein (gag) and pol polyprotein (pol) genes. complete cds	0.63	1519696	C. elegans cDNA yk126f9.5; coded for by C. elegans cDNA yk159h6.3; coded for by C. elegans cDNA yk126f9.3; coded for by C. elegans cDNA yk159h6.5 [Caenorhabditis elegans]	0.38
276	U52909	Arabidopsis thaliana U1 snRNP 70K protein gene, complete cds	0.62	<NONE>	<NONE>	<NONE>
277	AF008192	Homo sapiens putative GR6 protein (GR6) mRNA, complete cds	0.62	3800934	(AF100655) contains similarity to ser/thr protein kinases [Caenorhabditis elegans]	9.7
278	U17081	Human fatty acid binding protein (FABP3) gene, complete cds	0.62	3617848	(AF049709) tyrosylprotein sulfotransferase-A; TPST-A	7.7
279	AB018340	Homo sapiens mRNA for KIAA0797 protein, partial cds	0.62	424044	VP5 protein - porcine rotavirus >gi 61355	7.7
280	Y00093	H.sapiens mRNA for leukocyte adhesion glycoprotein p150,95	0.62	1054945	(U38621) polyprotein [Tobacco vein mottling virus]	4.5
281	M63138	Human cathepsin D (catD) gene, exons 7, 8, and 9.	0.62	136810	GLYCOPROTEIN M >gi 73791 pir WMBE51 UL10 protein - human herpesvirus 1 1-473 [Human herpesvirus 1] >gi 221732 gnl PID d1002131	3.5
282	X76056	N. sylvestris DNA for spacer region between 25S and 18S ribosomal RNA genes	0.62	2661176	(U76671) putative cds [Rhodobacter sphaeroides]	2.0
283	X74501	B.taurus mRNA for ACTH receptor	0.62	4249552	(AB001075) galectin-2 related protein	2.0
284	M57634	Rat FI-ATPase beta subunit mRNA, 3' end.	0.62	2119692	transforming growth factor-beta type III receptor - chicken >gi 511843 (L01121) transforming growth factor-beta type III receptor [Gallus gallus]	1.5

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
285	Y15724	Homo sapiens SERCA3 gene, exons 1-7 (and joined CDS)	0.62	2498164	ASPARTYL/ASPARAGINYL BETA-HYDROXYLASE (ASPARTATE BETA- HYDROXYLASE) (ASP BETA- HYDROXYLASE) (PEPTIDE- ASPARTATE BETA- DIOXYGENASE) beta- dioxxygenase (EC 1.14.11.16) - bovine >gi 162694 taurus]	0.52
286	AL010142	Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-72, complete sequence	0.62	3183206	HYPOTHETICAL PROTEIN KIAA0009 sapiens]	4e-07
287	AB008160	Mus musculus Stat3 gene, 5'-flanking region and exon 1 partial sequence	0.62	466097	HYPOTHETICAL 63.5 KD PROTEIN ZK353.1 IN CHROMOSOME III >gi 1078903 pir S44654 ZK353.1 protein - Caenorhabditis elegans >gi 289757 (L15313) putative [Caenorhabditis elegans] (Z48583) similar to ATPases associated with various cellular activities (AAA); cDNA EST EMBL:Z14623 comes from this gene; cDNA EST EMBL:D75090 comes from this gene; cDNA EST EMBL:D72255 comes from this gene; cDNA EST yk200e4...	1e-35
288	AB018795	Halomonas marina gene for alginate lyase, complete cds	0.62	3877493		3e-46
289	Z69906	Human DNA sequence from cosmid E141E2, on chromosome 22, complete sequence [Homo sapiens]	0.61	<NONE>	<NONE>	<NONE>
290	U18259	Human clone CIITA- 8 MHC class II transactivator CIITA mRNA, complete cds.	0.61	1483567	(X79983) viral proteinase [Pseudorabies virus]	9.8
291	X98890	S.tuberosum mRNA for inorganic phosphate transporter, StPT1	0.61	475724	(U08884) protein VIII precursor [Bovine adenovirus type 3]	7.6

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
292	U70825	Rattus norvegicus 5-oxo-L-prolinase mRNA, complete cds	0.61	733543	(U23448) similar to genome polyprotein (SP:POLG_BVDVN, P19711); alternative splicing to C04A2.7a	4.4
293	L81667	Homo sapiens (subclone 2_a9 from P1 H49) DNA sequence	0.61	2565087	(U80759) CAGH4 alternate open reading frame [Homo sapiens]	3.3
294	AE000760	Aquifex aeolicus section 92 of 109 of the complete genome	0.61	2811092	HOMEBOX PROTEIN HOX-A3 (HOX-1.5) homeobox-containing transcription factor [Mus musculus]	2.6
295	U58512	Mus musculus Rho-associated, coiled-coil forming protein kinase p160 ROCK-1 mRNA, complete cds	0.61	295671	(L11275) selected as a weak suppressor of a mutant of the subunit AC40 of DNA dependant RNA polymerase I and III	1.5
296	U27459	Human origin. recognition complex protein 2 homolog hORC2L mRNA, complete cds	0.61	200285	(M97900) putative open reading frame [Mus musculus]	0.66
297	L36680	Pisum sativum S-adenosylmethionine synthase mRNA, 3' end.	0.61	2285790	(AB002086) p47 [Rattus norvegicus]	4e-12
298	AE000673	Aquifex aeolicus section 5 of 109 of the complete genome	0.61	3395782	(AF058446) histone macroH2A1.2 [Gallus gallus]	6e-27
299	AF086310	Homo sapiens full length insert cDNA clone ZD51F08	0.61	3646450	(AL031603) conserved hypothetical protein. [Schizosaccharomyces pombe]	8e-29
300	AJ009675	Agrotis ipsilon mRNA for 3-hydroxy-3-methylglutaryl coenzyme A reductase	0.61	4176370	(AC005058) similar to calcium-independent phospholipase A2; similar to AC004392 (PID:g3367519) [Homo sapiens]	2e-73
301	AC005577	Homo sapiens chromosome 19, cosmid F18382B, centromeric end, complete sequence [Homo sapiens]	0.60	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Candida albicans				
302	U40454	topoisomerase type I (CATOP1) gene, complete cds	0.60	<NONE>	<NONE>	<NONE>
303	J01390	Emericella nidulans mtDNA between h2/h5 and bh2/b2 junctions. genes for ATPase subunit 6, cytochrome oxidase subunit 3, seven. unidentified proteins, twentyfour tRNA's and L-rRNA.	0.60	<NONE>	<NONE>	<NONE>
304	L11172	Plasmodium falciparum RNA polymerase I gene, complete cds.	0.60	<NONE>	<NONE>	<NONE>
305	Z81079	Caenorhabditis elegans cosmid F39H11, complete sequence [Caenorhabditis elegans]	0.60	<NONE>	<NONE>	<NONE>
306	Z49627	S.cerevisiae chromosome X reading frame ORF YJR127c	0.60	118751	MAJOR DNA-BINDING PROTEIN herpesvirus 1 (strain 11) >gi 60327 (X64346) major ssDNA-binding protein [Saimiriine herpesvirus 2]	9.6
307	U94911	Rattus norvegicus H-K-ATPase alpha 2 gene, alternatively spliced products and partial cds	0.60	2213862	(AF003086) PfSNF2L [Plasmodium falciparum]	7.4
308	U67476	Methanococcus jannaschii section 18 of 150 of the complete genome	0.60	1749688	(D89240) unnamed protein product	5.7
309	U67513	Methanococcus jannaschii section 55 of 150 of the complete genome	0.60	3327421	(U97068) zonadhesin [Mus musculus]	4.3
310	U57817	Haemophilus ducreyi lipoprotein gene, complete cds	0.60	4008577	(AL034491) conserved hypothetical protein [Schizosaccharomyces pombe]	2.5

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					probable protein-tyrosine kinase (EC 2.7.1.112) RTK - Pacific electric ray >gi290858	1.5
311	X80700	H.sapiens G17 gene	0.60	422541	(AF033823) moira [Drosophila melanogaster]	0.51
312	L42167	Mus musculus (clone R24) rds gene, partial cds	0.60	4220848	(AF031087) mismatch repair protein MSH6 [Mus musculus]	5e-07
313	U54777	Human hMSH6 mRNA, complete cds	0.60	2665637	(U97006) No definition line found [Caenorhabditis elegans]	2e-07
314	D86985	Human mRNA for KIAA0232 gene, complete cds	0.60	1938462	(U55376) coded for by C. elegans cDNA cm21e6; coded for by C. elegans cDNA cm01e2; similar to melibiose carrier protein (thiomethylgalactoside permease II)	5e-15
315	D43964	Rat liver mRNA for Kan-1, complete cds	0.60	1280135	(U37500) RNA polymerase II largest subunit [Mus musculus]	1e-19
316	U49058	Rattus norvegicus CTD-binding SR-like protein rA4 mRNA, partial cds	0.60	2145091	(Z70205) predicted using Genefinder	2e-37
317	X84388	U.ruddi mitochondrial 12S ribosomal RNA	0.60	3874247		
318	AF125447	Caenorhabditis elegans cosmid Y14H12B	0.59	<NONE>	<NONE>	<NONE>
319	U20189	Hyoscyamus muticus clone cVS2 vetispiradiene synthase mRNA, partial cds.	0.59	<NONE>	<NONE>	<NONE>
320	M63962	Human gastric H,K-ATPase catalytic subunit gene, complete cds.	0.59	<NONE>	<NONE>	<NONE>
321	AJ132366	Helicobacter pylori (strain P1) comB and pmi/algA (partial) genes, and partial ORF1 and ORF2	0.59	<NONE>	<NONE>	<NONE>

36.9

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Mus musculus				
322	U17289	transcription factor AP-2 (AP-2) gene, alternative exon 1a, and isoform 2, partial cds.	0.59	2459419	(AC002332) hypothetical protein [Arabidopsis thaliana]	9.4
323	Z71466	S.cerevisiae chromosome XIV reading frame ORF YNL190w	0.59	3875542	(Z67990) Similarity to Rat amiloride-sensitive sodium channel beta-subunit	7.3
324	Z66493	Beet soil-borne virus genes for 13K, 22K and 48K proteins	0.59	2119867	cryV465 protein - Bacillus thuringiensis thuringiensis]	7.2
325	L41351	Homo sapiens prostasin mRNA, complete cds	0.59	729212	CRYSTALLIN J1C crystallin [Tripedalia cystophora]	4.2
326	X79854	S.lincolnensis gene for 16S ribosomal RNA	0.59	3702828	(AF056577) high mobility group protein 1.2	3.2
327	AJ223356	Strongylocentrotus purpuratus mRNA for SuDp98 protein	0.59	2495704	HYPOTHETICAL PROTEIN KIAA0129 product is novel. [Homo sapiens]	2.5
328	X86019	H.sapiens mRNA for PRPL-2 protein	0.59	1743341	(Y10027) transcription factor TEF-1 [Mus musculus]	2.5
329	U75528	Xiphias gladius creatine kinase gene, partial cds	0.59	1845995	(U69477) envelope glycoprotein [Human immunodeficiency virus type 1]	2.4
330	AC005573	Homo sapiens chromosome 5, PAC clone 202e13	0.59	2506366	DNA POLYMERASE EPSILON SUBUNIT B DNA-directed DNA polymerase (EC 2.7.7.7) II chain B - yeast. (Saccharomyces cerevisiae) >gi 786319 (U25842) DNA Polymerase epsilon, subunit B (Swiss Prot. accession number P24482) [Saccharomyces cerevisiae]	1.4
331	L19180	Rat receptor-linked protein tyrosine phosphatase	0.59	1235974	(X96713) collagen [Globodera pallida]	1.1
332	L32090	Listeria monocytogenes secA gene, complete cds.	0.59	2291129	(AF016415) No definition line found [Caenorhabditis elegans]	0.83

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Xenopus laevis			(AL031124) hypothetical	
333	U24433	syndecan-2 mRNA, complete cds.	0.59	3355692	protein SC1C2.25c [Streptomyces coelicolor]	0.64
334	M23412	Drosophila muscarinic acetylcholine receptor mRNA, complete cds.	0.59	168237	(M76546) hydroxyproline-rich protein [Helianthus annuus]	0.22
335	AF060729	Synaphea media chloroplast atpB-rbcL intergenic spacer region, partial sequence	0.59	731596	HYPOTHETICAL 67.5 KD PROTEIN IN PRPS4-STE20 INTERGENIC REGION >gi 626567 pir S46825 hypothetical protein YHL010c - yeast (Saccharomyces cerevisiae) >gi 2289881 (U11582) No definition line found [Saccharomyces cerevisiae]	0.16
336	AF029734	Xanthobacter autotrophicus transcriptional activator AldR (aldR) gene, partial cds; and NAD-dependent chloroacetaldehyde dehydrogenase (aldB) gene, complete cds	0.59	2498801	PERIAXIN >gi 2143901 pir I58157 periaxin - rat >gi 505297 (Z29649) periaxin [Rattus norvegicus]	0.13
337	X95307	C.reinhardtii LI818r-1 gene	0.59	1723781	HYPOTHETICAL 34.3 KD PROTEIN IN TAF145-YOR1 INTERGENIC REGION >gi 2131717 pir S64612 hypothetical protein YGR277c - yeast (Saccharomyces cerevisiae) >gi 1323505 gnl PID c243248 (Z73062) ORF YGR277c [Saccharomyces cerevisiae]	1e-04
338	M24572	Dictyostelium discoideum tRNA-Glu-GAA gene, clone yGluGA.A8.	0.59	1176186	HYPOTHETICAL 43.3 KD GTP-BINDING PROTEIN IN DACB-RPMA INTERGENIC REGION >gi 606121 coli	3e-06
339	U73733	Human hMSH6 gene, exon 2	0.59	2665637	(AF031087) mismatch repair protein MSH6 [Mus musculus]	5e-07

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Escherichia coli				
340	D90747	genomic DNA. (25.2 - 25.6 min)	0.59	134286	DOLICHOL KINASE	6e-08
341	J05211	Human desmoplakin mRNA. 3' end.	0.59	246796	major centromere protein, CENP-B [human, Peptide, 594 aa]	4e-08
342	L24441	Loligo pealii kinesin light chain mRNA, complete cds.	0.59	547800	KINESIN LIGHT CHAIN (KLC) sea urchin (Strongylocentrotus purpuratus) >gi161530	5e-14
343	M25140	Human cardiac alpha-myosin heavy chain (MYH6) gene, exons 2, 3 and 4.	0.58	<NONE>	<NONE>	<NONE>
344	L81932	Homo sapiens (subclone 9_h2 from P1 H21) DNA sequence	0.58	<NONE>	<NONE>	<NONE>
345	AF087966	Homo sapiens full length insert cDNA clone YU51G04	0.58	<NONE>	<NONE>	<NONE>
346	Z78574	H.sapiens flow-sorted chromosome 6 TaqI fragment, SC6pA10G11	0.58	<NONE>	<NONE>	<NONE>
347	AF068061	Blattella germanica allatostatin neuropeptide precursor, gene, complete cds	0.58	<NONE>	<NONE>	<NONE>
348	AF015592	Homo sapiens Cdc7 (CDC7) mRNA, complete cds	0.58	<NONE>	<NONE>	<NONE>
349	AF028006	Methanosarcina barkeri atp operon: ATP synthase beta subunit (atpD), ATP synthase epsilon subunit (atpC), ATP synthase gene 1 (atpI), ATP synthase a subunit subunit (...)	0.58	3184291	(AC004136) putative DNA polymerase III gamma subunit	9.4
350	AB017032	Mus musculus gene for pancreatic trypsin, complete cds	0.58	3170561	(AF056704) synapsin IIIa [Rattus norvegicus]	9.2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
351	AF081585	Dictyostelium discoideum developmental protein DG1110 (DG1110) gene, partial cds	0.58	105417	basic proline-rich peptide IB-8a human	9.2
352	AF086322	Homo sapiens full length insert cDNA clone ZD53E01	0.58	93026	hypothetical protein - African swine fever virus (strain Malawi Lil-20/1) >gi 450758 (X71982) myeloid differentiation antigen homologue [African swine fever virus] >gi 903686 (M95672) unknown protein	7.1
353	AF088025	Homo sapiens full length insert cDNA clone ZC19C04	0.58	2384644	(U92805) thrombospondin-3 [Xenopus laevis]	7.0
354	AB002339	Human mRNA for KIAA0341 gene, partial cds	0.58	2135587	M130 antigen (cytosolic variant 2) - human	5.4
355	U67548	Methanococcus jannaschii section 90 of 150 of the complete genome	0.58	2911094	(AL021957) hypothetical protein Rv2174	4.2
356	L07868	Homo sapiens receptor tyrosine kinase (ERBB4) gene, complete cds.	0.58	461922	PYRUVATE DECARBOXYLASE (8-10 NM CYTOPLASMIC FILAMENT-ASSOCIATED PROTEIN) (P59NC) 4.1.1.1 - Neurospora crassa >gi 293948 (L09125) pyruvate decarboxylase [Neurospora crassa] >gi 1655909	4.2
357	X03897	Bacillus subtilis sigma 43 operon with P23-dnaE-rpoD genes (dnaE for DNA primase, rpoD for RNA polymerase)	0.58	1323704	(U55387) similar to C. elegans F38E1.9 gene product encoded by GenBank Accession Number U41996 [Cricetulus griseus]	4.1
358	D76419	Desulfovibrio vulgaris rbo gene for desulfoferrodoxin and rub gene for rubredoxin, complete cds	0.58	3420047	(AC004680) putative protein kinase [Arabidopsis thaliana]	2.4

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Human DNA				
359	Z82174	sequence from cosmid B20F6 on chromosome 22, complete sequence [Homo sapiens]	0.58	2145455	(Y07866) catalase-peroxidase	2.4
360	M33642	F.solani ST135 protein gene, complete cds.	0.58	2896706	(AL021897) hypothetical protein Rv1069c	2.4
361	U64873	Mus musculus transforming growth factor alpha (TGF alpha) gene, partial cds	0.58	3874437	(Z81038) predicted using Genefinder; cDNA EST yk488a2.5 comes from this gene [Caenorhabditis elegans]	1.8
362	AB002132	Macrophthalmus banzai mitochondrial DNA for 12S and 16S rRNA, partial and complete sequence	0.58	2960022	(AJ224676) rho type GEF [Drosophila melanogaster]	1.8
363	AF070070	Caenorhabditis elegans MutS homolog (msh-5) mRNA, partial cds	0.58	4098205	(U75869) Omp22 [Helicobacter pylori]	1.8
364	AF045240	Staphylococcus epidermidis plasmid pIP1629 mobilization protein (mobC1), (orf69-1), (mobA1),	0.58	4218117	(AL035353) protein (fragment)	0.62
365	X61637	H.sapiens Wilms tumor gene 1, exons 8 and 9	0.58	2331059	(U88211) unknown [Gallus gallus]	0.62
366	AF039312	Moraxella catarrhalis strain 4223 transferrin binding protein A (tbpA) and transferrin binding protein B (tbpB) genes, complete cds; and unknown gene	0.58	120155	FIBER PROTEIN >gi 74229 pir ERADFM fiber protein - mouse adenovirus 1 >gi 209758 (M30594) fiber protein [Mastadenovirus mus1]	0.27
367	D87463	Human mRNA for KIAA0273 gene, complete cds	0.58	3861477	(U94177) androgen receptor [Pan troglodytes]	0.12
368	U40342	Mus musculus ninein mRNA, complete cds.	0.58	4115936	(AF118223) No definition line found [Arabidopsis thaliana]	0.004

209

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
369	S57235	CD68=110kda transmembrane glycoprotein (human, promonocyte cell line U937, mRNA, 1722 nt)	0.58	2072501	(U96113) WWP1 [Homo sapiens]	1e-04
370	U39391	Mus musculus serotonin1A receptor mRNA, complete cds.	0.58	1469876	(D63481) The KIAA0147 gene product is related to adenylyl cyclase. [Homo sapiens]	1e-07
371	D00056	Monkey B-lymphotropic papovavirus genes for VP-1, 2, 3 and large T antigen, complete and partial cds, strain LPV-76 > :: gb M14494 PPMVP1 M Monkey B-lymphotropic papovavirus mutant (LPV-76) PstI B fragment encoding VP1, VP2, VP3 and T-antigen.	0.58	2462069	(AJ001774) vanadium chloroperoxidase	1e-08
372	M77182	Amsacta entomopoxvirus spheroidin gene, complete cds, and four vaccinia related orfs. > :: gb I16670 I16670 Sequence 1 from patent US 5476781	0.58	1730722	HYPOTHETICAL 43.8 KD PROTEIN IN NCE3-HHT2 INTERGENIC REGION >gi 2131871 pir S62957 hypothetical protein YNL035c - yeast (Saccharomyces cerevisiae) >gi 1301880 gnl PID e239670 (Z71311) ORF YNL035c [Saccharomyces cerevisiae]	8e-14
373	S72579	igloo-S=growth-associated protein GAP-43 homolog	0.58	2689720	(AF037168) DnaJ homologue [Arabidopsis thaliana]	7e-14
374	AF018165	Tetraodon fluviatilis amyloid precursor protein mRNA, complete cds	0.58	3219938	HYPOTHETICAL 34.9 KD PROTEIN C57A10.11C IN CHROMOSOME I >gi 2058378 gnl PID e314002 pombe]	5e-22

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
375	U81803	Filobasidiella neoformans translation elongation factor EF1-alpha (CnTEF1) mRNA, complete cds	0.57	<NONE>	<NONE>	<NONE>
376	U09781	Candida albicans ATCC 18804, CBS 562 peptide transporter gene, complete cds.	0.57	<NONE>	<NONE>	<NONE>
377	AC002143	Homo sapiens (subclone 4_b10 from BAC H102) DNA sequence	0.57	<NONE>	<NONE>	<NONE>
378	U23442	Tetrahymena thermophila RR internal deletion sequence.	0.57	<NONE>	<NONE>	<NONE>
379	U17289	Mus musculus transcription factor AP-2 (AP-2) gene, alternative exon 1a, and isoform 2, partial cds.	0.57	<NONE>	<NONE>	<NONE>
380	X70844	Buzura suppressaria nuclear polyhedrosis virus gene for polyhedrin protein	0.57	<NONE>	<NONE>	<NONE>
381	AJ012159	Homo sapiens 5T4 oncofetal trophoblast glycoprotein gene	0.57	<NONE>	<NONE>	<NONE>
382	X76571	H.sapiens simple DNA sequence region clone wg1a8.	0.57	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
383	AF034434	Vibrio cholerae pathogenicity island, putative transposase, aldehyde dehydrogenase (aldA), toxR-activated gene A protein (tagA), putative inner membrane protein, and putative zinc metalloprotease genes, complete cds; and...	0.57	<NONE>	<NONE>	<NONE>
384	AB017031	Mus musculus gene for TESP4, complete cds	0.57	<NONE>	<NONE>	<NONE>
385	X89788	S.hispidus mitochondrial DNA for SSU ribosomal RNA gene	0.57	<NONE>	<NONE>	<NONE>
386	L16921	Rat progesteron receptor gene, 5' untranslated region.	0.57	3323116	(AE001251) femA protein, putative [Treponema pallidum]	8.9
387	AF027292	Homo sapiens interferon regulatory factor 6	0.57	259790	(S48157) DNA polymerase-primase 180 kda subunit [Drosophila melanogaster, Peptide, 1490 aa]	6.7
388	AJ012581	Cicer arietinum mRNA for cytochrome P450	0.57	2131498	hypothetical protein YDR446w - yeast CAI: 0.11 [Saccharomyces cerevisiae]	5.3
389	L15363	Human transfer RNA-Met (TRMEP1) pseudogene, complete gene	0.57	3228680	(AF070935) GABA receptor subunit [Musca domestica]	5.2
390	AE000525	Helicobacter pylori 26695 section 3 of 134 of the complete genome	0.57	1938478	(U97008) weak similarity to family 1 of G-protein coupled receptors [Caenorhabditis elegans]	4.0
391	AF020189	Amblyomma americanum ecdysteroid receptor (AamEcR) mRNA, 3'UTR, region 1	0.57	2072224	(U94875) p40 [Borna disease virus]	4.0

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
392	X56997	Human UbA52 gene coding for ubiquitin-52 amino acid fusion protein	0.57	2960113	(AL022121) hypothetical protein Rv3689	4.0
393	AL010260	Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 4-81, complete sequence	0.57	117233	CYTOCHROME P450 2C14 (CYPI1C14) phenobarbital-inducible, hepatic - rabbit P-450 [Oryctolagus cuniculus] >gi 358265 prf 1306317A cytochrome P450 [Oryctolagus cuniculus]	3.9
394	M99581	Xenopus laevis gamma-crystallin (gcry3) gene, complete cds.	0.57	141647	GASTRULA ZINC FINGER PROTEIN XLCGF44.2 >gi 85736 pir S06571 finger protein (clone XlcGF44-2) - African clawed frog (fragment)	3.0
395	M38384	Drosophila melanogaster seven in absentia mRNA, complete cds.	0.57	1707127	(U80454) T16A1.1 [Caenorhabditis elegans]	3.0
396	U32795	Haemophilus influenzae Rd section 110 of 163 of the complete genome	0.57	1173433	IRON(III)-TRANSPORT SYSTEM PERMEASE PROTEIN SFUB >gi 152861 (M33815) protein (sufB)	2.3
397	X12600	Klebsiella pneumoniae nifX, nifU, nifS, nifV and nifW genes	0.57	2909562	(AL021925) hypothetical protein Rv2256c	1.4
398	AB014526	Homo sapiens mRNA for KIAA0626 protein, complete cds	0.57	482390	insect-stage-specific protein - Trypanosoma cruzi >gi 162099 (M65021) insect stage-specific antigen	0.61
399	AF063587	Rhodococcus fascians strain NRRL-B-15096 hypothetical protein gene, complete cds	0.57	4104321	(AF034582) vesicle associated protein [Rattus norvegicus]	0.46
400	L11117	Guinea pig estrone sulfotransferase gene.	0.57	82584	alpha/beta-gliadin precursor (clone A212) - wheat	0.35

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
401	V00829	Mouse complete gene for a mouse kallikrein gene. Genes are mGK1 (complete gene) and mGK-2 of hormones, e.g., grow... > :: gb J00390 MUSKAL07 Mouse pseudo-kallikrein 2, exons 4 and 5, and kallikrein 1 gene, complete cds.	0.57	2500916	NUCLEAR HORMONE RECEPTOR NOR-2 receptor [Rattus norvegicus] >gi 1583604 prf 2121281A NOR-2 protein [Rattus norvegicus]	0.20
402	X53092	Chicken mRNA for beta-2 subunit of neuronal nicotinic acetylcholine receptor	0.57	1072256	(U40953) similar to matrin F/G (SP:Q00910) containing C4-type zinc-fingers [Caenorhabditis elegans] (Z81035) predicted using Genefinder; Similarity to dehydrogenases; cDNA EST EMBL:D65800 comes from this gene; cDNA EST EMBL:D76184 comes from this gene; cDNA EST EMBL:D69322 comes from this gene; cDNA EST EMBL:C08158 comes f...	0.031
403	L07939	Ovis ovis granulocyte colony stimulating factor	0.57	3874345	(AC003974) putative ubiquitin specific protease	3e-07
404	U18061	Colletotrichum gloeosporioides CAP20 (cap20) gene, complete cds.	0.57	2914695	TUMOR NECROSIS FACTOR, ALPHA-INDUCED PROTEIN 3 (PUTATIVE DNA BINDING PROTEIN A20) (ZINC FINGER PROTEIN A20) >gi 107549 pir A35797 probable DNA-binding protein A20 - human >gi 177866 (M59465) A20	9e-08
405	Z73955	L.japonicus mRNA for small GTP-binding protein, RAB11G	0.57	112894		7e-08

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
406	X04335	Petunia grp-1 gene for glycine-rich protein	0.57	3876901	(Z77660) Similarity to Human enoyl-CoA hydratase (SW:ECHM_HUMAN); cDNA EST EMBL:T00611 comes from this gene; cDNA EST yk203d10.3 comes from this gene; cDNA EST yk203d10.5 comes from this gene; cDNA EST yk457h5.3 comes from t...	1e-27
407	U40718	Rattus norvegicus S-adenosylmethionine decarboxylase (AMDP2) pseudogene	0.56	<NONE>	<NONE>	<NONE>
408	M60318	S.cerevisiae SSDI protein gene, complete cds. > :: gb AR013983 AR013983 Sequence 8 from patent US 5773245	0.56	<NONE>	<NONE>	<NONE>
409	X60057	Nicotiana tabacum blp4 mRNA for luminal binding protein (BiP)	0.56	<NONE>	<NONE>	<NONE>
410	AF085930	Homo sapiens full length insert cDNA clone YR55A09	0.56	<NONE>	<NONE>	<NONE>
411	AL010189	Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-102, complete sequence	0.56	<NONE>	<NONE>	<NONE>
412	X05402	Murine G-CSF gene for granulocyte colony stimulating factor precursor	0.56	<NONE>	<NONE>	<NONE>
413	U92280	Rattus norvegicus regulator of G-protein signalling 12 (RGS12) mRNA, complete cds	0.56	<NONE>	<NONE>	<NONE>
414	U85660	Human papillomavirus strain RTRX7 complete genome	0.56	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
415	X57626	M. javanica mitochondrion ATPase 6, and putative tRNA-f-Met and tRNA-His genes	0.56	<NONE>	<NONE>	<NONE>
416	AB003363	Sus scrofa S100C gene, complete cds	0.56	<NONE>	<NONE>	<NONE>
417	L42291	Danio rerio DANA element, intron 4.	0.56	2650002	(AE001062) conserved hypothetical protein [Archaeoglobus fulgidus]	8.7
418	AF031826	Mus musculus leukocystatin gene, complete cds	0.56	462493	L-LACTATE DEHYDROGENASE (IMMUNOGENIC PROTEIN P36) >gi 479296 pir S33362 L-lactate dehydrogenase (EC 1.1.1.27) - Mycoplasma hyopneumoniae	6.7
419	U17068	Pennisetum glaucum Ac-like element, AcL2.	0.56	399449	ESCARGOT/SNAIL PROTEIN HOMOLOG	6.7
420	Z48042	H.sapiens mRNA encoding GPI-anchored protein p137	0.56	141232	HYPOTHETICAL 8.7 KD PROTEIN (READING FRAME D) >gi 76316 pir QQSA7C hypothetical protein E-74	6.7
421	AF027657	Choristoneura fumiferana entomopoxvirus nucleotide triphosphate phosphohydrolase I (NPHI) gene, complete cds	0.56	464999	PUTATIVE ACETYLCHOLINE REGULATOR UNC-18 >gi 480359 pir S36747 acetylcholine regulator unc-18 - Caenorhabditis elegans >gi 247392 bbs 100294 putative acetylcholine regulator unc-18	5.1
422	AB011540	Homo sapiens mRNA for MEGF7, partial cds	0.56	1718033	URACIL-DNA GLYCOSYLASE (UDG) herpesvirus 2 >gi 695219 (U20824) uracil DNA glycosylase	5.1
423	X59941	X.maculatus NGF gene for nerve growth factor	0.56	1169081	COMMON PLANT REGULATORY FACTOR CPRF-1 >gi 515621 (X58575) light-inducible protein CPRF-1 [Petroselinum crispum] >gi 1498301 (U46217) CPRF1	3.8

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
424	M72711	Rat transcriptional repressor of myelin-specific genes (SCIP) mRNA, complete cds.	0.56	501027	(U01849) ORF2 [Trypanosoma brucei]	2.3
425	AL023850	Caenorhabditis elegans cosmid Y67D11A, complete sequence [Caenorhabditis elegans]	0.56	266771	CHORISMATE MUTASE (CM) / PREPHENATE DEHYDRATASE (PDT) (P-PROTEIN) >gi 281791 pir S26053 chorismate mutase (EC 5.4.99.5) P / prephenate dehydratase (EC 4.2.1.51) - Erwinia herbicola >gi 43344	2.3
426	U47862	Schistosoma mansoni gynecophoral canal protein mRNA, complete cds	0.56	2147138	ATP synthase chain 6 - Platymonas subcordiformis mitochondrion >gi 633582 (Z47797) ATP synthase subunit 6 [Platymonas subcordiformis]	2.3
427	V00574	Human germ line gene homologous to bladder carcinoma oncogene T24 (Gene code c-Ha-ras-1) with four exons.	0.56	1518672	(U60289) receptor protein tyrosine phosphatase psi [Homo sapiens]	1.7
428	Z71502	X.laevis H1(0)-1 gene	0.56	1651674	(D90899) ferrichrome-iron receptor	1.3
429	M37278	R.norvegicus renin gene, exons 1-9.	0.56	2853019	(AF045141) putative serine proteinase [Scirpophaga incertulas]	1.0
430	D28878	Thermus thermophilus polA gene for thermostable DNA polymerase I, complete cds	0.56	3659692	(AF068748) sphingosine kinase [Mus musculus]	0.77
431	Z15027	H.sapiens HLA class III DNA	0.56	1304141	(D43758) fibrinogen A-alpha-chain	0.76
432	M14362	Human T-cell surface antigen CD2 (T11) mRNA, complete cds.	0.56	2462979	(Y11915) Tenascin-X [Bos taurus]	0.59
433	Z50801	Z.mays mRNA for chlorophyll a/b-binding protein CP29	0.56	109677	collagen alpha 1(I) chain - mouse >gi 50487	0.50

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					HYPOTHETICAL 86.0 KD	
434	Z38114	<i>S.cerevisiae</i> chromosome XIII cosmid 9745	0.56	140372	PROTEIN IN GLK1-SRO9 INTERGENIC REGION >gi 83159 pir S19367 hypothetical protein YCL039w - yeast (<i>Saccharomyces cerevisiae</i>)	0.35
435	AF052254	<i>Escherichia coli</i> DNA gyrase A (gyrA) gene, partial cds	0.56	2724126	(AF038535) synaptotagmin VII [<i>Homo sapiens</i>]	0.12
436	AF080649	<i>Tegula pulligo</i> 12S small subunit ribosomal RNA gene, mitochondrial gene for mitochondrial RNA, partial sequence	0.56	3913223	CYCLIN-DEPENDENT KINASE INHIBITOR 1 p21/WAF1 [<i>Felis catus</i>]	0.11
437	AJ005690	<i>Danio rerio</i> mRNA for protein tyrosine kinase	0.56	2623830	(AF030962) unknown [<i>Schistosoma mansoni</i>]	7e-06
438	U31202	Human noggin (NOGGIN) gene, complete cds.	0.56	3875475	(Z78411) F02D8.3 [<i>Caenorhabditis elegans</i>]	1e-06
439	X51695	<i>Ovis sp.</i> trichohyalin mRNA, partial	0.56	3386622	(AC004665) unknown protein [<i>Arabidopsis thaliana</i>]	1e-10
440	U28938	<i>Rattus norvegicus</i> protein tyrosine phosphatase D30 mRNA, complete cds	0.56	3293547	(AF072709) putative oxidoreductase [<i>Streptomyces lividans</i>]	1e-14
441	AE001171	<i>Borrelia burgdorferi</i> (section 57 of 70) of the complete genome	0.56	2315521	(AF016452) similar to the beta transducin family	4e-16
442	AF036685	<i>Caenorhabditis elegans</i> cosmid C05B10	0.56	1519671	(U67951) contains similarity to ATP/GTP-binding site motif (PS:PS00017) [<i>Caenorhabditis elegans</i>]	6e-20
443	X01173	<i>Xenopus laevis</i> vitellogenin gene A1 5' flanking region	0.56	1118102	(U41558) K02B2.3 gene product [<i>Caenorhabditis elegans</i>]	2e-31
444	D10911	<i>Mus musculus</i> DNA for MS2 protein, complete cds	0.55	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Rice mRNA EN117,				
445	D30010	partial sequence	0.55	<NONE>	<NONE>	<NONE>
446	U51991	Escherichia coli phosphoprotein phosphatase	0.55	<NONE>	<NONE>	<NONE>
447	M18858	Mouse T cell receptor C-gamma-7.1 mRNA, 3' end.	0.55	<NONE>	<NONE>	<NONE>
448	U95218	Homo sapiens T cell-death associated protein gene, complete cds	0.55	<NONE>	<NONE>	<NONE>
449	M14948	Human R-ras gene, exon 1.	0.55	<NONE>	<NONE>	<NONE>
450	AB002353	Human mRNA for KIAA0355 gene, complete cds	0.55	<NONE>	<NONE>	<NONE>
451	L81689	Homo sapiens (subclone 1_d6 from P1 H54) DNA sequence	0.55	<NONE>	<NONE>	<NONE>
452	M68955	Human myristoylated alanine-rich C-kinase substrate (MACS) gene, 5' end.	0.55	3322710	(AE001220) V-type ATPase, subunit B (atpB-1) [Treponema pallidum]	5.0
453	X62953	R.norvegicus mRNA (pJG116) with repetitive elements	0.55	1076802	extensin-like protein - maize >gi 600118 mays]	5.0
454	L34630	Synechocystis sp. mntABC transporter system: periplasmic-binding protein (mntC), complete cds; (mntA) gene, complete cds; membrane protein (mntB) gene, complete cds.	0.55	2117632	hydrogen dehydrogenase (EC 1.12.1.2) - Clostridium acetobutylicum >gi 557064 (U15277) hydrogenase I [Clostridium acetobutylicum]	5.0
455	U43521	Plasmodium berghei merozoite surface protein-1 gene, complete cds	0.55	127654	MYOGLOBIN	4.9

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
456	Z64937	H.sapiens CpG DNA, clone 17g7, reverse read cpg17g7.r1a.	0.55	417298	MFS18 PROTEIN PRECURSOR	3.8
457	U10914	Macaca mulatta clone irh83 T-cell receptor alpha chain mRNA, partial cds.	0.55	310406	(L09212) tat protein [Simian immunodeficiency virus] virus]	3.8
458	AF022838	Homo sapiens multidrug resistance protein	0.55	1585251	traB gene [Amycolatopsis methanolica]	2.8
459	M35603	Mouse Hox-3.1 gene and Hox-3.2-Hox-3.1 intergenic region.	0.55	818849	(U25430) nucleotide pyrophosphatase precursor [Oryza sativa]	2.0
460	AE001395	Plasmodium falciparum chromosome 2, section 32 of 73 of the complete sequence	0.55	137532	PROTEIN C2 >gi 74386 pir WZVZB6 59K HindIII-C protein - vaccinia virus (strain WR)	1.7
461	AE001395	Plasmodium falciparum chromosome 2, section 32 of 73 of the complete sequence	0.55	137532	PROTEIN C2 >gi 74386 pir WZVZB6 59K HindIII-C protein - vaccinia virus (strain WR)	1.7
462	U59736	Human transcription factor (NFATc.b) mRNA, complete cds	0.55	3327144	(AB014565) KIAA0665 protein [Homo sapiens]	0.096
463	U34860	Saccharomyces cerevisiae origin recognition complex large subunit (ORC1) gene, complete cds	0.55	140372	HYPOTHETICAL 86.0 KD PROTEIN IN GLK1-SRO9 INTERGENIC REGION >gi 83159 pir S19367 hypothetical protein YCL039w - yeast (Saccharomyces cerevisiae)	0.017
464	AF012341	Homo sapiens glutaryl-CoA dehydrogenase (GCDH) gene, exons 6, 7, 8, 9, and 10	0.55	1166611	(U46674) coded for by C. elegans cDNA yk27d9.5; coded for by C. elegans cDNA yk27d9.3; short region of weak homology to drosophila suppressor of sable protein	0.008

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		HIV-1 isolate Q98-				
465	AF004891	CxA from Kenya, envelope glycoprotein C2V3 region (env) gene, partial cds	0.54	<NONE>	<NONE>	<NONE>
466	Y10159	D.discoideum racGAP gene	0.54	<NONE>	<NONE>	<NONE>
467	AB001895	Homo sapiens mRNA for B120, complete cds	0.54	<NONE>	<NONE>	<NONE>
468	X12357	Bovine gene for aspartyl protease NM1 exons 3 and 4 > :: lcl X12357 Bovine aspartyl protease NM1 gene, exons 3 and 4.	0.54	<NONE>	<NONE>	<NONE>
469	AE001151	Borrelia burgdorferi (section 37 of 70) of the complete genome	0.54	<NONE>	<NONE>	<NONE>
470	X92052	H.sapiens mRNA for T cell receptor alpha chain	0.54	<NONE>	<NONE>	<NONE>
471	U00938	Mus musculus ileal lipid-binding protein gene. complete cds	0.54	1009712	(U27698) calreticulin [Arabidopsis thaliana]	4.9
472	X68367	M.thermoformicum complete plasmid pFZ1 DNA	0.54	125272	CASEIN KINASE II, ALPHA CHAIN (CK II) >gi 419938 pir A43297 casein kinase II (EC 2.7.1.-) alpha chain - Theileria parva >gi 161871 (M92084) casein kinase II alpha subunit [Theileria parva]	4.7
473	Z61098	H.sapiens CpG DNA, clone 44c4, reverse read cpg44c4.r1a .	0.54	4191274	(AJ131094) Xvent-1B protein [Xenopus laevis]	3.7
474	M63962	Human gastric H.K-ATPase catalytic subunit gene, complete cds.	0.54	3881648	(Z70757) similar to serine protease inhibitor [Caenorhabditis elegans]	3.7
475	XS6019	H.sapiens mRNA for PRPL-2 protein	0.54	1648828	(D87963) ETF-related factor-1 (ETFR-1)	2.1

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
476	X89010	S.glaucens genes strU, strX, strV and strW for 5'-hydroxystreptomycin production and transport polypeptides	0.54	3550345	(AF084524) cellular repressor of E1A-stimulated genes CREG [Mus musculus]	0.25
477	AB007836	Homo sapiens mRNA for Hic-5. partial cds	0.54	1097213	ORF 1 [Streptomyces lavendulae]	0.15
478	U32622	Comamonas testosteroni TsaR (tsaR), toluenesulfonate methyl-monooxygenase oxygenase component component (tsaB), toluenesulfonate zinc-independent alcohol dehydrogenase...	0.54	3875351	(Z96047) DY3.6 [Caenorhabditis elegans]	0.006
479	D61394	Arabidopsis thaliana gene for beta-VPE, complete cds	0.53	<NONE>	<NONE>	<NONE>
480	D61394	Arabidopsis thaliana gene for beta-VPE, complete cds	0.53	<NONE>	<NONE>	<NONE>
481	Z33072	M.capricolum DNA for CONTIG MC097	0.53	<NONE>	<NONE>	<NONE>
482	U45975	Human phosphatidylinositol (4,5)bisphosphate 5-phosphatase homolog mRNA. partial cds.	0.53	<NONE>	<NONE>	<NONE>
483	Z71324	S.cerevisiae chromosome XIV reading frame ORF YNL048w	0.53	2135586	M130 antigen (cytosolic variant 1) - human	2.1
484	L32090	Listeria monocytogenes secA gene. complete cds.	0.53	2291129	(AF016415) No definition line found [Caenorhabditis elegans]	0.70

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Mus musculus mRNA				
485	D86423	for HGT keratin, partial cds	0.53	1235974	(X96713) collagen [Globodera pallida]	0.41
486	Y15969	Mus musculus V kappa 21-6 gene, partial	0.52	<NONE>	<NONE>	<NONE>
487	M27480	Mus musculus (clone 3F9) transcribed germline T cell receptor gamma chain (Tcr-g) mRNA, VJ4 C4 region.	0.52	3875542	(Z67990) Similarity to Rat amiloride-sensitive sodium channel beta-subunit	4.6
488	D87004	Human (lambda) DNA for immunoglobulin light chain	0.52	1766073	(U37272) winged helix protein CWH-1 [Gallus gallus]	3.5
489	Z99704	Human DNA sequence from cosmid E75B8 on chromosome 22, complete sequence [Homo sapiens]	0.51	<NONE>	<NONE>	<NONE>
490	U76523	Sambucus nigra lectin precursor mRNA, complete cds	0.51	<NONE>	<NONE>	<NONE>
491	U32795	Haemophilus influenzae Rd section 110 of 163 of the complete genome	0.50	<NONE>	<NONE>	<NONE>
492	M14602	Human myoglobin gene, exon 2.	0.49	478384	helicase homolog g10L protein - African swine fever virus >gi414091 (X72951) G10L 125 KDa protein	7.0
493	D87075	Human mRNA for KIAA0238 gene, partial cds	0.24	1938429	(U97002) similar to Schizosaccharomyces pombe 4-nitrophenylphosphatase (PNPPASE) (SP:Q00472, NID:g5004) [Caenorhabditis elegans]	2.5
494	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	0.23	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		<i>N.crassa</i>				
495	J05254	mitochondrial small (19S) rRNA and Cys-tRNA.	0.23	192150	(L05670) clustrin [Mus musculus]	5.1
496	X16399	Gene for glutamate dehydrogenase (EC 1.4.1.4), put. bacterial origin	0.23	790933	(L07867) invariant surface glycoprotein [Trypanosoma brucei]	0.030
497	AE001251	Treponema pallidum section 67 of 87 of the complete genome	0.22	<NONE>	<NONE>	<NONE>
498	AF026919	Homo sapiens amyloid lambda light chain variable region mRNA, partial cds	0.21	<NONE>	<NONE>	<NONE>
499	Z27247	D.melanogaster mRNA for defensin	0.21	<NONE>	<NONE>	<NONE>
500	Y15608	Candida albicans UBI3 gene	0.21	<NONE>	<NONE>	<NONE>
501	V00598	Human beta-tubulin pseudogene.	0.21	<NONE>	<NONE>	<NONE>
502	X79426	A.thaliana microsatellite [repeated motif (gat)7]	0.21	<NONE>	<NONE>	<NONE>
503	X75772	A.caerulescens mitochondrial genes for cytochrome b and NADH dehydrogenase 5	0.21	139626	PROTEIN T1 PRECURSOR	7.8
504	AF028736	Serratia marcescens site specific recombinase	0.21	3645960	(AL031583) 1-evidence=predicted by content; 1-method=genefinder;084; 1-method_score=47.46; 1-evidence_end; 2-evidence=predicted by match; 2-match_accession=SWISS-PROT:P23792; 2-match_description=DISCONNECTED PROTEIN.; 2-matc...	4.6
505	X97545	S.cerevisiae OST5 gene	0.21	2275631	(AF014940) No definition line found [Caenorhabditis elegans]	2.7

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
506	M24543	Human prostate-specific antigen (PA) gene, complete cds.	0.21	1938527	(U97012) C04E6.2 gene product [Caenorhabditis elegans]	2.7
507	M62470	Mouse thrombospondin (THBS1) gene, complete cds.	0.21	548563	RNA REPLICASE POLYPROTEIN 2.7.7.48) - Erysimum latent virus >gi 3892232 (AF098523) replicase protein [Erysimum latent virus]	2.1
508	Y13544	Homo sapiens cosmid C1	0.21	1235710	(L40584) polypeptide [Infectious pancreatic necrosis virus]	2.0
509	M24193	Chicken MHC B complex protein (C123) mRNA, complete cds.	0.21	3600102	(AF090441) extracellular reelin [Gallus gallus]	0.52
510	X97161	H.sapiens TFE3 gene, exon 4,5 & 6	0.21	854065	(X83413) U88 [Human herpesvirus 6]	0.30
511	X67649	R.norvegicus DNA sequence for LFB1/HNF1 promoter	0.21	3913114	TRANSCRIPTION FACTOR COUP 2 COUP-TFII - chicken >gi 392817 (U00697) orphan receptor COUP-TFII [Gallus gallus]	0.004
512	U63807	Fugu rubripes growth hormone (GH) gene, complete cds	0.21	3510505	(AF030881) pol polypeptide [Fugu rubripes]	3e-04
513	Z95636	H.sapiens mRNA for laminin alpha 5 chain	0.21	400350	NAM7 PROTEIN (NONSENSE MEDIATED MRNA DECA Y PROTEIN 1) (UP-FRAMESHIFT SUPPRESSOR 1) factor NAM7 - yeast (Saccharomyces cerevisiae) >gi 4023	1e-07
514	U91907	Mirounga leonina major histocompatibility complex class II (DQA) gene, partial cds	0.20	<NONE>	<NONE>	<NONE>
515	Z35758	Transmissible gastroenteritis virus TFI virion protein genes	0.20	<NONE>	<NONE>	<NONE>
516	X00334	Drosophila virilis simple DNA sequence (pDv-19)	0.20	<NONE>	<NONE>	<NONE>

365

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
517	M76741	Homo sapiens biliary glycoprotein (BGP) gene, partial cds.	0.20	<NONE>	<NONE>	<NONE>
518	D78515	Mus musculus rae28 gene, exon 1 and 5'flanking region	0.20	<NONE>	<NONE>	<NONE>
519	M62975	Drosophila melanogaster RNA polymerase II second largest subunit upstream (DmRP 140) gene, exons 1-4.	0.20	<NONE>	<NONE>	<NONE>
520	M27260	Chicken 78-kD glucose-regulated protein, complete cds.	0.20	<NONE>	<NONE>	<NONE>
521	AF076470	Rice tungro bacilliform virus Serdang strain, complete genome	0.20	<NONE>	<NONE>	<NONE>
522	AF076470	Rice tungro bacilliform virus Serdang strain, complete genome	0.20	<NONE>	<NONE>	<NONE>
523	U04636	Human cyclooxygenase-2 (hCox-2) gene, complete cds.	0.20	<NONE>	<NONE>	<NONE>
524	AE001430	Plasmodium falciparum chromosome 2, section 67 of 73 of the complete sequence	0.20	<NONE>	<NONE>	<NONE>
525	AF043514	Mus musculus phosphomannomutase (Pmm2) mRNA, complete cds	0.20	3025006	HYPOTHETICAL 15.5 KD PROTEIN IN MOAE-RHLE INTERGENIC REGION >gi 1787009 (AE000181) orf, hypothetical protein [Escherichia coli]	9.8

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
526	U23144	Xenopus laevis FTZ-F1-related nuclear orphan receptor variant (xFTZrAshort) mRNA, complete cds.	0.20	3184402	(AB014477) period protein [Chymomyza costata]	9.6
527	U14621	Paracentrotus lividus Pax-6 (suPax-6) mRNA, complete cds.	0.20	465894	PROBABLE MICROSOMAL SIGNAL PEPTIDASE 23 KD SUBUNIT (SPC22/23) >gi 630688 pir S44854 K12H4.4 protein - Caenorhabditis elegans >gi 289708 (L14331) homology with signal peptidase; coded for by C. elegans cDNAs GenBank: M79661, M79662 and M79663; putative	7.7
528	AF030511	Actinobacillus pleuropneumoniae MRP ATPase homolog (mrp) gene, partial cds; ApxIVA var3 (apxIVA) gene, complete cds; and beta-galactosidase (lacZ) gene, partial cds	0.20	1175966	HYPOTHETICAL 45.3 KD PROTEIN IN THIS 5'REGION >gi 1084720 pir S56193 probable membrane protein YFL062w - yeast (Saccharomyces cerevisiae)	7.2
529	AF070581	Homo sapiens clone 24540 mRNA sequence	0.20	542394	glyoxal oxidase (EC 1.2.3.-) precursor - basidiomycete (Phanerochaete chrysosporium) >gi 1050302	5.8
530	X75437	T.maritima pgK gene for 3-phosphoglycerate kinase	0.20	825648	(Z34531) coproporphyrinogen oxidase [Homo sapiens]	5.8
531	U32686	Haemophilus influenzae Rd section 1 of 163 of the complete genome	0.20	3309593	(AF072878) ciliary outer arm dynein beta heavy chain	5.6
532	Z28081	S.cerevisiae chromosome XI reading frame ORF YKL081w	0.20	2507201	CARBON CATABOLITE DEREPRESSING PROTEIN KINASE >gi 1469803 (L78129) serine/threonine kinase [Candida albicans]	5.5

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Hordeum vulgare				
533	AF022725	limit dextrinase (HvLD99) gene, complete cds	0.20	3139154	(AF064077) adrenocorticotrophic hormone receptor [Sus scrofa]	4.3
534	AL021726	Drosophila melanogaster cosmid 171E4	0.20	3885334	(AC005623) putative argonaute protein [Arabidopsis thaliana]	2.6
535	AB012106	Brassica rapa mRNA for SRK45, complete cds	0.20	4008334	(Z92824) B0413.4 [Caenorhabditis elegans]	1.5
536	Z46606	H.sapiens HLTF gene for helicase-like transcription factor	0.20	132946	60S RIBOSOMAL PROTEIN L30B (RP29) cytosolic - yeast (Saccharomyces cerevisiae) >gi 171821 not determined [Saccharomyces cerevisiae] >gi 1045254 cerevisiae] >gi 1323250 gnl PID e243708 (Z72933) ORF YGR148c [Saccharomyces cerevisiae]	1.5
537	X87193	H.sapiens mRNA for 2.19 gene	0.20	139820	DNA-REPAIR PROTEIN XRCC1	1.5
538	L77965	Clostridium perfringens C beta 2 toxin gene, complete cds	0.20	1175950	HYPOTHETICAL 33.5 KD PROTEIN IN SEC53-ACT1 INTERGENIC REGION >gi 1084703 pir S56211 probable membrane protein YFL044c - yeast (Saccharomyces cerevisiae) >gi 836711 gnl PID d1009835 (D50617) YFL044C	1.4
539	M15938	Chicken neural cell-adhesion molecule (NCAM) gene, exon 18.	0.20	2133082	regulatory protein MSR1 - yeast	1.1
540	AJ003220	Solanum tuberosum mRNA for extensin-like protein, partial	0.20	2496932	HYPOTHETICAL 55.9 KD PROTEIN C56G2.1 IN CHROMOSOME III >gi 726413 (U23177) C56G2.1 gene product [Caenorhabditis elegans]	1.1
541	X98108	A.thaliana psbP gene	0.20	119227	EPIDERMAL GROWTH FACTOR PRECURSOR precursor - mouse >gi 309210 (J00380) prepro-egf [Mus musculus]	0.49

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
542	AB011179	Homo sapiens mRNA for KIAA0607 protein, partial cds	0.20	2143753	gene VGF protein - rat >gi 205690 (M60525) nerve growth factor inducible protein [Rattus norvegicus] >gi 205701 (M60522) nerve growth factor-inducible protein [Rattus norvegicus] >gi 207651	0.39
543	X75318	H.sapiens ITIH1 gene (exon 22) and ITIH3 gene	0.20	629557	RNA-binding protein mpD - Arabidopsis thaliana (fragment) >gi 510240 (X61108) RNA binding protein [Arabidopsis thaliana]	0.38
544	AB008374	Oncorhynchus mykiss mRNA for alpha 3 type I collagen, partial cds	0.20	1082610	muf1 protein - human >gi 762953 (X86018) muf1 [Homo sapiens]	0.37
545	U09809	Limulus polyphemus arginine kinase mRNA, complete cds.	0.20	3882016	(AJ012650) CP [Papaya ringspot virus]	0.37
546	AB020671	Homo sapiens mRNA for KIAA0864 protein, partial cds	0.20	2674350	(U93121) M-phase phosphoprotein-1 [Homo sapiens]	0.18
547	L04457	Phytophthora megasperma mitochondrial ORF152, complete cds, cytochrome c oxidase subunit I (cox1) gene, complete cds, cytochrome c oxidase subunit II	0.20	746516	(U23517) D1022.7 [Caenorhabditis elegans] >gi 3258651 elegans]	0.043
548	L04457	Phytophthora megasperma mitochondrial ORF152, complete cds, cytochrome c oxidase subunit I (cox1) gene, complete cds, cytochrome c oxidase subunit II	0.20	746516	(U23517) D1022.7 [Caenorhabditis elegans] >gi 3258651 elegans]	0.042

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Cdk2=cyclin-				
549	S82819	dependent kinase 5 regulatory subunit p35 [mice, brain, 129/SvJ, C57BL/6, Genomic/mRNA, 5528 nt]	0.20	3413870	(AB007923) KIAA0454 protein [Homo sapiens]	0.020
550	D31792	Streptomyces griseus DNA for serine/threonine protein kinases, complete cds	0.20	861405	(U29154) T07F12.2 gene product [Caenorhabditis elegans]	0.019
551	U97499	Homo sapiens butyrophilin (BT3.2) gene, exons 5-10, and complete cds	0.20	2773341	(AF040954) putative protein phosphatase 1 nuclear targeting subunit [Rattus norvegicus]	0.008
552	U31463	Rattus norvegicus nonmuscle myosin heavy chain-A mRNA, complete cds.	0.20	3880111	(Z81130) predicted using Genefinder	0.002
553	X78401	Bacteriophage P22 right operon, orf 48, replication genes 18 and 12, nin region genes, ninG phosphatase, late control gene 23, orf 60, complete cds, late control region, start of lysis gene 13	0.20	1123087	(U42436) C49H3.3 gene product [Caenorhabditis elegans]	4e-04
554	X57310	Nocardia lactamdurans pcbAB and pcbC genes for alpha-aminoadipyl-L-cysteiny-D-valine synthetase and isopenicillin N synthase	0.20	1723511	PUTATIVE ENDONUCLEASE C1F12.06C yeast (Schizosaccharomyces pombe) >gi 1217980 (Z69944) unknown [Schizosaccharomyces pombe]	4e-09
555	X62386	S.epidermidis genes epiY, epiA, epiB, epiC, epiD, epiQ, epiP	0.20	3874927	(Z73424) C44B9.1 [Caenorhabditis elegans]	3e-10

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
556	X59000	Epizootic haemorrhagic disease virus gene segment 6 for NS1	0.20	3879755	(Z80220) similar to nucleotide binding protein; cDNA EST EMBL:M75897 comes from this gene; cDNA EST EMBL:M89054 comes from this gene; cDNA EST EMBL:D26713 comes from this gene; cDNA EST EMBL:D26718 comes from this gene; cDNA...	8e-16
557	M98776	Human keratin 1 gene, complete cds	0.20	1086900	(U41278) contains similarity to G beta repeats	2e-30
558	AF011446	Mus musculus granzyme K gene, complete cds	0.19	<NONE>	<NONE>	<NONE>
559	AF074708	Macaca mulatta clone MMU1.5 FRG1-like pseudogene, exons 7 and 8, partial sequence	0.19	<NONE>	<NONE>	<NONE>
560	X13287	Medicago sativa nodulin-25 gene	0.19	<NONE>	<NONE>	<NONE>
561	Z49509	S.cerevisiae chromosome X reading frame ORF YJR009c	0.19	<NONE>	<NONE>	<NONE>
562	D89041	Bovine DNA for prostaglandin F2alpha receptor, partial cds	0.19	<NONE>	<NONE>	<NONE>
563	D29644	Streptococcus salivarius DNA for dextranase	0.19	<NONE>	<NONE>	<NONE>
564	AE001461	Helicobacter pylori, strain J99 section 22 of 132 of the complete genome	0.19	<NONE>	<NONE>	<NONE>
565	L38559	Homo sapiens galactocerebrosidase (GALC) gene, exon 17.	0.19	<NONE>	<NONE>	<NONE>
566	Z82628	R.prowazekii genomic DNA fragment (clone A405F)	0.19	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
567	U25641	Tetrahymena thermophila telomerase component p80 mRNA, complete cds	0.19	<NONE>	<NONE>	<NONE>
568	AB002343	Human mRNA for KIAA0345 gene, complete cds	0.19	<NONE>	<NONE>	<NONE>
569	D10064	Erwinia carotovora gene for pectate lyase III, complete cds	0.19	<NONE>	<NONE>	<NONE>
570	U31734	Homo sapiens clone MF118 A4A10 hypoxanthine phosphoribosyltransferase (hppt) 130 kb deletion mutant mRNA, partial cds, contains human Alu element	0.19	<NONE>	<NONE>	<NONE>
571	AE001386	Plasmodium falciparum chromosome 2, section 23 of 73 of the complete sequence	0.19	<NONE>	<NONE>	<NONE>
572	M95623	Homo sapiens hydroxymethylbilane synthase gene, complete cds.	0.19	<NONE>	<NONE>	<NONE>
573	S67478	(GC*IS)=vitamin D-binding protein/group specific component [human, peripheral blood leukocytes, Genomic, 794 nt, segment 4 of 9]	0.19	<NONE>	<NONE>	<NONE>
574	X99075	H.sapiens NRGN gene, exon 1	0.19	<NONE>	<NONE>	<NONE>
575	AF044775	Homo sapiens breakpoint cluster region BCRder14 sequence	0.19	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Human mRNA for KIAA0335 gene, complete cds	0.19	<NONE>	<NONE>	<NONE>
576	AB002333					
577	U53566	Macaca mulatta pit-1/GHF-1 transcription factor mRNA, complete cds	0.19	1078068	probable membrane protein YLR311c - yeast	9.2
578	U73664	Human t(11;14)(q13;q32) breakpoint junction sequence	0.19	116734	COAT PROTEIN (CAPSID PROTEIN) virus >gi 58901 (X62133) CyMV coat protein gene product	8.8
579	AF004054	Heterophyllaea pustulata rps16 gene, chloroplast gene, partial intron sequence	0.19	1928991	(U92815) heat shock protein 70 precursor [Citrus lanatus]	8.7
580	Z27081	Caenorhabditis elegans cosmid M01A8, complete sequence [Caenorhabditis elegans]	0.19	2496247	HYPOTHETICAL ATP-BINDING PROTEIN MJ0625 >gi 2128413 pir A64378 hypothetical protein MJ0625 - Methanococcus jannaschii >gi 1591336 (U67510) M. jannaschii predicted coding region MJ0625	8.6
581	Z74145	S.cerevisiae chromosome IV reading frame ORF YDL097c	0.19	1174425	TYROSINE-PROTEIN KINASE SPK-1	6.7
582	D38547	Small round structured virus genomic RNA, 3'terminal sequence containing ORF2 and ORF3	0.19	971318	(Z48053) putative protein [Bovine herpesvirus 1]	5.1

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
583	D88000	Ralstonia eutropha DNA 16S ribosomal RNA >:: dbj D88002 D88002 Ralstonia eutropha DNA for 16S ribosomal RNA >:: dbj D88003 D88003 Ralstonia eutropha DNA for 16S ribosomal RNA >:: dbj D88004 D88004 Ralstonia eutropha DNA for 16S ribosomal RNA	0.19	3800952	(AF100657) No definition line found [Caenorhabditis elegans]	5.1
584	U67462	Methanococcus jannaschii section 4 of 150 of the complete genome	0.19	3183617	(AJ005586) MYB-related transcription factor [Antirrhinum majus]	4.0
585	L23906	Gallus domesticus microsatellite DNA marker.	0.19	1947094	(U93074) voltage-gated sodium channel homolog BdNa1	3.9
586	AE001462	Helicobacter pylori, strain J99 section 23 of 132 of the complete genome	0.19	1730177	GLUCOSE-6-PHOSPHATE ISOMERASE (GPI) ISOMERASE) (PHI) >gi 2118333 pir I48073 glucose phosphate isomerase - Chinese hamster >gi 987046 griseus] (Z82256) cDNA EST yk251g7.3 comes from this gene; cDNA EST yk251g7.5 comes from this gene; cDNA EST EMBL:D68223 comes from this gene; cDNA EST EMBL:C12737 comes from this gene; cDNA EST yk389c8.5 comes from this gene; cDNA E...	3.9
587	M19460	P.putida catBC operon encoding cis,cis-muconate lactonizing enzyme I and muconolactone isomerase genes, complete cds.	0.19	3873843		3.9
588	U22349	Tetrahymena australis telomerase RNA gene, complete sequence	0.19	4105782	(AF049922) PGP169-12 [Petunia x hybrida]	3.2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
589	L27745	Homo sapiens voltage operated calcium channel, alpha-I subunit mRNA, complete cds.	0.19	3763926	(AC004450) unknown protein [Arabidopsis thaliana]	3.0
590	AF049588	Canis familiaris synapsin I gene, partial cds	0.19	4104931	(AF042196) auxin response factor 8 [Arabidopsis thaliana]	3.0
591	X06627	Staphylococcus aureus plasmid pS194 sequence	0.19	137927	PRE-NECK APPENDAGE PROTEIN (LATE PROTEIN GP12) >gi 75856 pir WMBP22 gene 12 protein - phage phi-29 >gi 215330 (M14782) pre-neck appendage protein [Bacteriophage phi-29] >gi 225367 prf 1301270G gene 12 [Bacteriophage phi-29]	2.3
592	X61597	M.musculus gene for kallikrein-binding protein	0.19	2982874	(AE000675) cobalamin synthesis related protein CobW	1.7
593	AF016242	Dictyostelium discoideum protein synthesis elongation factor 1-alpha (tef2) gene, partial cds	0.19	133659	PUTATIVE RNA-DIRECTED RNA POLYMERASE	1.4
594	AF004447	Venezuelan equine encephalitis virus strain 1327 polyprotein gene, partial cds >:: gb AF004460 AF004460 Venezuelan equine encephalitis virus strain 1385 polyprotein gene, partial cds	0.19	4096173	(U25968) early embryogenesis protein [Oryza sativa]	1.3
595	J04821	Human elastin (ELN) gene, exon 1, clones HELC-5 and HELC-6.	0.19	1170523	INHIBIN BETA B CHAIN PRECURSOR inhibin precursor - bovine >gi 563753 (U16241) betaB inhibin/activin precursor [Bos taurus]	1.3
596	AF059650	Homo sapiens histone deacetylase 3 (HDAC3) gene, complete cds	0.19	3024881	PROBABLE TRANSPORT PROTEIN CY21C12.11 >gi 2078066 gnl PID e315171 (Z95210) betP	0.83

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
597	M69053	D.melanogaster calcium-activated K+ channel subunit	0.19	1707984	FERREDOXIN-DEPENDENT GLUTAMATE SYNTHASE 1 (FD-GOGAT) >gi 2126524 pir S60228 glutamate synthase (ferredoxin) (EC 1.4.7.1) gltB - Synechocystis sp. (PCC 6803) >gi 515938 (X80485) glutamate synthase	0.80
598	AF076279	Dictyostelium firmibasis plasmid Dfp1, complete plasmid sequence	0.19	453986	(U00008) yjeA [Escherichia coli]	0.79
599	D28873	Mouse MCNP gene for C-type natriuretic peptide, complete cds (exon 1, exon 2)	0.19	2650444	(AE001092) acetyl-CoA synthetase (acs-1) [Archaeoglobus fulgidus]	0.63
600	U06071	Oxytricha nova macronuclear actin II gene, complete cds.	0.19	1584024	complement control protein [Botryllus schlosseri]	0.48
601	L54057	Homo sapiens CLP mRNA, partial cds.	0.19	3036883	(AL022374) putative ABC transporter	0.46
602	X89806	P.lividiu s cDNA for COLL2alpha gene	0.19	3638957	(AC004877) sco-spondin-mucin-like; similar to P98167 uncertain [Homo sapiens]	0.41
603	AE001104	Archaeoglobus fulgidus section 3 of 172 of the complete genome	0.19	2315192	(Y11739) transcription factor [Homo sapiens]	0.35
604	U54501	Rattus norvegicus microsatellite sequence D0Mco22	0.19	228951	D-MeAsp receptor:ISOTYPE=epsilon3 [Mus musculus]	0.32
605	X74468	Human papillomavirus type 15 genomic DNA	0.19	3695390	(AF096371) contains similarity to Rattus norvegicus cyclin G-associated kinase (SW:P97874) [Arabidopsis thaliana]	0.28
606	U20285	Human Gps1 (GPS1) mRNA, complete cds	0.19	2582659	(AJ002527) glucitol-6-phosphate dehydrogenase [Clostridium beijerinckii]	0.27
607	D49408	Human gene for interleukin 3 receptor alpha subunit, exon 10	0.19	2522368	(AF008596) alpha 1,3-fucosyltransferase [Helicobacter pylori]	0.16

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
608	AF041141	Homo sapiens pituitary specific homeodomain protein (PROP1) gene, exon 3 and complete cds	0.19	37403	(X03541) trk gene product (aa 1-641) [Homo sapiens]	0.091
609	L12531	Discopyge ommata Ca2+ channel alpha 1 subunit gene sequence.	0.19	3618274	(AJ223219) hypothetical protein	0.069
610	AF052445	Yellow fever virus clone HONG9 polyprotein gene, complete cds	0.19	1932822	(U15928) KH-domain putative RNA binding protein	0.001
611	Z36946	B.anthraxis sap gene encoding S-layer protein	0.19	173241	(L06487) ZIP1 protein [Saccharomyces cerevisiae]	2e-04
612	AF087984	Homo sapiens full length insert cDNA clone YW29A12	0.19	3786014	(AC005499) hypothetical protein [Arabidopsis thaliana]	1e-06
613	AE001010	Archaeoglobus fulgidus section 97 of 172 of the complete genome	0.19	3135493	(AF060248) unknown [Arabidopsis thaliana]	7e-08
614	L08965	Trichosporon cutaneum carbamoyl phosphate synthetase large subunit (argA) gene, partial cds.	0.19	1086901	(U41278) F33G12.3 gene product [Caenorhabditis elegans]	2e-08
615	M91466	Rattus norvegicus A2b-adenosine receptor mRNA, complete cds.	0.19	2984320	(AE000773) acetoin utilization protein [Aquifex aeolicus]	6e-09
616	X95971	S.lividans groEL2 gene	0.19	3925277	(AL032643) similar to Uncharacterized protein family UPF0034, Double-stranded RNA binding motif; cDNA EST yk489b3.5 comes from this gene; cDNA EST yk439g7.5 comes from this gene [Caenorhabditis elegans]	7e-10
617	U12539	Schizosaccharomyces pombe scd2 (scd2) gene, complete cds.	0.19	1938549	(U97016) similar to drosophila Rlc1 gene product ribosomal protein L4 (YML4) (NID:g459259)	3e-14

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
618	U12539	Schizosaccharomyces pombe scd2 (scd2) gene, complete cds.	0.19	1938549	(U97016) similar to drosophila Rlc1 gene product ribosomal protein L4 (YML4) (NID:g459259)	9e-15
619	Z68327	Human DNA sequence from cosmid U25D11, between markers DXS366 and DXS87 on chromosome X.	0.19	3875774	EMBL:D32434 comes from this gene; cDNA EST EMBL:D33710 comes from this gene; cDNA EST EMBL:D34467 comes from this gene; cDNA EST EMBL:D35005 comes from this gene; cDNA EST EMBL:D37535 comes from this gene; ... >gi 3878710 gnl PID e1348373 EST EMBL:D33710 comes from this gene; cDNA EST EMBL:D34467 comes from this gene; cDNA EST EMBL:D35005 comes from this gene; cDNA EST EMBL:D37535 comes from this gene; ...	6e-15
620	U66525	Dictyostelium discoideum ORFveg114 mRNA, complete cds	0.19	3540281	(AF056116) All-1 related protein [Fugu rubripes]	2e-17
621	U25830	Newcastle disease virus isolate Herts/33 matrix protein mRNA, complete cds	0.19	2228750	(U93868) RNA polymerase III subunit [Homo sapiens]	1e-18
622	U89407	Mus musculus strain BALB/c delta-aminolevulinic acid dehydratase (Lv) mRNA, partial cds	0.19	1825764	(U88314) C46H11.11 gene product [Caenorhabditis elegans]	3e-25
623	AF095598	Bison bison athabasca microsatellite BBJ 2	0.18	<NONE>	<NONE>	<NONE>
624	AF064260	Strongylocentrotus purpuratus SRC8 mRNA, complete cds	0.18	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
625	U69533	Arabidopsis thaliana AtKAP alpha mRNA, complete cds	0.18	<NONE>	<NONE>	<NONE>
626	D89041	Bovine DNA for prostaglandin F2alpha receptor, partial cds	0.18	<NONE>	<NONE>	<NONE>
627	M24571	Dictyostelium discoideum tRNA-Glu-GAA gene, clone yGluGAA7.	0.18	<NONE>	<NONE>	<NONE>
628	X59772	D.melanogaster ovo gene required for female germ line development	0.18	<NONE>	<NONE>	<NONE>
629	AL010209	Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-104, complete sequence	0.18	<NONE>	<NONE>	<NONE>
630	U67575	Methanococcus jannaschii section 117 of 150 of the complete genome	0.18	111839	inositol 1,4,5-triphosphate receptor 2 - rat	8.5
631	U28730	Caenorhabditis elegans cosmid K10B2	0.18	1787604	(AE000232) orf, hypothetical protein [Escherichia coli]	8.3
632	X99798	L.lactis pepF1 & pepF2 genes	0.18	3406624	(AF079110) glycosomal malate dehydrogenase [Trypanosoma brucei]	8.1
633	AF025306	Danio rerio band 4.1-like protein 4 (nbl4) mRNA, complete cds	0.18	465445	PROBABLE NUCLEAR ANTIGEN herpesvirus 1 (strain Kaplan) >gi 334072 (M34651) ORF-3 protein [Pseudorabies virus]	7.9
634	AF059251	Mus musculus lipoxigenase (alox) mRNA, complete cds	0.18	1655667	(Z81368) hypothetical protein Rv2393	6.6
635	Z22605	G.domesticus CTCF protein mRNA.	0.18	481864	3-methyl-2-oxobutanoate dehydrogenase	6.6
636	AB011086	Homo sapiens mRNA for KIAA0514 protein, complete cds	0.18	3874158	(Z81464) predicted using Genefinder	6.4

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Caenorhabditis				
637	Z78536	elegans cosmid C07A4, complete sequence [Caenorhabditis elegans]	0.18	3702121	(AJ011681) retinoblastoma-related protein [Chenopodium rubrum]	6.4
638	U67530	Methanococcus jannaschii section 72 of 150 of the complete genome	0.18	3877946	(Z81094) Weak similarity to 65 KDA heat shock protein (TR:G602231); cDNA EST EMBL:D71705 comes from this gene; cDNA EST EMBL:D74382 comes from this gene [Caenorhabditis elegans] (Z69634) cDNA EST EMBL:D71510 comes from this gene; cDNA EST EMBL:C08449 comes from this gene; cDNA EST yk266b12.3 comes from this gene; cDNA EST yk266b12.5 comes from this gene; cDNA EST yk461h7.3 comes from this gene; cDNA...	6.3
639	M63781	Influenza A/Duck/England/1/62 (H4N6) nucleoprotein mRNA, complete cds.	0.18	3873663		6.2
640	M73781	Oryctolagus cuniculus integrin beta-8 subunit mRNA, complete cds. >:: gb I44828 I44828 Sequence 3 from patent US 5635601	0.18	1362129	major allergen OLE17 - common olive	5.8
641	X67219	D.melanogaster Rop gene	0.18	3449286	(AB011527) MEGF1 [Rattus norvegicus]	4.8
642	AF106941	Homo sapiens beta-arrestin 2 mRNA, complete cds	0.18	548353	[PROTEIN-PII] URIDYLYLTRANSFERASE vinelandii >gi 39257 (X59610) uridylyl transferase	3.7
643	AF052602	Danio rerio huntingtin (HD) mRNA, complete cds	0.18	241058	potential IGF binding protein [chickens, Peptide Partial, 77 aa, segment 2 of 3]	3.6

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
644	AB020709	Homo sapiens mRNA for KIAA0902 protein, complete cds	0.18	3875570	(Z68314) predicted using GeneFinder; cDNA EST EMBL:M75775 comes from this gene; cDNA EST EMBL:M89255 comes from this gene; cDNA EST EMBL:M89127 comes from this gene; cDNA EST EMBL:T00141 comes from this gene; cDNA EST EMBL:T...	2.1
645	AF096883	HIV-1 isolate patient 3 country USA pol polyprotein (pol) gene, partial cds	0.18	3250696	(AL024486) putative protein	1.7
646	L39928	Pyrocoelia miyako (clone pB-PmL41) luciferase mRNA, complete cds	0.18	2914702	(AC003974) unknown protein [Arabidopsis thaliana]	0.73
647	M17082	Human carcinoembryonic nonspecific crossreacting antigen (CEA; NCA) gene, exons 1 and 2.	0.18	1351833	REGULATORY PROTEIN ABAA	0.72
648	X75318	H.sapiens ITIH1 gene (exon 22) and ITIH3 gene	0.18	629557	RNA-binding protein mpD - Arabidopsis thaliana (fragment) >gi 510240 (X61108) RNA binding protein [Arabidopsis thaliana]	0.41
649	AF011908	Mus musculus apoptosis associated tyrosine kinase (AATYK) mRNA, complete cds	0.18	330442	(K03332) nuclear antigen 2 [Epstein-Barr virus]	5e-04
650	U04004	Simian immunodeficiency virus SIVagmVER-2 envelope protein gene, partial cds.	0.18	135102	ASPARTYL-tRNA SYNTHETASE aspartate--tRNA ligase (EC 6.1.1.12) - Escherichia coli coli] >gi 1736513 gnl PID d1016401 (D90829) Aspartate--tRNA ligase (EC 6.1.1.12) [Escherichia coli]	6e-11
651	U88155	Xenopus laevis RanGTPase activating protein	0.18	995714	(X91258) pid:e198503 [Saccharomyces cerevisiae]	2e-13

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
652	Z18921	B.oleracea gene for S-receptor kinase-like protein	0.18	3875535	(Z66511) similar to ribokinase; cDNA EST EMBL:D69553 comes from this gene; cDNA EST EMBL:D65938 comes from this gene; cDNA EST yk280h9.3 comes from this gene; cDNA EST yk280h9.5 comes from this gene; cDNA EST yk223d11.3 come...	1e-19
653	M60650	S.cerevisiae STA2 gene, complete cds.	0.16	<NONE>	<NONE>	<NONE>
654	U80912	Eucalyptus globulus NADP-isocitrate dehydrogenase (EgICDH) mRNA, complete cds	0.16	3766172	(AF057298) ornithine decarboxylase antizyme 2 [Mus musculus]	4.2
655	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	0.16	76749	hypothetical protein 4 - fowl adenovirus 1	4.0
656	AF027174	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-B) mRNA, complete cds	0.16	3044086	(AF055904) unknown [Myxococcus xanthus]	0.60
657	AF030231	Glycine max sucrose synthase (SS) mRNA, complete cds	0.078	<NONE>	<NONE>	<NONE>
658	M19183	Woodchuck hepatitis virus (WHV), complete genome, clone WHV 59.	0.072	1076190	cell wall glycoprotein, 75K, precursor - diatom (Cylindrotheca fusiformis) >gi 515363 (X80394) P75K gene product [Cylindrotheca fusiformis]	6.3
659	U31557	Ovine adenovirus IVa2 protein gene, DNA polymerase gene, terminal protein gene and 52.55 kDa protein gene, partial cds	0.072	3511143	(AF061244) unknown [Agrocybe aegerita]	6.2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Caenorhabditis				
660	AL021491	elegans cosmid Y44A6B, complete sequence [Caenorhabditis elegans]	0.070	<NONE>	<NONE>	<NONE>
661	M33874	X.laavis Xotch protein mRNA, complete cds.	0.070	1654096	(Y09076) RAD3 [Schizosaccharomyces pombe]	0.23
662	AB012725	Mus musculus ZAN75 mRNA for zinc finger protein, complete cds	0.069	1350800	MITOCHONDRIAL RIBOSOMAL PROTEIN S5	2.0
663	AL021491	Caenorhabditis elegans cosmid Y44A6B, complete sequence [Caenorhabditis elegans]	0.068	<NONE>	<NONE>	<NONE>
664	Z60318	H.sapiens CpG DNA, clone 1e1, reverse read cpg1e1.rla.	0.068	1280134	(U55376) F16H11.2 gene product [Caenorhabditis elegans]	2.6
665	Z35973	S.cerevisiae chromosome II reading frame ORF YBR104w	0.068	2493000	PROBABLE SUCCINYL-COA:3-KETOACID-COENZYME A TRANSFERASE PRECURSOR EMBL:Z14816 comes from this gene; cDNA EST EMBL:Z14946 comes from this gene; cDNA EST EMBL:D69746 comes from this gene; cDNA EST yk219b6.3 comes from this gene; cDNA ES...	0.68
666	Z86111	Streptomyces lividans rpsP, trmD, rplS, sipW, sipX, sipY, sipZ, mutT genes and 4 open reading frames	0.068	1235974	(X96713) collagen [Globodera pallida]	4e-04
667	M72980	Anthonomus grandis vitellogenin gene (VTG), complete cds.	0.068	3242750	(AC005164) match to ESTs AA731149 (NID:g2140138), AA731908 (NID:g2752719), AA287837 (NID:g1933519), AA262811 (NID:g1898382), and AA825820 (NID:g2899132)	1e-59

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
668	M34161	Rat tachykinin (PPT) gene, exons 5 and 6.	0.067	<NONE>	<NONE>	<NONE>
669	L03811	Aspergillus niger zinc finger protein (creA) gene, complete cds.	0.067	<NONE>	<NONE>	<NONE>
670	M64983	Human fibrinogen beta chain gene, complete mRNA. >gb I47706 I47706 Sequence 3 from patent US 5639940	0.067	<NONE>	<NONE>	<NONE>
671	AF014051	Nicotiana tabacum Mg chelatase subunit (ChlH) mRNA, partial cds	0.067	<NONE>	<NONE>	<NONE>
672	Y07540	H.sapiens sil gene	0.067	92331	glycoprotein GP330, renal - rat (fragments)	7.5
673	AJ000347	Rattus norvegicus mRNA for 3'(2'),5'-bisphosphate nucleotidase	0.067	129238	25 KD OOKINETE SURFACE ANTIGEN PRECURSOR (PRS25) >gi 320962 pir A44966 25k ookinete surface antigen precursor - Plasmodium reichenowi reichenowi]	7.4
674	L19979	Squid sodium channel mRNA, complete cds.	0.067	2128473	hypothetical protein MJ0750 - Methanococcus jannaschii >gi 1592304 (U67521) ferredoxin-type protein	1.5
675	X08050	Yeast tRNA-Glu(3) gene and flanking regions	0.067	1334398	(X15081) MURF2 protein (AA 1-348)	0.65
676	X17115	Human mRNA for IgM heavy chain complete sequence	0.067	1731331	HYPOTHETICAL 51.6 KD PROTEIN CY49.14C >gi 1370241 gnl PID e247089 (Z73966) hypothetical protein Rv2075c [Mycobacterium tuberculosis]	0.51
677	AF032871	Homo sapiens uncoupling protein 3 (UCP3) gene, exon 1 and partial exon 2	0.067	112900	ALPHA-2C-1 ADRENERGIC RECEPTOR human >gi 178194 (J03853) kidney alpha-2-adrenergic receptor [Homo sapiens] >gi 1628638 (U72648) alpha2-C4-adrenergic receptor [Homo sapiens]	0.50

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
678	X05319	Mouse class II MHC E-beta 2 (d) gene exon 3	0.067	585074	DYNAMIN 3 (DYNAMIN, TESTICULAR) rat >gi 391872 gnl PID d1003668 (D14076) testicular dynamin [Rattus norvegicus]	3e-04
679	AB006362	Candida albicans CaSLN1 gene, complete cds	0.067	3417296	(AC003007) Unknown gene product (partial) [Homo sapiens]	9e-56
680	AF021236	African horse sickness virus capsid VP3 (L3) mRNA, complete cds	0.066	<NONE>	<NONE>	<NONE>
681	AE001507	Helicobacter pylori, strain J99 section 68 of 132 of the complete genome	0.066	<NONE>	<NONE>	<NONE>
682	AF039717	Caenorhabditis elegans cosmid R13H8	0.066	<NONE>	<NONE>	<NONE>
683	AF029027	Syncerus caffer isolate Queen Elizabeth Mweya 14 mitochondrial DNA control region	0.066	<NONE>	<NONE>	<NONE>
684	AF087967	Homo sapiens full length insert cDNA clone YU51G05	0.066	2982476	(X97203) C1 protein [Beet curly top virus]	9.5
685	J02037	Baboon endogenous virus proviral long terminal repeat DNA.	0.066	972767	(L37868) POU-domain transcription factor [Homo sapiens]	7.3
686	AF000141	Lycopersicon esculentum class I knotted-like homeodomain protein (LeT6) mRNA, complete cds	0.066	3157926	(AC002131) Strong similarity to extensin-like protein gb Z34465 from Zea mays. [Arabidopsis thaliana]	5.6
687	AB001746	Bensingtonia sp. OK255 gene for 18S rRNA >:: dbj AB001747 AB001747 Bensingtonia sp. OK259 gene for 18S rRNA	0.066	3859889	(AF070064) cap 'n' collar isoform C [Drosophila melanogaster]	0.38

Nearest Neighbor (BlastN vs. Genbank)				Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Helicobacter pylori,				
688	AE001461	strain J99 section 22 of 132 of the complete genome	0.065	<NONE>	<NONE>	<NONE>
689	M30821	Chicken erythroid transport proteins c1 and c2	0.065	<NONE>	<NONE>	<NONE>
690	AB009802	Homo sapiens gene for osteonidogen, intron 3	0.065	<NONE>	<NONE>	<NONE>
691	AF086062	Homo sapiens full length insert cDNA clone YZ06B11	0.065	<NONE>	<NONE>	<NONE>
692	AB002369	Human mRNA for KIAA0371 gene, complete cds	0.065	2500884	SIGNAL SEQUENCE BINDING PROTEIN binding protein [Synechococcus sp.]	5.5
693	AF086864	Cyclopodia sp. large subunit ribosomal RNA gene, mitochondrial gene for mitochondrial RNAs, partial sequence > :: gb AF086866 AF086866 Penicillidia sp. large subunit ribosomal RNA gene, mitochondrial gene for mitochondrial RNAs, partial sequence	0.065	3721684	(AB012957) probable glycosyl transferase [Vibrio cholerae]	5.5
694	L44593	Bacteriophage BK5-T ORF410, 3' end pf cds, 20 ORFs, repressor protein, and Cro repressor protein genes, complete cds, ORF70' gene, 5' end of cds.	0.065	1172067	PEPTIDASE T (AMINOTRIPEPTIDASE) [influenzae Rd]	3.2
695	U80079	Ciona intestinalis MyoD-family protein (CiMDFa) mRNA, complete cds	0.065	4218110	(AL035353) contains EST gb:F15281	2.5

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
696	AB020718	Homo sapiens mRNA for KIAA0911 protein, complete cds	0.065	1722734	MINOR CAPSID PROTEIN L2 >gi 1020192 type 23]	1.9
697	AF082137	Zea mays copia-like retrotransposon Stl-14 leader region, partial sequence	0.065	1877501	(U89278) polyhomeotic 2 homolog [Homo sapiens]	1.1
698	X64053	R.norvegicus ZnBP gene for zinc binding protein	0.065	464963	TRYPSIN PRECURSOR	0.36
699	U67065	Mus musculus butyrophilin (BTN) gene, promoter region and complete cds	0.065	2132252	hypothetical protein YPL263c - yeast	3e-10
700	M64862	Rat matrix F/G mRNA, complete cds.	0.065	3420183	(AF041105) organic anion transporter protein 3 [Rattus norvegicus]	4e-19
701	K02205	Yeast (<i>S.cerevisiae</i>) transcriptional activator of amino acid-biosynthetic genes (GCN4) gene, complete cds.	0.064	<NONE>	<NONE>	<NONE>
702	X58282	Maize mRNA for a high mobility group protein	0.064	<NONE>	<NONE>	<NONE>
703	AC001545	Homo sapiens (subclone 1_f3 from P1 H69) DNA sequence	0.064	<NONE>	<NONE>	<NONE>
704	AF023461	Homo sapiens FRA3B region sequence	0.064	<NONE>	<NONE>	<NONE>
705	U50307	Caenorhabditis elegans cosmid F43H9.	0.064	<NONE>	<NONE>	<NONE>
706	U46542	Streptococcus crista HmpA gene, partial cds, putative adhesin/ABC transport system protein (scbA) gene, complete cds	0.064	1209391	(D83659) TPR protein pombe] >gi 2894282 gnl PID c1251103 (AL021838) pre-mrna splicing factor. [Schizosaccharomyces pombe]	9.2
707	X57564	A.rusticana mRNA for neutral peroxidase	0.064	1492037	(U60315) MC094R [Molluscum contagiosum virus subtype 1]	6.9

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
708	U06986	Human alpha-2-macroglobulin receptor/lipoprotein receptor protein (A2MR/LRP) gene, exons 39-41.	0.064	100800	rab15B protein - wheat >gi 21853 (X62476) rab protein [Triticum aestivum]	5.3
709	D85773	Human CpG island sequence, clone Q28B8	0.064	2245382	(U88325) suppressor of cytokine signalling-1 [Mus musculus]	5.3
710	L06178	Apis mellifera ligustica complete mitochondrial genome	0.064	3695379	(AF096370) contains similarity to a C. elegans hypothetical protein F44G4.1 (GB:Z49910) and several yeast hypothetical proteins such as 35.1 KD protein in NAM8-GAR1 intergenic region (SP:P38805) [Arabidopsis thaliana]	3.2
711	Y16242	Triticum aestivum mRNA for beta-amylase	0.064	1175958	HYPOTHETICAL 70.5 KD PROTEIN IN AGP3-DAK3 INTERGENIC REGION >gi 1084712 pir S56201 probable membrane protein YFL054c - yeast (Saccharomyces cerevisiae) >gi 836701 gnl PID d1009825 (D50617) YFL054C	3.1
712	L81779	Homo sapiens (subclone 2_a2 from P1 H25) DNA sequence	0.064	3845169	(AE001391) phosphatase (acid phosphatase family)	0.81
713	X13826	C.reinhardtii psb1 mRNA for OEE1 protein of photosystem II (oxygen-evolving enhancer protein)	0.064	171040	(M94535) ATPase [Saccharomyces cerevisiae] cerevisiae, Peptide, 377 aa [Saccharomyces cerevisiae]	0.054
714	X06487	H.sapiens mRNA for bcl2-Ig fusion gene	0.064	2429362	(AF020261) proline rich protein [Santalum album]	0.016
715	U79638	Mus musculus cyclin-dependent kinase inhibitor protein (p15 ^{INK4b}) gene, exon 2 and partial cds	0.064	3929221	(AF082557) TRF1-interacting ankyrin-related ADP-ribose polymerase [Homo sapiens]	1e-10

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Human T cell				
716	U39099	receptor alpha chain mRNA, partial cds	0.063	<NONE>	<NONE>	<NONE>
717	U39673	Clostridium acetobutylicum KdpC (kdpC) gene, partial cds, sensor histidine kinase homolog (kdpD) and response regulator homolog (kdpE) genes, complete cds	0.063	<NONE>	<NONE>	<NONE>
718	AL022317	Human DNA sequence from clone 140L1 on chromosome 22q13.1-13.31, complete sequence [Homo sapiens]	0.063	1931640	(U95973) Serine carboxypeptidase isolog [Arabidopsis thaliana]	5.2
719	U28972	Spiroplasma citri orfA and orfB genes, partial cds, orfB, orfC, and orfE genes and Spiroplasma virus SpVI-derived ORF1 and ORF3 genes, complete cds, and SpVI-derived ORF14 gene, partial cds.	0.063	4091939	(AF070704) envelope glycoprotein [Human immunodeficiency virus type 1]	5.2
720	U15159	Mus musculus limk kinase (limk) mRNA, complete cds	0.063	3638957	(AC004877) sco-spondin-mucin-like; similar to P98167 uncertain [Homo sapiens]	5.1
721	AF058416	Homo sapiens lipoprotein receptor-related protein (LRP1), exons 39, 40, and 41	0.063	1788123	(AE000276) orf, hypothetical protein [Escherichia coli]	4.0
722	AE001430	Plasmodium falciparum chromosome 2, section 67 of 73 of the complete sequence	0.063	2244849	(Z97337) hypothetical protein	4.0

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		<i>Sireptococcus</i>			(Z70203) cDNA EST	
723	L29323	pneumoniae methyl transferase gene cluster, complete sequence	0.063	3874022	EMBL:D72339 comes from this gene; cDNA EST EMBL:D75197 comes from this gene [Caenorhabditis elegans] (Z73105) predicted using Genefinder; cDNA EST EMBL:T01277 comes from this gene; cDNA EST EMBL:T01796 comes from this gene; cDNA EST EMBL:D32545 comes from this gene; cDNA EST EMBL:D33060 comes from this gene; cDNA EST EMBL:D...	2.3
724	X72631	H.sapiens mRNA encoding Rev-ErbAalpha > :: emb[X72632]HSREV ERB2 H.sapiens mRNA encoding Rev-ErbAalpha (internal fragment)	0.063	3979878	(AF025467) contains similarity to drosophila DNA-binding protein K10 (NID:g8148) [Caenorhabditis elegans]	1.7
725	U17969	Human initiation factor eIF-5A gene, complete cds.	0.063	2429509	(AF082486) nef protein [Human immunodeficiency virus type 1]	1.4
726	AE001000	Archaeoglobus fulgidus section 107 of 172 of the complete genome	0.063	3462802	(U58734) weak similarity to ankyrin G [Caenorhabditis elegans]	0.35
727	S80986	svp[40]=svp-related nuclear receptor/retinoid signaling modulator [zebrafishes, mRNA, 3876 nt]	0.063	1326288	proline-rich proteoglycan 2 precursor, parotid - rat >gi 310200 (L17318) proline-rich proteoglycan [Rattus norvegicus]	0.093
728	AF109134	Homo sapiens 7-60 mRNA, complete cds	0.063	1083764	(AL021816) SPBC24E9.03c, unknown, len:251aa [Schizosaccharomyces pombe]	0.001
729	D87466	Human mRNA for KIAA0276 gene, partial cds	0.063	2879865	(AF053455) tetraspan TM4SF [Homo sapiens]	6e-05
730	AB018269	Homo sapiens mRNA for KIAA0726 protein, complete cds	0.063	2995865	HYPOTHETICAL 47.6 KD PROTEIN C16C10.5 IN CHROMOSOME III >gi 3874383 gnl PID e1344077 type (RING finger) [Caenorhabditis elegans]	2e-16
731	D86954	Cricetulus griseus mRNA for Cytochrome P-450 2A14, complete cds	0.063	2496896		1e-22

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Plasmodium				
732	AL010232	falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 4-58, complete sequence	0.062	<NONE>	<NONE>	<NONE>
733	U90714	Mycoplasma gallisepticum haemagglutinin precursor genes, complete cds	0.062	<NONE>	<NONE>	<NONE>
734	AF107044	Homo sapiens clone pCL4 DNA-binding protein SOX21 (SOX21) gene, complete cds	0.062	<NONE>	<NONE>	<NONE>
735	L41729	Caenorhabditis elegans Ro ribonucleoprotein autoantigen mRNA, complete cds	0.062	2983060	(AE000687) putative protein [Aquifex aeolicus]	8.6
736	Z99287	Caenorhabditis elegans cosmid Y7A9D, complete sequence [Caenorhabditis elegans]	0.062	1176542	POTATIVE SERINE/THREONINE- PROTEIN KINASE D1044.3 IN CHROMOSOME III >gi 495684 (U00065) contains EGF-like repeats; highly similar to ZC84.1; 3' exons similar to protein kinase [Caenorhabditis elegans]	5.8
737	AB014514	Homo sapiens mRNA for KIAA0614 protein, partial cds	0.062	4033395	DNA GYRASE SUBUNIT B subunit [Myxococcus xanthus]	3.9
738	L29165	Human germline immunoglobulin light chain variable region (lambda-IIIb subgroup) from IgM rheumatoid factor.	0.062	1914685	(Y12014) RAD23 protein, isoform II	1.3
739	U09364	Schistosoma japonicum Chinese clone pY6 paramyosin mRNA, partial cds.	0.062	1350800	MITOCHONDRIAL RIBOSOMAL PROTEIN S5	1.3
740	Y16242	Triticum aestivum mRNA for beta- amylase	0.062	79834	hypothetical protein 1246 (uvrA region)- Micrococcus luteus (fragment)	0.59

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
741	M97695	Leishmania pifanoi cysteine proteinase (cys2) gene, complete cds.	0.062	1174754	TROPOMYOSIN I (TMI) (POLYPEPTIDE 49) >gi 320989 pir A60607 tropomyosin - fluke	0.018
742	U67526	Methanococcus jannaschii section 68 of 150 of the complete genome	0.062	1330345	(U58755) coded for by C. elegans cDNA yk34b1.5; coded for by C. elegans cDNA yk13h10.5; coded for by C. elegans cDNA yk46e8.5; coded for by C. elegans cDNA yk46d5.5; coded for by C. elegans cDNA yk43c2.5; coded for by C. elegans cDNA yk46e8....	1e-40
743	Z78414	Caenorhabditis elegans cosmid W09D12, complete sequence [Caenorhabditis elegans]	0.061	<NONE>	<NONE>	<NONE>
744	Y13606	Mus musculus gene encoding filensin, exons 6, 7	0.061	2314715	(AE000651) H. pylori predicted coding region HP1527	4.9
745	J04374	Eggplant mosaic virus genome.	0.061	141449	HYPOTHETICAL 35.5 KD PROTEIN IN TRANSPOSON TN4556 >gi 80759 pir JQ0431 hypothetical 35.5K protein - Streptomyces fradiae transposon Tn4556	3.8
746	AB022200	Marine obligately oligotrophic bacterium POO-10 DNA for 16S ribosomal RNA, partial sequence	0.061	3983593	(AB000307) transcarboxylase-beta	2.2
747	X54250	Rat mRNA for zinc finger protein AT-BP2, partial cds	0.061	1377886	(L46815) DNA binding protein Rc [Mus musculus]	0.98
748	X69942	M.musculus mRNA of enhancer-trap-locus 1	0.061	2983969	(AE000748) putative protein [Aquifex aeolicus]	0.57
749	AJ223206	Mus musculus mRNA for scrapie responsive protein 1	0.061	4204265	(AC005223) 45643 [Arabidopsis thaliana]	5e-31
750	Y10205	H.sapiens mRNA for CD88 protein	0.060	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
751	U79260	Human clone 23745 mRNA, complete cds	0.060	<NONE>	<NONE>	<NONE>
752	X07453	Plasmodium falciparum 11-1 gene part 1	0.060	<NONE>	<NONE>	<NONE>
753	U57502	Rattus norvegicus protein tyrosine phosphatase delta gene, catalytic domain, partial cds.	0.060	3452285	(AF044915) polar tube protein PTP55 precursor	0.28
754	X68359	M. fascicularis gene for apolipoprotein C-III	0.060	730843	SHUTTLE CRAFT PROTEIN >gi 487400	2e-04
755	X51634	Pseudomonas braB gene for branched chain amino acid transport carrier (LIV-II)	0.059	1835622	(U85718) CCML [Pseudomonas putida GB-1]	8.1
756	AF072405	Gossypium hirsutum cotton fiber expressed protein 2 (CFE2) mRNA, complete cds	0.059	423766	alkaline phosphatase, 145K - Synechococcus sp.	4.7
757	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	0.056	2662481	(AF034859) juvenile hormone resistance protein	3.3
758	AF093268	Rattus norvegicus homer-1c mRNA, complete cds	0.054	547847	LECTIN PRECURSOR	7.0
759	X61046	Hydra N-COL 2 mRNA for mini-collagen, partial cds	0.053	<NONE>	<NONE>	<NONE>
760	AJ005813	Arabidopsis thaliana mRNA for neoxanthin cleavage enzyme	0.052	<NONE>	<NONE>	<NONE>
761	S79843	{random amplified hybridization microsatellite RAHM} [Beta vulgaris=sugar beets. Genomic, 537 nt]	0.025	1730145	GAMETOGENESIS EXPRESSED PROTEIN GEG-154 >gi 2137331 pir 48361 gene GEG-154 protein - mouse >gi 550123 (X71642) pid:g550123 [Mus musculus]	2e-16

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Mouse mRNA for				
762	AB000096	GATA-2 protein, complete cds	0.023	<NONE>	<NONE>	<NONE>
763	Z62366	H.sapiens CpG DNA, clone 67h7, forward read cpg67h7.ft1a	0.023	3123312	ZINC FINGER PROTEIN 142 (KIAA0236) to Human zinc finger protein(ZNF142) [Homo sapiens]	5.9
764	L11670	Human transmembrane glycoprotein (CD53) gene, exons 2 through 8.	0.023	80636	hypothetical 67K protein - Mycobacterium fortuitum plasmid pAL5000 >gi 149986 (M60875) ORF2	3.4
765	D83984	Sulculus diversicolor DNA for IDO-like myoglobin, complete cds	0.023	3114665	(AF061267) inner membrane component HtxE [Pseudomonas stutzeri]	3.4
766	X98890	S.tuberosum mRNA for inorganic phosphate transporter, StPT1	0.023	683532	(X02155) thyroglobulin [Bos taurus]	1.1
767	U58835	Dissostichus mawsoni preprotrypsin gene, complete cds	0.022	<NONE>	<NONE>	<NONE>
768	AJ009630	Glomus versiforme chitin synthase gene (clone Gvchs3)	0.022	<NONE>	<NONE>	<NONE>
769	J04040	Human glucagon mRNA, complete cds.	0.022	<NONE>	<NONE>	<NONE>
770	X74908	L.esculentum Asr3 gene	0.022	<NONE>	<NONE>	<NONE>
771	L07293	Shigella dysenteriae O-antigen polysaccharide biosynthesis rfbX, O-antigen polymerase (rfc), rhamnosyl transferase I and II (rfbR and rfbQ) and rfbD genes, complete cds.	0.022	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Mus musculus				
772	AF040094	inositol polyphosphate 5-phosphatase II (INPP5P) mRNA, complete cds	0.022	<NONE>	<NONE>	<NONE>
773	X76776	H.sapiens HLA-DMB gene	0.022	<NONE>	<NONE>	<NONE>
774	AE001521	Helicobacter pylori, strain J99 section 82 of 132 of the complete genome	0.022	<NONE>	<NONE>	<NONE>
775	X16004	A.longa rbcL, rpl5, rps8, rpl36, rps14, rps2, trnI, trnF, trnC and rpoB (partial) genes > :: emb X75651 ALRIBP A.longa plastid genes for ribosomal proteins, tRNAs, RNA polymerase subunit beta and rubisco large subunit	0.022	<NONE>	<NONE>	<NONE>
776	Y12707	Lactococcus lactis cremoris plasmid pHW393 DNA, rrladii, mlladii genes	0.022	<NONE>	<NONE>	<NONE>
777	U27118	Arabidopsis thaliana glutamyl-tRNA reductase	0.022	<NONE>	<NONE>	<NONE>
778	Z96622	H.sapiens telomeric DNA sequence, clone SPTEL002, read SPTELOO002.seq	0.022	191333	(J05503) carbamoyl-phosphate synthetase (E.C.6.3.5.5)	9.8
779	D83984	Sulculus diversicolor DNA for IDO-like myoglobin, complete cds	0.022	1078509	probable membrane protein YDR018c - yeast	9.7
780	Z77952	H.sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA-4A3	0.022	4204206	(AB022786) N-acetyl-beta-D-glucosaminidase [Enterobacter sp.]	7.5

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Xenopus laevis				
781	M10217	mitochondrial DNA, complete genome.	0.022	2145763	B2168_C2_205 protein - Mycobacterium leprae	7.3
782	M55147	Pea chloroplast glyceraldehyde-3-phosphate dehydrogenase (Cpb1) gene, complete cds.	0.022	417308	PROBABLE HELICASE MOT1 Mot1p is a probable helicase essential for vegetative growth on rich glucose medium at 30 degree C: Swiss-Prot Accession number P32333; similar to S. cerevisiae RAD26 gene product: Swiss-Prot Accession number P40352	4.2
783	X58839	Acholeplasma virus MV-L1 DNA for complete circular genome	0.022	3273189	(AB008757) subunit II of c(o/b)3-type cytochrome c oxidase [Bacillus stearothermophilus]	4.1
784	M26185	Mouse c-myb oncogene, exon 1 and exon 2 (partial).	0.022	138592	VITELLOGENIN I PRECURSOR (YOLK PROTEIN 1) >gi 72270 pir VJFFI vitellogenin I precursor unnamed protein product [Drosophila melanogaster]	2.5
785	AF061195	Streptomyces albus valine dehydrogenase (Vdh) gene, complete cds	0.022	2088768	(AF003145) B0414.8 gene product [Caenorhabditis elegans]	0.86
786	AF053622	Homo sapiens alpha 1,2-mannosidase IB gene, exon 9	0.022	1352361	EARLY GROWTH RESPONSE PROTEIN 1 fish >gi 531456 (U12895) egr1 [Danio rerio] rerio]	0.36
787	Z71500	S.cerevisiae chromosome XIV reading frame ORF YNL224c	0.022	1708875	PUTATIVE TUMOR SUPPRESSOR LUCA15 sapiens]	0.16
788	D10471	Herpes simplex virus type 2 genomic DNA for 0.74-0.84 region, complete cds	0.022	3132276	(AB011486) short ORF [TT virus]	0.13
789	U43082	Zea mays T cytoplasm male sterility restorer factor 2 (rf2) mRNA, complete cds	0.022	3319720	(AL031035) putative aldehyde dehydrogenase [Streptomyces coelicolor]	0.011

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		H.sapiens simple tandem repeat DNA (clone wg3a6)	0.021	<NONE>	<NONE>	<NONE>
790	X86913	Mus musculus Pontin52 mRNA, complete cds	0.021	<NONE>	<NONE>	<NONE>
791	AF100694	Nannostomus sp. large subunit rRNA gene, mitochondrial gene encoding mitochondrial rRNA, partial sequence.	0.021	<NONE>	<NONE>	<NONE>
792	U34016	Yeast mitochondrial genes for 15S rRNA and tRNA-Trp	0.021	<NONE>	<NONE>	<NONE>
793	X00845	Homo sapiens gene for CC chemokine PARC precursor, complete cds	0.021	<NONE>	<NONE>	<NONE>
794	AB012113	Daucus carota globulin-like protein (Gea8) gene, complete cds	0.021	<NONE>	<NONE>	<NONE>
795	U62395	P.falciparum actin II gene, complete cds.	0.021	2623773	(AF004835) tyrocidine synthetase 3 [Brevibacillus brevis]	8.8
796	M22718	Arabidopsis thaliana glutamyl-tRNA reductase	0.021	3549885	(AJ006631) cysteine-rich secretory protein-1 [Equus caballus]	8.8
797	U27118	H.sapiens CLN3 gene, complete CDS	0.021	262249	(S52010) orf1 5' of EpoR [mice, Peptide. 85 aa] [Mus sp.]	8.7
798	X99832	Homo sapiens TRAIL receptor 2 mRNA, complete cds	0.021	729048	SUCCINYL-COA:COENZYME A TRANSFERASE transferase [Clostridium kluyveri]	8.7
799	AF016266	Human DNA sequence from PAC 179I15, BRCA2 gene region chromosome 13q12-13 contains lactase-phlorizin hydrolase (LCT)	0.021	585820	LIPOPOLYSACCHARIDE 1,2-N-ACETYLGLUCOSAMINETRANSFERASE >gi 466761 (U00039) rfaK [Escherichia coli] >gi 1790053 (AE000440) probably hexose transferase; lipopolysaccharide core biosynthesis	5.3
800	Z92541					

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		dopamine D2				
801	S58588	receptor [human, brain, Genomic, 3794 nt, segment 4 of 5]	0.021	2677620	(Y08029) NAD(P)(+)-arginine ADP-ribosyltransferase [Oryctolagus cuniculus]	5.1
802	M60522	Rat nerve growth factor-inducible protein (VGF) gene, complete cds.	0.021	4103934	(AF030050) replication factor C [Rattus norvegicus]	3.1
803	AF045654	Gallus gallus neuregulin beta-1a mRNA, complete cds	0.021	2746829	(AF040647) No definition line found [Caenorhabditis elegans]	3.0
804	M69023	Human globin gene.	0.021	3880259	(Z82056) T26H5.8 [Caenorhabditis elegans] >gi 3880787 gnl PID e1350288 (AL032620) T26H5.8	2.4
805	Z65960	H.sapiens CpG DNA, clone 69d2, reverse read cpg69d2.rt1b.	0.021	1707245	(U80845) similar to family 1 of G-protein coupled receptors [Caenorhabditis elegans]	0.79
806	X97073	A.oligospora gene encoding lectin	0.021	116949	CORE ANTIGEN >gi 73601 pir NKVLC2 core antigen - woodchuck hepatitis virus 2 >gi 336135	0.47
807	X56491	D. melanogaster mRNA for gene containing opa repetitive element	0.021	2842750	HOMEBOX PROTEIN DLX-7 >gi 1620520	0.16
808	L78760	Homo sapiens (subclone 1_f6 from P1 H31) DNA sequence	0.021	113671	!!!! ALU CLASS F WARNING ENTRY !!!!	0.15
809	AB007864	Homo sapiens KIAA0404 mRNA, partial cds	0.021	118144	CYSTEINE SYNTHASE A (O-ACETYL SERINE SULFHYDRYLASE A) (O-ACETYL SERINE (THIOL)-LYASE A) (CSASE A) >gi 68323 pir SYEBAC cysteine synthase (EC 4.2.99.8) A - Salmonella typhimurium >gi 153935 (M21450) cysK protein [Salmonella typhimurium]	0.12
810	AL021932	Mycobacterium tuberculosis H37Rv complete genome; segment 22/162	0.021	2909514	(AL021932) hypothetical protein Rv0439c	7e-10

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
811	U89991	Hypocrea jecorina mannose-1-phosphate guanylyltransferase (MPG1) mRNA, complete cds	0.021	3581924	(AL031538) mannose-1-phosphate guanylyltransferase [Schizosaccharomyces pombe]	6e-20
812	X00641	Sugar beet mitochondrial minicircle pO sequence	0.020	<NONE>	<NONE>	<NONE>
813	Z50097	D.melanogaster mRNA for hdc protein.	0.020	<NONE>	<NONE>	<NONE>
814	AF044866	Phoebe sennae large subunit ribosomal RNA gene, partial sequence; tRNA-Val gene, complete sequence; and small subunit ribosomal RNA gene, partial sequence, mitochondrial genes for mitochondrial RNAs	0.020	<NONE>	<NONE>	<NONE>
815	AF074386	Sambucus nigra hevein-like protein mRNA, complete cds	0.020	<NONE>	<NONE>	<NONE>
816	AF027174	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-B) mRNA, complete cds	0.020	<NONE>	<NONE>	<NONE>
817	AE001405	Plasmodium falciparum chromosome 2, section 42 of 73 of the complete sequence	0.020	2196776	(AF003342) bunched gene product [Drosophila melanogaster]	8.4
818	AF074387	Sambucus nigra hevein-like protein mRNA, complete cds	0.020	627071	histidine-rich protein - Plasmodium lophurae	2.8

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
819	Y13304	Hylobates hoolock mitochondrial DNA for cytb gene, Horace	0.020	285580	(D10043) ORF [Acetobacter pasteurianus] (U80439) coded for by C. elegans cDNA yk7c8.5; coded for by C. elegans cDNA yk133b3.5; coded for by C. elegans cDNA yk65a4.5; coded for by C. elegans cDNA yk7c8.3; coded for by C. elegans cDNA CEESQ66F; coded for by C. elegans cDNA yk65a4.3;...	2.1
820	Z66539	H.sapiens creatine transporter gene	0.020	1703594	EARLY GROWTH RESPONSE PROTEIN 1 fish >gi 531456 (U12895) egr1 [Danio rerio] rerio]	0.98
821	AF053622	Homo sapiens alpha 1,2-mannosidase IB gene, exon 9	0.020	1352361	HYPOTHETICAL 38.1 KD PROTEIN IN SBCB-HISL INTERGENIC REGION >gi 405956 (U00009) ORF_ID:o349#4; similar to [SwissProt Accession Number P33015] [Escherichia coli] >gi 1736693 gnl PID d1016570 Number.P33015] [Escherichia coli] >gi 1788323 (AE000292) putative transport system permease protein [Escherichia coli]	0.72
822	M20555	Human MHC class II HLA-DRw53-beta (DR4,w4) gene, exons 2,3,4,5,6.	0.020	465569	COENZYME PQQ SYNTHESIS PROTEIN F synthesis F - Pseudomonas fluorescens >gi 929802	0.43
823	M20555	Human MHC class II HLA-DRw53-beta (DR4,w4) gene, exons 2,3,4,5,6.	0.020	1709751		0.42

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
824	AJ005015	Homo sapiens mRNA for putative SMC-like protein, partial	0.020	267449	PROTEIN ZK637.2 IN CHROMOSOME III >gi 102507 pir S15787 hypothetical protein 1 (cosmid ZK637) - Caenorhabditis elegans Genefinder; cDNA EST yk217b5.3 comes from this gene; cDNA EST yk217b5.5 comes from this gene; cDNA EST yk340g12.3 comes from this gene; cDNA EST yk340g12.5 comes from this gene; cDNA EST yk428c5.5 co...	1e-12
825	AF034099	Laccaria bicolor glyoxal malate synthase protein mRNA, complete cds	0.020	1109847	(U41538) No definition line found [Caenorhabditis elegans]	1e-22
826	AF100694	Mus musculus Pontin52 mRNA, complete cds	0.019	132836	60S RIBOSOMAL PROTEIN L28 protein L28 [Rattus norvegicus]	5.7
827	AF093268	Rattus norvegicus homer-1c mRNA, complete cds	0.019	2633401	(Z99109) similar to DNA exonuclease	4.5
828	AF100694	Mus musculus Pontin52 mRNA, complete cds	0.019	2492604	MULTIDRUG RESISTANCE PROTEIN CDR2 albicans]	4.4
829	U67538	Methanococcus jannaschii section 80 of 150 of the complete genome	0.019	1723566	PUTATIVE GLUCOSYLTRANSFERASE C17C9.07 >gi 1314159 gnl PID e241760 (Z73099) SPAC17C9.07, putative glucosyl transferase len: 501, similar to SW:ALG8_YEAST P40351 glucosyltransferase ALG8 pombe]	2.7
830	U56088	Human periodic tryptophan protein 2 (PWP2) gene, exons 3 to 14	0.019	2144804	collagen alpha 1(II) chain - bovine	0.040
831	U76524	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	0.018	1916976	(U91682) vitelline membrane protein homolog [Aedes aegypti]	7.2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
832	AF026258	Onobrychis viciifolia chalcone synthase (CHS) mRNA, complete cds	0.018	763076	(Z48799) ZP3 [Cyprinus carpio] >gi 777724 (L41637) egg membrane protein [Cyprinus carpio]	5.2
833	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	0.009	3955011	(AJ005438) beta adrenoreceptor B	0.60
834	X71603	C.jejuni VST DNA >:: emb A39603 A39603 Sequence 2 from Patent WO9417205 >:: gb I76090 I76090 Sequence 2 from patent US 5691138	0.008	<NONE>	<NONE>	<NONE>
835	AF093268	Rattus norvegicus homer-1c mRNA, complete cds	0.008	138116	HEAD FIBER PROTEIN (LATE PROTEIN GP8.5) >gi 75846 pir WMBP8H gene 8.5 protein - phage PZA >gi 216057 (M11813) head fiber protein	8.1
836	X91751	Bovine herpesvirus type 1 UL7 gene	0.008	1711436	SUPEROXIDE DISMUTASE (FE) 1.15.1.1 (Fe) - Pseudomonas aeruginosa >gi 409767	5.9
837	M95594	Arabidopsis thaliana l-aminocyclopropane-1-carboxylate synthase (ACS2) gene, complete cds.	0.008	683698	(Z48229) orf1 gene product [Saccharomyces cerevisiae]	1e-06
838	U67465	Methanococcus jannaschii section 7 of 150 of the complete genome	0.008	3874664	(Z68493) predicted using Genefinder	1e-07
839	X72388	B.taurus mRNA for filensin	0.008	100174	l-aminocyclopropane-1-carboxylate synthase	7e-09
840	U22398	Human Cdk-inhibitor p57KIP2 (KIP2) mRNA, complete cds.	0.008	2228750	(U93868) RNA polymerase III subunit [Homo sapiens]	2e-18
841	L42546	Xenopus laevis LIM class homeodomain protein	0.007	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Homo sapiens				
842	AF041428	ribosomal protein s4 X isoform gene, complete cds	0.007	<NONE>	<NONE>	<NONE>
843	AF000227	Secale cereale omega secalin gene, complete cds	0.007	<NONE>	<NONE>	<NONE>
844	D86254	Human MHC (HLA) DRB intron 1 DNA, partial sequence	0.007	<NONE>	<NONE>	<NONE>
845	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	0.007	<NONE>	<NONE>	<NONE>
846	Y07738	M.musculus gene for vimentin	0.007	<NONE>	<NONE>	<NONE>
847	AJ005813	Arabidopsis thaliana mRNA for neoxanthin cleavage enzyme	0.007	<NONE>	<NONE>	<NONE>
848	AF055119	Homo sapiens alpha-tectorin (TECTA) gene, exon 6	0.007	<NONE>	<NONE>	<NONE>
849	M61195	Zucchini 1-aminocyclopropane-1-carboxylate synthase	0.007	<NONE>	<NONE>	<NONE>
850	Y11050	Homo sapiens DSG3 gene, partial intron and partial exon 6, 140 bp	0.007	<NONE>	<NONE>	<NONE>
851	X61204	M.voltae vhuD, vhuG, vhuA, vhuU & vhuB genes	0.007	<NONE>	<NONE>	<NONE>
852	AB012105	Brassica rapa mRNA for SLG45, complete cds	0.007	<NONE>	<NONE>	<NONE>
853	S43882	telomere: {minichromosome, repeats} [Trypanosoma brucei, Genomic, 1170 nt]	0.007	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
854	L32674	Geomydoecus nadleri mitochondrial cytochrome oxidase I gene, partial cds.	0.007	<NONE>	<NONE>	<NONE>
855	U58732	Caenorhabditis elegans cosmid F48D6.	0.007	<NONE>	<NONE>	<NONE>
856	U76524	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	0.007	<NONE>	<NONE>	<NONE>
857	Z35284	H.sapiens mRNA for MDR3 P-glycoprotein	0.007	1730696	HYPOTHETICAL 121.1 KD PROTEIN IN BIO3-HXT17 INTERGENIC REGION PRECURSOR YNR067c - yeast (Saccharomyces cerevisiae)	9.5
858	X15217	Human sno oncogene mRNA for snoA protein, ski-related	0.007	902455	(U24203) membrane protein [Escherichia coli]	8.8
859	AF027173	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-A) mRNA, complete cds	0.007	1684636	(Y09454) ORF3 [Lactobacillus casei bacteriophage A2]	8.3
860	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	0.007	3878803	(Z48795) R05H5.7 [Caenorhabditis elegans]	8.3
861	S76317	119=180-200 kDa membrane protein scavenger receptor homolog (clone 18, intron and flanking exons 14 and 15) (sheep, lymph node, lymphocytes, Genomic, 308 nt, segment 2 of 2)	0.007	294747	(L08174) ORF2 [Romanomermis culicivorax]	7.4

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
862	D88084	Pedicularis verticillata chloroplast DNA, intergenic region between trnT(UGU) and trnL(UAA)5'exon	0.007	2555187	(AF026789) vitellogenin [Pimpla nipponica]	6.9
863	X58869	Chicken mRNA for aldehyde dehydrogenase	0.007	115978	CD30L RECEPTOR PRECURSOR (LYMPHOCYTE ACTIVATION ANTIGEN (250075) 110mc ncr domain,	6.5
864	D87120	Homo sapiens mRNA for GS3786, complete cds	0.007	3879589	cDNA EST EMBL:D35637 comes from this gene; cDNA EST yk322a3.5 comes from this gene; cDNA EST yk397b2.5 comes from this gene; cDNA EST yk348b11.5 comes from this gene; cDNA EST yk397b2.3 comes fr...	5.1
865	X68793	H.sapiens gene for antithrombin III	0.007	2358285	>gi 3880965 gnl PID e 1350578 comes from this gene; cDNA EST yk322a3.5 comes from this gene; cDNA EST yk397b2.5 comes from this gene; cDNA EST yk348b11.5 comes from this gene; cDNA EST yk397b2.3 comes ...	3.8
866	AJ001596	Danio rerio mRNA for opioid receptor homologue	0.007	2507509	(AF010403) ALR [Homo sapiens]	1.9
867	AF061195	Streptomyces albus valine dehydrogenase (Vdh) gene. complete cds	0.007	2088768	HYPOTHETICAL 29.8 KD PROTEIN IN HOLB-PTSG INTERGENIC REGION >gi 1787342 (AE000210) orf, hypothetical protein [Escherichia coli] protein in holB 3'region . [Escherichia coli]	1.9
868	AJ005813	Arabidopsis thaliana mRNA for neoxanthin cleavage enzyme	0.007	1710105	(AF003145) B0414.8 gene product [Caenorhabditis elegans]	1.7

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Zebrafish retinoic acid receptor alpha 2.A	0.007	2239219	(Z97210) hypothetical protein	0.77
869	L03398	Human mRNA for KIAA0150 gene, partial cds	0.007	19917	(Z14014) Pistil extensin like protein, partial CDS only	0.61
870	D63484	Maize glyceraldehyde 3-phosphate dehydrogenase, 3' end.	0.007	543068	mucin, tracheobronchial - dog >gi 402558	0.45
871	M31483	Lycopersicon esculentum cytosolic class II small heat shock protein HCT2 (HSP17.4) mRNA, complete cds	0.007	2494941	ALPHA-2B ADRENERGIC RECEPTOR adrenoceptor [Cavia porcellus] >gi 1587159 prf 2206293B adrenoceptor alpha2B [Cavia porcellus]	0.42
872	AF090115	Helianthus tuberosus lectin 1 mRNA, complete cds	0.007	1110587	(S79410) nuclear localization signals Peptide, 140 aa [Mus sp.]	0.26
873	AF064029	H.sapiens PAL2A gene	0.007	1706176	CUTINASE TRANSCRIPTION FACTOR 1 ALPHA >gi 1262912 (U51671) cutinase transcription factor 1 [Fusarium solani f. sp. pisi]	0.21
874	X88931	zRAR alpha =retinoic acid receptor alpha [zebrafish, embryos, mRNA, 1773 nt]	0.007	2239219	(Z97210) hypothetical protein	0.11
875	S74155	Petromyzon marinus plasma albumin mRNA, complete cds.	0.007	730888	OCTAPEPTIDE-REPEAT PROTEIN T2	0.011
876	M74193	Saccharomyces cerevisiae Spp41p (SPP41) gene, complete cds.	0.007	3820885	(AL033126) 65G3.k [Drosophila melanogaster]	0.001
877	U03673	Homo sapiens mRNA for Laminin-5 beta3 chain, complete cds	0.007	1235974	(X96713) collagen [Globodera pallida]	3e-06
878	D37766					

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		<i>Caenorhabditis</i>				
879	AF022388	<i>elegans</i> putative transcription factor MAB-3 (mab-3) gene, complete cds	0.007	3747107	(AF095741) unknown [<i>Rattus norvegicus</i>]	5e-09
880	U89984	<i>Acanthamoeba castellanii</i> transformation-sensitive protein homolog mRNA, complete cds	0.007	1890281	(U89984) transformation-sensitive protein homolog (U89984) similar to 1.1 kb rat rabGAP domains; cDNA EST EMBL:D34945 comes from this gene; cDNA EST EMBL:D27313 comes from this gene; cDNA EST EMBL:D34829 comes from this gene; cDNA EST EMBL:D27312 comes from this gene; cDNA ... Probable rabGAP domains; cDNA EST EMBL:D34945 comes from this gene; cDNA EST EMBL:D27313 comes from this gene; cDNA EST EMBL:D34829 comes from this gene; cDNA EST EMBL:D27312 comes from this gene; cDNA ...	2e-09
881	AB020689	Homo sapiens mRNA for KIAA0882 protein, partial cds	0.007	3880809		1e-23
882	AF100694	<i>Mus musculus</i> Pontin52 mRNA, complete cds	0.006	<NONE>	<NONE>	<NONE>
883	AF027173	<i>Arabidopsis thaliana</i> cellulose synthase catalytic subunit (Ath-A) mRNA, complete cds	0.006	<NONE>	<NONE>	<NONE>
884	U76524	<i>Sambucus nigra</i> ribosome inactivating protein precursor mRNA, complete cds	0.006	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
885	U76524	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	0.006	<NONE>	<NONE>	<NONE>
886	AJ005813	Arabidopsis thaliana mRNA for neoxanthin cleavage enzyme	0.006	<NONE>	<NONE>	<NONE>
887	AB012106	Brassica rapa mRNA for SRK45, complete cds	0.006	<NONE>	<NONE>	<NONE>
888	M80529	Rattus norvegicus ceruloplasmin gene, exon 1 and 5' flank	0.006	<NONE>	<NONE>	<NONE>
889	AF027173	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-A) mRNA, complete cds	0.006	99408	hypothetical protein 6 - Chlamydomonas reinhardtii transposon >gi 1360717 gnl PID e33461 reinhardtii]	9.6
890	U76523	Sambucus nigra lectin precursor mRNA, complete cds	0.006	4039024	(AF039110) polyprotein [Rubella virus]	9.3
891	AF093268	Rattus norvegicus homer-1c mRNA, complete cds	0.006	160533	(M94428) merozoite surface antigen 1 [Plasmodium vivax]	7.5
892	AB012106	Brassica rapa mRNA for SRK45, complete cds	0.006	4019458	(AF093984) envelope glycoprotein [Human immunodeficiency virus type 1]	7.0
893	AJ005813	Arabidopsis thaliana mRNA for neoxanthin cleavage enzyme	0.006	1916976	(U91682) vitelline membrane protein homolog [Aedes aegypti]	6.8
894	AF093268	Rattus norvegicus homer-1c mRNA, complete cds	0.006	102059	promastigote surface antigen-2 (clone 4.6) - Leishmania major (fragment) >gi 9583 (X57135) surface antigen P2 [Leishmania major]	2.4
895	AF093268	Rattus norvegicus homer-1c mRNA, complete cds	0.006	3171241	(AF067204) transcription factor BF-1 [Danio rerio]	1.0
896	X99384	M.musculus mRNA for paladin gene	0.003	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
897	AF027174	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-B) mRNA, complete cds	0.003	<NONE>	<NONE>	<NONE>
898	AE001148	Borrelia burgdorferi (section 34 of 70) of the complete genome	0.003	4160388	(AJ011856) ORF Q0255 [Saccharomyces cerevisiae]	7.6
899	AF027173	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-A) mRNA, complete cds	0.003	1709213	NUCLEAR ENVELOPE PORE MEMBRANE PROTEIN POM 121 (PORE MEMBRANE PROTEIN OF 121 KD) (P145)	1.5
900	U72396	Lycopersicon esculentum class II small heat shock protein Le-HSP17.6 mRNA, complete cds	0.002	<NONE>	<NONE>	<NONE>
901	AF100694	Mus musculus Pontin52 mRNA, complete cds	0.002	<NONE>	<NONE>	<NONE>
902	AF104631	Chlamydomonas reinhardtii light harvesting complex II protein precursor (Lhcb3) mRNA, complete cds	0.002	<NONE>	<NONE>	<NONE>
903	AF100694	Mus musculus Pontin52 mRNA, complete cds	0.002	<NONE>	<NONE>	<NONE>
904	AB012106	Brassica rapa mRNA for SRK45, complete cds	0.002	<NONE>	<NONE>	<NONE>
905	M21339	Human non-histone chromosomal protein HMG-14 gene, complete cds.	0.002	<NONE>	<NONE>	<NONE>
906	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	0.002	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Human h-lys gene for				
907	X57103	lysozyme (upstream region)	0.002	<NONE>	<NONE>	<NONE>
908	AF074386	Sambucus nigra hevein-like protein mRNA, complete cds	0.002	<NONE>	<NONE>	<NONE>
909	U01066	Human CD4 promoter, partial sequence.	0.002	<NONE>	<NONE>	<NONE>
910	L28094	Barley mRNA sequence.	0.002	<NONE>	<NONE>	<NONE>
911	AD000833	Homo sapiens DNA from chromosome 19-cosmid f19399 (~17 kb EcoRI restriction fragment)	0.002	<NONE>	<NONE>	<NONE>
912	AJ011701	Homo sapiens TRHR gene promoter and exons 1-2, partial	0.002	<NONE>	<NONE>	<NONE>
913	AF100694	Mus musculus Pontin52 mRNA, complete cds	0.002	<NONE>	<NONE>	<NONE>
914	AF037062	Homo sapiens retinol dehydrogenase gene, complete cds	0.002	<NONE>	<NONE>	<NONE>
915	AF093268	Rattus norvegicus homer-1c mRNA, complete cds	0.002	<NONE>	<NONE>	<NONE>
916	U67608	Methanococcus jannaschii section 150 of 150 of the complete genome	0.002	<NONE>	<NONE>	<NONE>
917	AF027173	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-A) mRNA, complete cds	0.002	<NONE>	<NONE>	<NONE>
918	Z46736	H.sapiens DNA for repeat region (ABM-C82)	0.002	<NONE>	<NONE>	<NONE>
919	AB012106	Brassica rapa mRNA for SRK45, complete cds	0.002	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
920	Z85983	X.laevis mRNA for NOVA protein	0.002	<NONE>	<NONE>	<NONE>
921	AF027173	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-A) mRNA, complete cds	0.002	<NONE>	<NONE>	<NONE>
922	S61977	medium-chain acyl-CoA dehydrogenase (exon 10, intron 10) [human, Genomic, 1407 nt]	0.002	<NONE>	<NONE>	<NONE>
923	AJ005813	Arabidopsis thaliana mRNA for neoxanthin cleavage enzyme	0.002	<NONE>	<NONE>	<NONE>
924	AB012105	Brassica rapa mRNA for SLG45, complete cds	0.002	<NONE>	<NONE>	<NONE>
925	AB012106	Brassica rapa mRNA for SRK45, complete cds	0.002	<NONE>	<NONE>	<NONE>
926	AF027173	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-A) mRNA, complete cds	0.002	<NONE>	<NONE>	<NONE>
927	X51646	H.sapiens DNA for dopamine D2 receptor gene	0.002	3329125	(AE001337) Yop C/Gen Secretion Protein D [Chlamydia trachomatis]	9.5
928	AF100694	Mus musculus Pontin52 mRNA, complete cds	0.002	465762	HYPOTHETICAL 112.1 KD PROTEIN C06G4.1 IN CHROMOSOME III >gi 630524 pir S44748 C06G4.1 protein - Caenorhabditis elegans >gi 409292 (L25598) homology with vigilin; coded for by C. elegans cDNA GenBank:M88954 (CEL12C9); putative [Caenorhabditis	8.9
929	U48478	Human skeletal muscle ryanodine receptor gene	0.002	2137221	co-repressor protein - mouse >gi 642619	6.9

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Mus musculus				
930	AF100694	Pontin52 mRNA, complete cds	0.002	806536	(Z22520) membrane protein [Bacillus acidopullulyticus]	6.3
931	AF100694	Mus musculus Pontin52 mRNA, complete cds	0.002	3881055	(AL023844) Y48A6B.1 [Caenorhabditis elegans]	5.8
932	AF090115	Lycopersicon esculentum cytosolic class II small heat shock protein HCT2 (HSP17.4) mRNA, complete cds	0.002	3878330	(Z81097) K07A1.4 [Caenorhabditis elegans]	4.8
933	AF093268	Rattus norvegicus homer-1c mRNA, complete cds	0.002	137640	REPLICATION PROTEIN E1 papillomavirus	4.0
934	AF019660	Mus musculus nuclear orphan receptor RORgamma	0.002	1330365	(U58757) similar to nucleotide pyrophosphatases	3.9
935	AF100694	Mus musculus Pontin52 mRNA, complete cds	0.002	1785972	(U46951) ORF5; Method: conceptual translation supplied by author	3.7
936	V00508	Human gene for epsilon-globin.	0.002	1333804	(X56082) protease [Ruminococcus flavefaciens]	3.5
937	AB012105	Brassica rapa mRNA for SLG45, complete cds	0.002	4153876	(AC005531) similar to mouse homeodomain-interacting protein kinase 2; similar to AF077659 (PID:g3702958)	3.0
938	AJ005813	Arabidopsis thaliana mRNA for neoxanthin cleavage enzyme	0.002	1070461	ornithine carbamoyltransferase (EC 2.1.3.3) - yeast (Saccharomyces cerevisiae) >gi 929866 (X83502) pid:e130025 [Saccharomyces cerevisiae] >gi 1008256	2.8
939	S41458	rod cGMP phosphodiesterase beta-subunit [human, mRNA, 3231 nt]	0.002	3450883	(AF083334) fibroin [Antheraea pernyi]	1.6

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Drosophila melanogaster Gart locus with genes for GARS=phosphoribosylamineglycine ligase, AIRS=phosphoribosylformylglycinamide cyclo-ligase, GART=glycinamide ribotide transformylase > :: gb J02527 DROGART D.melanogaster Gart gene encoding two polypeptides with GAR synthase, AIR synthase, and GAR transformylase enzyme activities and a pupal cuticle gene nested within intron A of the Gart gene.				
940	X06286		0.002	2662054	(AB004651) isocitrate lyase	1.5
941	AF015812	Homo sapiens RNA helicase p68 (HUMP68) gene, complete cds	0.002	3641659	(AB008374) alpha 3 type I collagen	1.1
942	X78925	H.sapiens HZF2 mRNA for zinc finger protein	0.002	141624	ZINC FINGER PROTEIN ZFP-37 (MALE GERM CELL SPECIFIC ZINC FINGER PROTEIN)	1.0
943	AF074386	Sambucus nigra hevein-like protein mRNA, complete cds	0.002	3879997	(Z49071) weak similarity with mu-type opioid receptor (Swiss Prot accession number (P33535)	1.0
944	Z69639	Human DNA sequence from cosmid L241B9, Huntington's Disease Region, chromosome 4p16.3 contains polymorphic VNTR pYNZ32.	0.002	3523162	(AF076292) TGF-beta/activin signal transducer FAST-1p	0.81

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
945	AF074387	Sambucus nigra hevein-like protein mRNA, complete cds	0.002	2984161	(AE000761) hypothetical protein [Aquifex aeolicus]	0.80
946	AF093268	Rattus norvegicus homer-1c mRNA, complete cds	0.002	101830	hypothetical protein B - chestnut blight fungus	0.72
947	AF017307	Homo sapiens Ets-related transcription factor (ERT) mRNA, complete cds	0.002	200531	(M18071) prion protein [Mus musculus]	0.72
948	U11383	Drosophila melanogaster Ovo-1028aa (ovo) mRNA, complete cds	0.002	2465207	(AF016045) OVO-like 1 binding protein [Homo sapiens]	0.35
949	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	0.002	3834294	(U80846) No definition line found [Caenorhabditis elegans]	0.29
950	AF086315	Homo sapiens full length insert cDNA clone ZD52F10	0.002	545067	(S68356) action potential broadening potassium channel=Shab [Aplysia, bag cell neurons, head ganglia. Peptide, 905 aa] [Aplysia] >gi 743110 prf 2011375A K channel [Aplysia californica]	0.15
951	X53096	S.aureus genes encoding Sau96I DNA methyltransferase and Sau96I restriction endonuclease	0.002	2529575	(AF018164) kinesin-like protein 3C [Homo sapiens]	0.11
952	AB012105	Brassica rapa mRNA for SLG45, complete cds	0.002	729918	LA PROTEIN HOMOLOG (LA RIBONUCLEOPROTEIN) (LA AUTOANTIGEN HOMOLOG)	0.092
953	X73973	G.gallus RAR-gamma2 mRNA for retinoic acid receptor	0.002	586122	TRICHOHYALIN >gi 423321 pir A40691 trichohyalin - sheep >gi 295941 (Z18361) trichohyalin	0.073
954	S41458	rod cGMP phosphodiesterase beta-subunit [human, mRNA, 3231 nt]	0.002	1017427	(X90569) elastic titin [Homo sapiens]	0.013

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		D.melanogaster			(U88169) similar to	
955	M35887	defective chorion-1 fc125 (dec-1) gene, complete cds.	0.002	1825606	molybdopterin biosynthesis MOEB proteins [Caenorhabditis elegans]	0.008
956	AF034099	Laccaria bicolor glyoxal malate synthase protein mRNA, complete cds	0.002	1825593	(U88167) D2092.2 gene product [Caenorhabditis elegans]	1e-06
957	AF033929	Bactrocera dorsalis strain Tahiti mitochondrial D-loop region, complete sequence	9e-04	<NONE>	<NONE>	<NONE>
958	AB012106	Brassica rapa mRNA for SRK45, complete cds	8e-04	<NONE>	<NONE>	<NONE>
959	AF029062	Homo sapiens DEAD- box protein (BAT1) gene, partial cds	8e-04	<NONE>	<NONE>	<NONE>
960	U70671	Human ataxin-2 related protein mRNA, partial cds	8e-04	<NONE>	<NONE>	<NONE>
961	AF051709	Dendrocopos leucopterus clone 2 microsatellite HrU2 repeat region	8e-04	<NONE>	<NONE>	<NONE>
962	X14077	Pea phy gene for phytochrome apoprotein	8e-04	<NONE>	<NONE>	<NONE>
963	AC004497	Homo sapiens chromosome 21, P1 clone LBNL#6	8e-04	457146	(L27838) rhostry protein [Plasmodium yoelii]	9.6
964	AF077344	Homo sapiens cartilage-derived C- type lectin	8e-04	3702123	(AJ011707) TraD protein [Escherichia coli]	8.5
965	X85117	H.sapiens epb72 gene exons 2,3,4,5,6,7	8e-04	2570059	(AJ004687) N-4 cytosine- specific methyltransferase [Neisseria gonorrhoeae]	6.8
966	AF100694	Mus musculus Pontin52 mRNA, complete cds	8e-04	1345859	COPPER TRANSPORT PROTEIN CTR1 transport protein - yeast (Saccharomyces cerevisiae) gene product [Saccharomyces cerevisiae]	6.7

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Homo sapiens				
967	AF031403	MLL/AF4 translocation breakpoint t(4;11)(q21;q23)	8e-04	2498926	SMALL PROTEIN B HOMOLOG A43259, from E. hirae [Mycoplasma pneumoniae]	6.6
968	L29252	Human (clone D13-2) L-iditol-2 dehydrogenase gene, exon 4, exon 5, exon 6 and exon 7.	8e-04	1488070	(U63997) putative transposase [Enterococcus faecium]	5.2
969	X16995	Mouse N10 gene for a nuclear hormonal binding receptor	8e-04	1493833	(U47323) stromal cell protein [Mus musculus]	3.2
970	M99412	Human interleukin-8 receptor (IL8RB) gene, complete cds	8e-04	1346101	4-AMINOBUTYRATE AMINOTRANSFERASE TRANSAMINASE) (GABA AMINOTRANSFERASE) homolog - smut fungus (Ustilago maydis) >gi 881562 Emericella nidulans gamma-amino-n-butyrate transaminase Swiss-Prot Accession Number P14010 [Ustilago maydis]	0.83
971	U37452	Human Down Syndrome region of chromosome 21 genomic sequence, clone A31D6-1C5.	8e-04	4164069	(AF111093) latrophilin 3 splice variant bbah [Bos taurus]	0.26
972	AF100694	Mus musculus Pontin52 mRNA, complete cds	8e-04	1352877	HYPOTHETICAL 13.0 KD PROTEIN IN RAD26-GEF1 INTERGENIC REGION >gi 1077881 pir S57057 probable membrane protein YJR038c - yeast (Saccharomyces cerevisiae) >gi 1015688 (Z49538) ORF YJR038c putative [Saccharomyces cerevisiae]	0.23
973	AF093268	Rattus norvegicus homer-1c mRNA, complete cds	8e-04	1788557	(AE000312) orf, hypothetical protein [Escherichia coli]	0.19

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
974	X83872	H.vulgaris mRNA for cAMP response element binding protein	8e-04	1175386	HYPOTHETICAL 37.7 KD PROTEIN C18B11.06 IN CHROMOSOME I >gi 2130289 pir S58305 hypothetical protein SPAC18B11.06 - fission yeast hypothetical protein [Schizosaccharomyces pombe]	0.005
975	M32514	Rat simple sequence DNA, clone 5.	8e-04	2394492	(AF024502) No definition line found [Caenorhabditis elegans]	0.002
976	AF074386	Sambucus nigra hevein-like protein mRNA, complete cds	8e-04	2981631	(AB012223) ORF2 [Canis familiaris]	0.001
977	X89211	H.sapiens DNA for endogenous retroviral like element	8e-04	2065210	(Y12713) Pro-Pol-dUTPase polyprotein	3e-04
978	U14391	Human myosin-IC mRNA, complete cds.	8e-04	3142302	(AC002411) Strong similarity to myosin heavy chain gb Z34293 from A. thaliana. [Arabidopsis thaliana]	4e-16
979	L13612	Drosophila melanogaster dead-box protein D.melanogaster DEAD-box gene, complete CDS	8e-04	3776027	(AJ010475) RNA helicase [Arabidopsis thaliana]	9e-24
980	AF074386	Sambucus nigra hevein-like protein mRNA, complete cds	7e-04	<NONE>	<NONE>	<NONE>
981	AF100694	Mus musculus Pontin52 mRNA, complete cds	7e-04	<NONE>	<NONE>	<NONE>
982	AF093268	Rattus norvegicus homer-1c mRNA, complete cds	7e-04	<NONE>	<NONE>	<NONE>
983	Z73987	Human DNA sequence from cosmid N120B6 on chromosome 22 Contains ESTs, complete sequence [Homo sapiens]	7e-04	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Brassica rapa mRNA				
984	AB012106	for SRK45, complete cds	7e-04	<NONE>	<NONE>	<NONE>
985	AF093268	Rattus norvegicus homer-1c mRNA, complete cds	7e-04	<NONE>	<NONE>	<NONE>
986	AF027174	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-B) mRNA, complete cds	7e-04	<NONE>	<NONE>	<NONE>
987	AF100694	Mus musculus Pontin52 mRNA, complete cds	7e-04	<NONE>	<NONE>	<NONE>
988	AJ005813	Arabidopsis thaliana mRNA for neoxanthin cleavage enzyme	7e-04	<NONE>	<NONE>	<NONE>
989	AF064029	Helianthus tuberosus lectin 1 mRNA, complete cds	7e-04	<NONE>	<NONE>	<NONE>
990	AF027174	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-B) mRNA, complete cds	7e-04	<NONE>	<NONE>	<NONE>
991	AF027173	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-A) mRNA, complete cds	7e-04	<NONE>	<NONE>	<NONE>
992	AF064029	Helianthus tuberosus lectin 1 mRNA, complete cds	7e-04	<NONE>	<NONE>	<NONE>
993	AF100694	Mus musculus Pontin52 mRNA, complete cds	7e-04	<NONE>	<NONE>	<NONE>
994	U76524	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	7e-04	3327230	(AB014608) KIAA0708 protein [Homo sapiens]	9.5

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
995	U76524	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	7e-04	3327230	(AB014608) KIAA0708 protein [Homo sapiens]	9.3
996	AF074387	Sambucus nigra hevein-like protein mRNA, complete cds	7e-04	3876455	(Z93380) predicted using Genefinder; similar to 7tm receptor protein [Caenorhabditis elegans]	7.1
997	U76524	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	7e-04	2128771	hypothetical protein MJ1293 - Methanococcus jannaschii >gi 1591931 (U67570) M. jannaschii predicted coding region MJ1293 [Methanococcus jannaschii]	6.2
998	U09412	Human zinc finger protein ZNF134 mRNA, complete cds	7e-04	1083336	glutathione transferase (EC 2.5.1.18) piA - mouse	5.4
999	AF027173	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-A) mRNA, complete cds	7e-04	473515	(M17619) NADH dehydrogenase subunit ND4 [Asterina pectinifera]	3.7
1000	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	7e-04	1724097	(U79772) female sex protein [Mercurialis annua]	3.3
1001	AF100694	Mus musculus Pontin52 mRNA, complete cds	7e-04	1197103	(D49747) core, env, and part of E2/NS1	3.2
1002	X16995	Mouse N10 gene for a nuclear hormonal binding receptor	7e-04	345372	unc-5 protein, long form - Caenorhabditis elegans >gi 258529 bbs 118648 (S47168) UNC-5=immunoglobulin and thrombospondin type 1 transmembrane protein {alternatively spliced} aa [Caenorhabditis elegans] >gi 2662596 (AF036698) C. elegans UNC-5 (NID:g25852)	2.7

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1003	U76524	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	7e-04	4204220	(AB022866) mobilization protein	2.5
1004	AF093268	Rattus norvegicus homer-1c mRNA, complete cds	7e-04	3201550	(Y17116) fibrinogen-binding protein	2.4
1005	AF074386	Sambucus nigra hevein-like protein mRNA, complete cds	7e-04	1174264	(U45966) polyprotein [Hepatitis G virus]	0.73
1006	AF027173	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-A) mRNA, complete cds	7e-04	135308	TRANSCRIPTION FACTOR JUN-D	0.065
1007	X98745	H.sapiens EWS gene, intron 6, polymorphism	7e-04	728836	!!!! ALU SUBFAMILY SP WARNING ENTRY	0.001
1008	AJ005813	Arabidopsis thaliana mRNA for neoxanthin cleavage enzyme	7e-04	1633564	(U47924) C8 [Homo sapiens]	9e-09
1009	AF074386	Sambucus nigra hevein-like protein mRNA, complete cds	6e-04	284171	Ig epsilon chain C region form 3 - human	1.3
1010	AB012106	Brassica rapa mRNA for SRK45, complete cds	6e-04	3845262	(AE001414) BRAHMA ortholog (DNA helicase superfamily II)	0.25
1011	AL034404	Human DNA sequence from clone 417C12 on chromosome Xp22.1122.2, complete sequence [Homo sapiens]	3e-04	<NONE>	<NONE>	<NONE>
1012	M99701	Homo sapiens (pp21) mRNA, complete cds.	3e-04	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1013	U00227	Ovis aries Merino breed DR beta-chain antigen binding domain, MHC class II DRB (Ovar-DRB24) gene, partial cds.	3e-04	<NONE>	<NONE>	<NONE>
1014	AF074387	Sambucus nigra hevein-like protein mRNA, complete cds	3e-04	<NONE>	<NONE>	<NONE>
1015	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	3e-04	999418	(L19655) ORF [Tomato ringspot virus]	8.3
1016	AB012106	Brassica rapa mRNA for SRK45, complete cds	3e-04	2367460	(AF011415) putative pheromone receptor [Mus musculus]	7.0
1017	AJ010737	Mus musculus DNA for microsatellite 3kb upstream lbp gene	3e-04	4106549	(AF104411) neuronal-specific septin 3 [Mus musculus]	5.5
1018	AF053137	Homo sapiens histone deacetylase 3 gene, exons 4, 5, 6, 7, 8, 9, and 10	3e-04	416702	NADH-DEPENDENT FLAVIN OXIDOREDUCTASE acid-inducible - Eubacterium sp >gi 1381570 (U57489) NADH:flavin oxidoreductase [Eubacterium sp. VPI 12708]	5.3
1019	AF027173	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-A) mRNA, complete cds	3e-04	1785789	(Y08502) orf111d [Arabidopsis thaliana]	5.1
1020	AC004173	Homo sapiens clone UWGC:y23x011 from 6p21, complete sequence [Homo sapiens]	3e-04	558521	(D28917) polyprotein [Hepatitis C virus]	1.1
1021	X57025	Human IGF-I mRNA for insulin-like growth factor I	3e-04	4206707	(AF118122) putative outer membrane protein OmpU	0.65
1022	X77090	H.sapiens IL-1Ra gene.	3e-04	1065941	(U40799) F42C5.7 gene product [Caenorhabditis elegans]	0.12

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Pseudorabies virus				
1023	M34651	with upstream and downstream sequences.	3e-04	2746853	(AF040650) contains similarity to sodium-potassium-chloride cotransport proteins	7e-05
1024	Z36011	S.cerevisiae chromosome II reading frame ORF YBR142w	3e-04	2500537	PROBABLE ATP-DEPENDENT RNA HELICASE HAS1 >gi 626265 pir S47451 hypothetical protein YMR290c RNA helicase [Saccharomyces cerevisiae]	4e-08
1025	AF020286	Dictyostelium discoideum 2034 gene, partial cds	3e-04	1465834	(U64857) No definition line found [Caenorhabditis elegans]	6e-14
1026	L26049	Chlamydomonas reinhardtii dynein heavy chain alpha (ODA11) gene, exons 2-15, and partial cds.	3e-04	3876775	(Z81077) predicted using Genefinder; Similarity to Yeast protein 8248 (TR:G587531)	9e-15
1027	AF020286	Dictyostelium discoideum 2034 gene, partial cds	3e-04	1465834	(U64857) No definition line found [Caenorhabditis elegans]	1e-17
1028	X79811	S.cerevisiae ACT3 gene	3e-04	3876090	(Z69655) Similarity to Yeast uridine kinase (SW:URK1_YEAST); cDNA EST EMBL:Z14695 comes from this gene; cDNA EST CEMSE17F comes from this gene; cDNA EST EMBL:D67355 comes from this gene; cDNA EST yk209h1.5 comes from this ge...	7e-31
1029	AF027173	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-A) mRNA, complete cds	2e-04	<NONE>	<NONE>	<NONE>
1030	M22970	Human pancreatic phospholipase A-2 (PLA-2) gene, exons 1 to 3.	2e-04	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Human DNA				
1031	Z68686	sequence from cosmid N2E9 on chromosome 22. Contains EST, complete sequence [Homo sapiens]	2e-04	<NONE>	<NONE>	<NONE>
1032	X95154	H.sapiens brca2 gene exon 4 > :: emb A62779 A62779 Sequence 20 from Patent WO9719110	2e-04	<NONE>	<NONE>	<NONE>
1033	AJ005813	Arabidopsis thaliana mRNA for neoxanthin cleavage enzyme	2e-04	<NONE>	<NONE>	<NONE>
1034	AF100694	Mus musculus Pontin52 mRNA, complete cds	2e-04	<NONE>	<NONE>	<NONE>
1035	AE001415	Plasmodium falciparum chromosome 2, section 52 of 73 of the complete sequence	2e-04	<NONE>	<NONE>	<NONE>
1036	AF090115	Lycopersicon esculentum cytosolic class II small heat shock protein HCT2 (HSP17.4) mRNA, complete cds	2e-04	<NONE>	<NONE>	<NONE>
1037	AC000958	Homo sapiens (subclone 6_d9 from P1 H21) DNA sequence	2e-04	<NONE>	<NONE>	<NONE>
1038	AF093268	Rattus norvegicus homer-1c mRNA, complete cds	2e-04	2501523	CD59 GLYCOPROTEIN PRECURSOR	7.1
1039	U76524	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	2e-04	2765360	(Y13925) cathepsin L2 [Penaeus vannamei]	6.8

H23

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					RNA POLYMERASE	
1040	AF027174	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-B) mRNA, complete cds	2e-04	133636	>gi 67126 pir RRXPLC RNA-directed RNA polymerase (EC 2.7.7.48) - lymphocytic choriomeningitis virus (strain Armstrong 53b) >gi 331369	5.2
1041	AB012106	Brassica rapa mRNA for SRK45, complete cds	2e-04	3822155	(AF074613) type II secretion protein [Escherichia coli O157:H7]	4.0
1042	U76524	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	2e-04	1718125	REGULATORY PROTEIN E2 >gi 1020222 type 36]	0.38
1043	X17058	Sus scrofa mRNA for glucose transport protein	2e-04	3341906	(AB009593) xylose transporter	2e-15
1044	AF008216	Homo sapiens candidate tumor suppressor pp32r1	1e-04	<NONE>	<NONE>	<NONE>
1045	X98890	S.tuberosum mRNA for inorganic phosphate transporter, StPT1	1e-04	624126	(U42580) a65L [Paramecium bursaria Chlorella virus 1]	7.9
1046	L14930	Glycine max (Rab7p) mRNA, complete cds.	9e-05	<NONE>	<NONE>	<NONE>
1047	AJ009970	Mus musculus thromboxane A2 receptor gene, exon 3, partial	9e-05	<NONE>	<NONE>	<NONE>
1048	Y11896	M.musculus mRNA for Brx gene, partial	9e-05	<NONE>	<NONE>	<NONE>
1049	L10832	Polistes annularis (clone pan48AAT) tandem repeat region.	9e-05	<NONE>	<NONE>	<NONE>
1050	AF055011	Homo sapiens clone 24587 mRNA sequence	9e-05	3880586	(Z79758) cDNA EST EMBL:D28009 comes from this gene; cDNA EST EMBL:D28008 comes from this gene; cDNA EST EMBL:D32478 comes from this gene; cDNA EST EMBL:D34508 comes from this gene; cDNA EST EMBL:D37581 comes from this gene; ...	7.6

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1051	U76524	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	9e-05	3024292	RHODOPSIN >gi 2290717 (AF000947) rhodopsin [Sepia officinalis]	6.7
1052	Z58294	H.sapiens CpG DNA, clone 34d6, forward read cpg34d6.ft1a	9e-05	3885496	(AF064825) heparin/heparan sulfate N-acetylglucosaminyl N-deacetylase/N-sulfotransferase [Bos taurus]	0.65
1053	D87451	Human mRNA for KIAA0262 gene, complete cds	9e-05	3874739	(Z66495) similar to claustrin like	0.004
1054	L37092	Mus musculus cyclin-dependent kinase homologue	9e-05	3080513	(AL022598) hypothetical protein	4e-09
1055	AF074386	Sambucus nigra hevein-like protein mRNA, complete cds	8e-05	<NONE>	<NONE>	<NONE>
1056	AF027174	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-B) mRNA, complete cds	8e-05	<NONE>	<NONE>	<NONE>
1057	AF074386	Sambucus nigra hevein-like protein mRNA, complete cds	8e-05	<NONE>	<NONE>	<NONE>
1058	D10102	Homo sapiens DNA from cosmid clone:844, GT repeat sequence	8e-05	<NONE>	<NONE>	<NONE>
1059	U72396	Lycopersicon esculentum class II small heat shock protein Le-HSP17.6 mRNA, complete cds	8e-05	1176475	HYPOTHETICAL 80.4 KD PROTEIN IN SMC3-MRPL8 INTERGENIC REGION >gi 1078237 pir S56849 probable membrane protein YJL073w - yeast (Saccharomyces cerevisiae) >gi 895898 (X88851) hypothetical protein YJL073w (Saccharomyces cerevisiae)	6.0
1060	X71934	H.sapiens XB gene for tenascin-X, repeat XIII	8e-05	285207	microtubule-associated protein, 110K tau - rat >gi 207158 (M84156) big tau [Rattus norvegicus]	3.7

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1061	AF027174	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-B) mRNA, complete cds	8e-05	4049682	(AF063866) ORF MSV092 hypothetical protein [Melanoplus sanguinipes entomopoxvirus]	2.1
1062	AF090115	Lycopersicon esculentum cytosolic class II small heat shock protein HCT2 (HSP17.4) mRNA, complete cds	8e-05	3861019	(AJ235271) unknown [Rickettsia prowazekii]	5e-14
1063	AF027174	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-B) mRNA, complete cds	7e-05	<NONE>	<NONE>	<NONE>
1064	L04193	Human lens membrane protein (mp19) gene, exon 11.	7e-05	<NONE>	<NONE>	<NONE>
1065	X61609	B.napus gene for LHC II Type III chlorophyll a/b binding protein	7e-05	2132314	hypothetical protein YPR174c - yeast similarity to a nuclear lamin from C. elegans (PIR accession number S42257) [Saccharomyces cerevisiae]	8.9
1066	AF064029	Helianthus tuberosus lectin I mRNA, complete cds	7e-05	2979422	(AB006757) PCDH7 (BH-Pcdh)c [Homo sapiens]	5.7
1067	AF027173	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-A) mRNA, complete cds	7e-05	2493696	HYPOTHETICAL 21.5 KD PROTEIN (ORF 185) >gi 1480440 (U34204) ORF185; hypothetical 21.4 kD protein [Brassica oleracea]	5.2
1068	AF093268	Rattus norvegicus homer-1c mRNA, complete cds	7e-05	2501029	PROBABLE LEUCYL-TRNA SYNTHETASE. MITOCHONDRIAL PRECURSOR (LEUCINE--TRNA LIGASE) (LEURS) KIAA0028 [Homo sapiens]	1.4

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Human DNA				
1069	Z68758	sequence from cosmid cN85E10 on chromosome 22q11.2-qter	3e-05	<NONE>	<NONE>	<NONE>
1070	X60653	human Histone H3.3 pseudogene (CIR-456)	3e-05	<NONE>	<NONE>	<NONE>
1071	Z58294	H.sapiens CpG DNA, clone 34d6, forward read cpg34d6.ft1a.	3e-05	1706241	GUANYLYL CYCLASE GC-E PRECURSOR cyclase receptor [Mus musculus]	9.6
1072	AF043251	Homo sapiens mitochondrial outer membrane protein (Tom40) gene, nuclear gene encoding mitochondrial protein, exons 1 through 6	3e-05	113980	AMINE OXIDASE [FLAVIN-CONTAINING] B oxidase (flavin-containing) (EC 1.4.3.4) B - human B [human, platelet, Peptide Partial, 520 aa] [Homo sapiens]	8.9
1073	M31104	Chicken progesterone receptor gene, encoding forms A and B, exons 1 and 2.	3e-05	1170841	IG GAMMA LAMBDA CHAIN V-II REGION	4.8
1074	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	3e-05	543684	ribosomal protein S3 - Chlamydomonas humicola chloroplast (fragment)	4.2
1075	L22206	Human vasopressin receptor V2 gene, complete cds.	3e-05	791207	(U20615) Gnot1 homeodomain protein [Gallus gallus]	1.8
1076	AF093268	Rattus norvegicus homer-1c mRNA, complete cds	3e-05	3237340	(AF033361) polyprotein [Hepatitis C virus]	0.94
1077	AF100694	Mus musculus Pontin52 mRNA, complete cds	3e-05	2879805	(AL021813) hypothetical protein	0.001
1078	AF100694	Mus musculus Pontin52 mRNA, complete cds	3e-05	3877951	(Z81555) predicted using Genefinder	3e-07

427

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1079	AF090115	Lycopersicon esculentum cytosolic class II small heat shock protein HCT2 (HSP17.4) mRNA, complete cds	2e-05	<NONE>	<NONE>	<NONE>
1080	AF064029	Helianthus tuberosus lectin 1 mRNA, complete cds	2e-05	3880197	(Z81132) predicted using Genefinder	2.4
1081	AF087989	Homo sapiens full length insert cDNA clone YX29D10	2e-05	113667	!!!! ALU CLASS B WARNING ENTRY !!!!	1.8
1082	AF064029	Helianthus tuberosus lectin 1 mRNA, complete cds	2e-05	474896	(L31967) mating type protein [Coprinus cinereus]	1.4
1083	AF064029	Helianthus tuberosus lectin 1 mRNA, complete cds	2e-05	2266988	(Y13274) M33 polycomb-like protein [Mus musculus]	0.62
1084	U67415	Equus caballus UCD-E-CA-467 dinucleotide repeat region, complete sequence	1e-05	<NONE>	<NONE>	<NONE>
1085	X67277	H.sapiens BGP gene for biliary glycoprotein, promoter region and exon 1	1e-05	<NONE>	<NONE>	<NONE>
1086	X85117	H.sapiens epb72 gene exons 2,3,4,5,6,7	1e-05	<NONE>	<NONE>	<NONE>
1087	U88328	Mus musculus suppressor of cytokine signalling-3	1e-05	443877	(Z29457) core region; pid:g443877 [Hepatitis C virus] virus]	3.9
1088	Y12853	Homo sapiens P2X7 gene, exon 4-8	1e-05	3878726	(Z66498) similar to cuticle collagen; cDNA EST EMBL:D75584 comes from this gene	0.36
1089	AE001140	Borrelia burgdorferi (section 26 of 70) of the complete genome	1e-05	3860719	(AJ235270) GLUTAMYL-tRNA AMIDOTRANSFERASE SUBUNIT A (gatA) [Rickettsia prowazekii]	4e-15

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1090	AJ224112	Homo sapiens gamma adaptin gene, exon 2 and flanking intronic sequences	9e-06	<NONE>	<NONE>	<NONE>
1091	AB000565	Homo sapiens DNA for repeat sequence Alu	9e-06	72879	translation initiation factor IF-2 - Escherichia coli	5.1
1092	Z78985	H.sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA20B4	9e-06	159975	(M65164) 51C surface protein [Paramecium tetraurelia]	4.8
1093	Z21677	Thermotoga maritima DNA for spc operon	9e-06	585879	50S RIBOSOMAL PROTEIN L2 maritima >gi 437926 (Z21677) ribosomal protein L2	7e-14
1094	AF031494	Drosophila hydei Dhc7 (Threads) mRNA, complete cds	9e-06	729377	DYNEIN BETA CHAIN, CILIARY sea urchin (Anthocidaris crassispina) chain [Anthocidaris crassispina]	4e-18
1095	AF051315	Homo sapiens placental protein 17a1 (PP17) mRNA, complete cds	4e-06	<NONE>	<NONE>	<NONE>
1096	AC001460	Homo sapiens (subclone 2_f4 from BAC H107) DNA sequence	4e-06	2648304	(AE000952) ISA1214-6, putative transposase	6.2
1097	X85030	H.sapiens mRNA for skeletal muscle-specific calpain	4e-06	4239857	(AB016726) calpain [Schistosoma japonicum]	0.006
1098	M75162	Human polymorphic arylamine N-acetyltransferase	3e-06	<NONE>	<NONE>	<NONE>
1099	AB009999	Rattus norvegicus mRNA for CDP-diacylglycerol synthase, complete cds	3e-06	3879045	(Z70309) R102.6 [Caenorhabditis elegans]	7.3
1100	Z78985	H.sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA20B4	3e-06	266529	MERCURIC REDUCTASE (HG(II) REDUCTASE) >gi 418744 pir S30168 mercury(II) reductase	6.5
1101	AB012190	Homo sapiens mRNA for Nedd8-activating enzyme hUba3, complete cds	3e-06	3877938	(Z79697) F58H10.1 [Caenorhabditis elegans]	6.3

1429

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Homo sapiens				
1102	AF041056	WSCR4 gene, exons 3 and 4	3e-06	1568583	(Z80775) hypothetical protein Rv0044c	1.9
1103	X00777	Mouse E(d) beta gene 5' flanking region and exon 1	3e-06	1680722	(U72497) fatty acid amide hydrolase [Rattus norvegicus]	0.008
1104	D21205	Human mRNA for estrogen responsive finger protein, complete cds	3e-06	563127	(U09825) acid finger protein [Homo sapiens]	1e-05
1105	Z47046	Human cosmid QLL2C9 from Xq28	1e-06	<NONE>	<NONE>	<NONE>
1106	L26261	Human MHC class III HLA-RP1 gene.	1e-06	<NONE>	<NONE>	<NONE>
1107	M13402	Rat 5S RNA gene, clone 5S-2.	1e-06	<NONE>	<NONE>	<NONE>
1108	X68793	H.sapiens gene for antithrombin III	1e-06	<NONE>	<NONE>	<NONE>
1109	AF003540	Homo sapiens Krueppel family zinc finger protein	1e-06	2507553	ZINC FINGER PROTEIN 33A (ZINC FINGER PROTEIN KOX31) (KIAA0065) (HA0946) Kruppel-related. [Homo sapiens]	0.098
1110	L42096	Homo sapiens (subclone 10_d2 from P1 H21) DNA sequence.	1e-06	1330401	(U58762) T27F7.1 gene product [Caenorhabditis elegans]	0.015
1111	Z69925	Human DNA sequence from cosmid cN116A5, between markers D22S280 and D22S86 on chromosome 22q12 contains EST	9e-07	<NONE>	<NONE>	<NONE>
1112	D90217	S. cerevisiae gene for YmL33, mitochondrial ribosomal proteins of large subunit	9e-07	3879097	(Z81109) predicted using Genefinder; similar to sodium/phosphate transporter; cDNA EST yk326f6.3 comes from this gene; cDNA EST yk326f6.5 comes from this gene [Caenorhabditis elegans]	7.1

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1113	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	9e-07	1330345	(U58755) coded for by C. elegans cDNA yk34b1.5; coded for by C. elegans cDNA yk13h10.5; coded for by C. elegans cDNA yk46e8.5; coded for by C. elegans cDNA yk46d5.5; coded for by C. elegans cDNA yk43c2.5; coded for by C. elegans cDNA yk46e8....	2e-29
1114	AF086562	Homo sapiens full length insert cDNA clone ZE16C03	4e-07	1072210	(U40945) coded for by C. elegans cDNA yk74b9.3; coded for by C. elegans cDNA yk74b9.5; similar to repeat of calcium channel alpha subunits; similar to tetracycline resistance protein; similar to hypothetical protein in HSP30-PMP1 region (SP...	3.9
1115	L39062	Homo sapiens interleukin 9 receptor IL9R pseudogene, exons 1-9	4e-07	3879983	(Z46795) similar to transforming protein etc2; cDNA EST EMBL:D34137 comes from this gene; cDNA EST EMBL:D37172 comes from this gene; cDNA EST EMBL:D76266 comes from this gene; cDNA EST EMBL:D70493 comes from this gene; cDNA ...	3.3
1116	Z69364	Human DNA sequence from cosmid L96F8, Huntington's Disease Region, chromosome 4p16.3 contains EST and cDNA. >:: emb Z69365 HSL96F8A Human DNA sequence from cosmid L96F8, Huntington's Disease Region, chromosome 4p16.3 contains EST and cDNA.	4e-07	3493176	(AF022889) latent TGF beta binding protein [Mus musculus]	3.0

431

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Human mRNA for KIAA0164 gene, complete cds	4e-07	4038031	(AC005936) hypothetical protein [Arabidopsis thaliana]	0.30
1117	D79986	Human mRNA for KIAA0098 gene, partial cds	3e-07	<NONE>	<NONE>	<NONE>
1118	D43950	Arabidopsis thaliana DnaJ homologue (AtJ6) mRNA, complete cds	3e-07	3881075	(AL032657) predicted using Genefinder; similar to DnaJ domain ; Thioredoxin; cDNA EST yk433f3.5 comes from this gene; cDNA EST EMBL:D32359 comes from this gene; cDNA EST EMBL:D34721 comes from this gene; cDNA EST yk433f3.3 c...	3e-09
1119	AF037168	H.sapiens mRNA for G9a	3e-07	3873414	(U00043) similar to D. melanogaster trithorax protein	3e-29
1120	X69838	Homo sapiens mRNA for KIAA0552 protein, complete cds	2e-07	2618749	(U90880) hypothetical protein 2; predicted using XGrail	2.0
1121	AB011124	Human cellular fms proto-oncogene, partial cds.	1e-07	<NONE>	<NONE>	<NONE>
1122	K03012	Homo sapiens DNA, microsatellite and Alu repeat region	1e-07	728837	!!!! ALU SUBFAMILY SQ WARNING ENTRY	0.095
1123	AB016195	Homo sapiens psihHaA pseudogene	4e-08	<NONE>	<NONE>	<NONE>
1124	Y16795	Homo sapiens FLII gene for ERGB transcription factor, intron 4 and partial cds	4e-08	728836	!!!! ALU SUBFAMILY SP WARNING ENTRY	3.6
1125	AB012624	Homo sapiens ogg1 gene, exons 1-7	4e-08	113668	!!!! ALU CLASS C WARNING ENTRY !!!!	3e-05
1126	AJ131341	Homo sapiens (subclone 1_c10 from P1 H69) DNA sequence	3e-08	4225950	(AJ132701) centaurin gamma 1B	1.8
1127	L81902	Gallus gallus mRNA for high mobility group 1 protein	3e-08	3041855	(AC004537) similar to tumor suppressor p33ING1; similar to AF044076 (PID:g282920S) [Homo sapiens]	3e-31
1128	Y17968	Homo sapiens FGFR-4 gene	1e-08	<NONE>	<NONE>	<NONE>
1129	Y13901					

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1130	L22024	Mesocricetus auratus serum amyloid P component gene, complete cds.	1e-08	<NONE>	<NONE>	<NONE>
1131	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	1e-08	<NONE>	<NONE>	<NONE>
1132	X14034	Human mRNA for phospholipase C > :: gb M37238 HUMPL C Human phospholipase C mRNA, complete cds.	1e-08	<NONE>	<NONE>	<NONE>
1133	Z59381	H.sapiens CpG DNA, clone 152b10, forward read cpg152b10.ft1a.	1e-08	<NONE>	<NONE>	<NONE>
1134	L81839	Homo sapiens (subclone 2_h3 from P1 H43) DNA sequence	1e-08	<NONE>	<NONE>	<NONE>
1135	X14448	Human GLA gene for alpha-D-galactosidase A (EC 3.2.1.22)	1e-08	3334427	HYPOTHETICAL PROTEIN MJ1207 Methanococcus jannaschii >gi 1591837 (U67562) protease synthase and sporulation negative regulator Pail, putative [Methanococcus jannaschii]	9.1
1136	AL023774	Human DNA sequence from clone 799F15 on chromosome Xq25, complete sequence [Homo sapiens]	1e-08	1354935	(U58330) probable copper-transporting atpase	1.2
1137	X64639	H.sapiens DNA repetitive subtelomeric-like sequence (522 bp)	1e-08	77356	hypothetical 70K protein - eggplant mosaic virus	0.098
1138	U97058	Human HuD gene, 5'UTR	5e-09	3387886	(AF070530) unknown [Homo sapiens]	9.5

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Human DNA				
1139	Z82181	sequence from cosmid E86D10 on chromosome 22. contains ESTs, exontrap, complete sequence	5e-09	728831	!!!! ALU SUBFAMILY J WARNING ENTRY	8.4
1140	AJ006587	Mus musculus mRNA for translation initiation factor eIF2 gamma X	5e-09	1872200	(U22376) alternatively spliced product using exon 13A	0.64
1141	Y11108	H.sapiens WNT8B gene	4e-09	2854198	(AF045646) contains similarity to collagens	4.0
1142	AE001223	Treponema pallidum section 39 of 87 of the complete genome	4e-09	3334189	CELL DIVISION PROTEIN FTSY HOMOLOG	1.5
1143	Z47046	Human cosmid QLL2C9 from Xq28	4e-09	104045	fibroblast growth factor receptor A1 precursor - African clawed frog >gi 214894 (M55163) fibroblast growth factor receptor [Xenopus laevis]	1.3
1144	AG000746	Homo sapiens genomic DNA, 21q region, clone: T171Bm40	4e-09	113666	!!!! ALU CLASS A WARNING ENTRY !!!!	0.33
1145	M74002	Human arginine-rich nuclear protein mRNA, complete cds.	4e-09	3875371	(Z50948) contains a valine and arginine rich domain, possesses weak similarity with the RNA binding domains from RNA splicing factor U2AF 65 KD subunit; cDNA EST EMBL:D64658 comes from this gene; cDNA EST EMBL:D66829 comes f... >gi 3878699 gnl PID e1351700 possesses weak similarity with the RNA binding domains from RNA splicing factor U2AF 65 KD subunit; cDNA EST EMBL:D64658 comes from this gene; cDNA EST EMBL:D66829 comes f...	3e-06
1146	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	2e-09	2494337	ENDO-1,4-BETA-XYLANASE PRECURSOR sp.]	4.9

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					UDP-	
1147	U20554	Drosophila melanogaster UDP-glucose:glycoprotein glucosyltransferase mRNA, complete cds.	2e-09	2499087	GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (DUGT) glucosyltransferase - fruit fly (Drosophila sp.) glucosyltransferase precursor [Drosophila melanogaster]	4e-24
1148	Z56162	H.sapiens CpG DNA, clone 91c9, forward read cpg91c9.ft1a	1e-09	<NONE>	<NONE>	<NONE>
1149	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-09	1002424	(U25739) YSPL-1 form 1 [Mus musculus]	8.9
1150	M85276	Homo sapiens NKG5 gene, complete cds.	1e-09	2315436	(AF016447) No definition line found [Caenorhabditis elegans]	8.3
1151	M94065	Human dihydroorotate dehydrogenase mRNA, 3' end.	1e-09	3892656	(AB014464) MGC-24v [Mus musculus]	6.2
1152	AJ131895	Homo sapiens genomic CAG repeat element, clone 60o2(250)	5e-10	<NONE>	<NONE>	<NONE>
1153	Z82181	Human DNA sequence from cosmid E86D10 on chromosome 22. contains ESTs, exontrap, complete sequence	5e-10	728831	!!!! ALU SUBFAMILY J WARNING ENTRY	7.9
1154	AJ224442	Homo sapiens mRNA for putative methyltransferase	5e-10	113667	!!!! ALU CLASS B WARNING ENTRY !!!!	0.15
1155	AJ010230	Homo sapiens RET finger protein-like 1 antisense transcript, partial	5e-10	728834	!!!! ALU SUBFAMILY SB2 WARNING ENTRY	0.006
1156	AF111116	Homo sapiens silencer of death domains (SODD) mRNA, complete cds	5e-10	4160014	(AF111116) silencer of death domains [Homo sapiens]	2e-08
1157	Z97017	Homo sapiens mRNA for hypothetical protein	4e-10	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Homo sapiens type II integral membrane protein	4e-10	<NONE>	<NONE>	<NONE>
1158	AF001298	H.sapiens mRNA for p40	2e-10	1000340	(U34384) CheW [Borrelia burgdorferi]	2.4
1159	Y11395	Human non-coding sequence upstream from DOC-2 gene on chromosome 5	2e-10	728837	!!!! ALU SUBFAMILY SQ WARNING ENTRY	0.28
1160	U41096	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	6e-11	<NONE>	<NONE>	<NONE>
1161	AF012899	S.cerevisiae chromosome II reading frame ORF YBR242w	6e-11	2213560	(Z97052) hypothetical protein (Z80220) Similarity to yeast protein TREMBL ID E246895); cDNA EST EMBL:T00018 comes from this gene; cDNA EST EMBL:C13908 comes from this gene; cDNA EST EMBL:C11656 comes from this gene; cDNA EST yk234a5.3 comes from this ge...	3e-27
1162	Z36111	Schizosaccharomyces pombe mRNA, partial cds, clone: SY 1004	6e-11	3879758		4e-30
1163	D89174	Human DNA sequence from cosmid A1 on chromosome 6 contains ESTs. HERV like retroviral sequence	5e-11	<NONE>	<NONE>	<NONE>
1164	Z95437	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	5e-11	3886065	(AF106581) contains similarity to C4-type zinc fingers	4.9
1165	AF012899	Human Uba52 gene coding for ubiquitin-52 amino acid fusion protein	2e-11	<NONE>	<NONE>	<NONE>
1166	X56997	Homo sapiens full length insert cDNA clone ZD40G12	2e-11	2134780	apoptosis inhibitor IAP homolog - human	3.8
1167	AF086253					

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1168	AB018314	Homo sapiens mRNA for KIAA0771 protein, partial cds	2e-11	3024343	P53-BINDING PROTEIN 53BP2 Bbp/53BP2 [Homo sapiens]	2e-11
1169	Z74972	S.cerevisiae chromosome XV reading frame ORF YOR064c	2e-11	3041855	(AC004537) similar to tumor suppressor p33ING1; similar to AF044076 (PID:g2829208) [Homo sapiens]	2e-40
1170	Z82181	Human DNA sequence from cosmid E86D10 on chromosome 22. contains ESTs, exontrap, complete sequence	7e-12	<NONE>	<NONE>	<NONE>
1171	X77738	H.sapiens red cell anion exchanger (EPB3, AE1, Band 3) gene, 3' region	7e-12	2135416	hypothetical protein - human >gi288145	0.012
1172	S61977	medium-chain acyl-CoA dehydrogenase (exon 10, intron 10) [human, Genomic, 1407 nt]	6e-12	113666	!!!! ALU CLASS A WARNING ENTRY !!!!	0.100
1173	X66285	M.musculus DNA for HCl locus	6e-12	854065	(X83413) U88 [Human herpesvirus 6]	2e-06
1174	S78744	protein S=activated protein C cofactor [rats, liver, mRNA, 3315 nt]	6e-12	2338292	(AF009243) proline-rich Gla protein 2 [Homo sapiens]	3e-10
1175	X58474	Bovine OXT gene for oxytocin, 5' noncoding region	2e-12	1296429	(L77967) small proline-rich protein with paired repeat	4.1
1176	Z56314	H.sapiens CpG DNA, clone 10h10, reverse read cpg10h10.r1a.	2e-12	2935221	(AF030154) pVII [bovine adenovirus type 3]	2.8
1177	Z56314	H.sapiens CpG DNA, clone 10h10, reverse read cpg10h10.r1a.	2e-12	2708659	(AF037440) putative 26 kDa protein [Edwardsiella ictaluri]	2.8
1178	Z19543	M.musculus h2-calponin cDNA	2e-12	2497945	BETA SCRUIIN >gi1015535 (Z47541) beta scruiin [Limulus polyphemus]	2e-04

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		erythropoietin				
1179	S45332	receptor [human, placental, Genomic, 8647 nt]	7e-13	728835	!!!! ALU SUBFAMILY SC WARNING ENTRY	0.074
1180	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	2e-13	<NONE>	<NONE>	<NONE>
1181	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	2e-13	<NONE>	<NONE>	<NONE>
1182	Z59509	H.sapiens CpG DNA, clone 15a1, reverse read cpg15a1.r1a.	2e-13	3150251	(AL023634) hypothetical protein	0.66
1183	D10170	Human CYP11B2 gene for steroid 18-hydroxylase	2e-13	728837	!!!! ALU SUBFAMILY SQ WARNING ENTRY	3e-05
1184	U65416	Human MHC class I molecule (MICB) gene, complete cds	2e-13	126295	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG	6e-11
1185	AJ006031	Mus musculus IHABP gene, promoter	8e-14	2132223	hypothetical protein YPL186c - yeast	1.1
1186	U34976	Human gamma-sarcoglycan mRNA, complete cds	8e-14	1054903	(U34976) gamma-sarcoglycan [Homo sapiens] >gi 4239660 sapiens]	0.034
1187	D30647	Rat mRNA for very-long-chain Acyl-CoA dehydrogenase, complete cds	8e-14	3183512	ACYL-COA DEHYDROGENASE, VERY-LONG-CHAIN SPECIFIC (VLCAD) >gi 2388724 (AF017176) very-long-chain acyl-CoA dehydrogenase [Mus musculus]	8e-23
1188	Z63247	H.sapiens CpG DNA, clone 7g4, forward read cpg7g4.f1a.	6e-14	86285	histone H1.01 - chicken	6.8
1189	U27196	Gallus gallus zinc finger protein (Fzf-1) mRNA, complete cds.	3e-14	2134436	zinc finger protein - chicken (fragment)	4e-10
1190	M26219	African green monkey origin of replication	2e-14	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Mus musculus				
1191	AF100694	Pontin52 mRNA, complete cds	2e-14	4235641	(AF119040) NL0D [Lycopersicon esculentum]	0.65
1192	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	2e-14	3043728	(AB011174) KIAA0602 protein [Homo sapiens]	0.28
1193	AJ005866	Homo sapiens mRNA for putative Sqv-7-like protein, partial	2e-14	4008517	(AJ005866) Sqv-7-like protein [Homo sapiens]	0.004
1194	U32709	Haemophilus influenzae Rd section 24 of 163 of the complete genome	2e-14	3861056	(AJ235272) POLYRIBONUCLEOTIDE NUCLEOTIDYLTRANSFERASE (pnp) [Rickettsia prowazekii]	6e-28
1195	AF073485	Homo sapiens MHC class I-related protein MR1 precursor (MR1) gene, partial cds	8e-15	728831	!!!! ALU SUBFAMILY J WARNING ENTRY	1.0
1196	AF052135	Homo sapiens clone 23625 mRNA sequence	8e-15	4098124	(U73522) AMSH [Homo sapiens]	8e-14
1197	AF100694	Mus musculus Pontin52 mRNA, complete cds	3e-15	<NONE>	<NONE>	<NONE>
1198	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	3e-15	113671	!!!! ALU CLASS F WARNING ENTRY !!!!	1.7
1199	Z75104	S.cerevisiae chromosome XV reading frame ORF YOR196c	3e-15	3878570	(Z46381) similar to lipoic acid synthase; cDNA EST yk283b6.3 comes from this gene; cDNA EST yk283b6.5 comes from this gene; cDNA EST yk472f5.3 comes from this gene; cDNA EST yk472f5.5 comes from this gene; cDNA EST yk476e7.3...	1e-15

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					(U42833) coded for by C.	
1200	X70052	S.cerevisiae sof1 gene	3e-15	1125754	elegans cDNA cm16f6; coded for by C. elegans cDNA CEESU63F; similar to S. cerevisiae SOF1 protein (SP:P33750) [Caenorhabditis elegans]	3e-29
1201	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	2e-15	<NONE>	<NONE>	<NONE>
1202	M92295	Gorilla gorilla gamma 1 and gamma-2 globin genes, complete cds.	1e-15	284078	hypothetical protein 2 - human >gi182220	7.4
1203	L34587	Homo sapiens RNA polymerase II elongation factor SIII, p15 subunit mRNA, complete cds. > :: gb AR022286 AR022286 Sequence 7 from patent US 5792634	9e-16	<NONE>	<NONE>	<NONE>
1204	D83649	Xenopus laevis mRNA for xSox7 protein, complete cds	8e-16	2447043	(D83649) xSox7 protein [Xenopus laevis]	4e-06
1205	AC005190	Homo sapiens PAC clone DJ1152D16 from Xq23; complete sequence [Homo sapiens]	3e-16	<NONE>	<NONE>	<NONE>
1206	J03626	Human UMP synthase mRNA, complete cds.	3e-16	113667	!!!! ALU CLASS B WARNING ENTRY !!!!	0.65
1207	J00083	Human Alu family interspersed repeat; clone BLUR11.	3e-16	728836	!!!! ALU SUBFAMILY SP WARNING ENTRY	4e-06
1208	U70674	Mus musculus m-Numb (m-nb) mRNA, complete cds	1e-16	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1209	U66619	Human SWI/SNF complex 60 KDa subunit (BAF60c) mRNA, complete cds	1e-16	1549247	(U66619) SWI/SNF complex 60 KDa subunit [Homo sapiens]	0.003
1210	U75467	Drosophila melanogaster Rga and Atu genes, complete cds	1e-16	1658503	(U75467) Atu [Drosophila melanogaster]	5e-32
1211	M72709	Human alternative splicing factor mRNA, complete cds.	3e-17	<NONE>	<NONE>	<NONE>
1212	U26556	Human ferritin H (FTHL13) pseudogene.	3e-17	<NONE>	<NONE>	<NONE>
1213	D32064	Human gene for 2-oxoglutarate dehydrogenase, complete cds	3e-17	2088843	(AF003386) F59E12.9 gene product [Caenorhabditis elegans]	0.12
1214	M76364	Human (Papua New Guinean) Mitochondrial DNA control region, sequence 131.	3e-17	114009	APAG PROTEIN >gi 72927 pir BVECAG apaG protein - Escherichia coli >gi 40918 (X04711) URF hypothetical protein [Escherichia coli]	0.006
1215	AF017466	Homo sapiens genomic sequence from subtelomeric region of chromosome 4q	1e-17	3947985	(U78948) MADS-box protein 2 [Malus domestica]	4.1
1216	AF004876	Homo sapiens 54TMp (54tm) mRNA, complete cds	1e-17	4101574	(AF004876) 54TMp [Homo sapiens]	0.006
1217	AF100694	Mus musculus Pontin52 mRNA, complete cds	9e-18	<NONE>	<NONE>	<NONE>
1218	AF086758	Rattus norvegicus Na-K-2Cl cotransporter	4e-18	3892703	(AL033545) putative glycine-rich protein [Arabidopsis thaliana]	0.30
1219	AF020089	Homo sapiens PEN11B mRNA, complete cds	4e-18	2642493	(AF023910) DNA topoisomerase I [Physarum polycephalum]	0.083
1220	X82333	H.sapiens IRLB gene (exon1-3)	4e-18	106837	irlB protein - human (fragment) >gi 33969	2e-11

4/4/01

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Human mRNA for				
1221	AB002383	KIAA0385 gene, complete cds	4e-18	3228540	(AF060181) zinc finger protein [Homo sapiens]	6e-25
1222	X98485	P.vivax PV14 gene	1e-18	<NONE>	<NONE>	<NONE>
1223	Z79057	H.sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA21E8	1e-18	2981631	(AB012223) ORF2 [Canis familiaris]	0.001
1224	L01457	Homo sapiens (clone JH4B1) PM-scl autoantigen mRNA, complete cds.	1e-18	346287	nucleolar 100K polymyositis-scleroderma protein - human >gi 35555 (X66113) PM/Scl 100kD nucleolar protein [Homo sapiens]	0.001
1225	L02897	Dog nonerythroid beta-spectrin mRNA, 3' end.	4e-19	3493358	(AB017037) nonstructural protein precursor [Himetobi P virus]	0.12
1226	AB012162	Homo sapiens mRNA for APCL protein, complete cds	4e-19	3894265	(AB012162) APCL protein [Homo sapiens]	0.002
1227	AB011093	Homo sapiens mRNA for KIAA0521 protein, partial cds	4e-19	3043566	(AB011093) KIAA0521 protein [Homo sapiens]	9e-09
1228	X78454	X.laevis AB21 mRNA for RPD3 homologue	4e-19	3023945	HISTONE DEACETYLASE (HD) thaliana]	5e-34
1229	U88895	Human endogenous retrovirus H D1 leader region/integrase-derived ORF1, ORF2, and putative envelope protein mRNA, complete cds	2e-19	59977	(Z14310) tripartite fusion transcript PLA2L [Human endogenous retrovirus]	1e-04
1230	U34377	Human tyrosine kinase TXK (txk) gene, exon 13.	1e-19	728831	!!!! ALU SUBFAMILY J WARNING ENTRY	3e-05
1231	X72966	M.musculus rab3A gene	1e-19	2408076	(Z99167) putative peroxisomal organisation and biogenesis protein [Schizosaccharomyces pombe]	2e-09
1232	AB007953	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484	4e-20	<NONE>	<NONE>	<NONE>

442

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					(AB001535) similar to	
1233	D14034	Human gene for Zn-alpha2-glycoprotein, complete cds	2e-20	3928756	C.elegans hypothetical protein CET01H8.1.CEC05C12.3.CEF54D1.5. similar to trp and trp-like proteins [Homo sapiens]	1e-07
1234	X82126	H.sapiens HOK-2 gene, exon 2	2e-20	2137269	DNA-binding protein - mouse >gij437444	1e-19
1235	AF093684	Luciferase reporter vector pXP2 *SA, complete sequence	5e-21	2773363	(AF041382) microtubule binding protein D-CLIP-190	5.5
1236	J05272	Human IMP dehydrogenase type I mRNA complete cds.	5e-21	124417	INOSINE-5'-MONOPHOSPHATE DEHYDROGENASE 1 (IMP DEHYDROGENASE 1) (IMPDH-I) (IMPD 1) I - human	2e-04
1237	D86997	Human (lambda) DNA for immunoglobulin light chain	5e-21	3878261	(Z75712) Similarity to S. Pombe BEM1/BUD5 suppressor; cDNA EST EMBL:Z14470 comes from this gene; cDNA EST yk482d4.3 comes from this gene; cDNA EST yk482d4.5 comes from this gene [Caenorhabditis elegans]	6e-46
1238	Z79865	H.sapiens chromosome 22 CpG island DNA genomic MseI fragment, clone 302f3, forward read 302f3.f	2e-21	2739037	(AF024614) ADAM 10 [Caenorhabditis elegans] Zinc-binding metalloprotease domain; cDNA EST CEMSA42F comes from this gene; cDNA EST yk218f3.3 comes from this gene; cDNA EST yk443d9.3 comes from this gene; cDNA EST yk443d9.5 comes from this gene; cDNA...	2.6

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1239	AF100694	Mus musculus Pontin52 mRNA, complete cds	6e-22	3924779	(U000505) similar to human B, cDNA EST yk450d8.5 comes from this gene; cDNA EST yk249a6.5 comes from this gene; cDNA EST yk219a2.5 comes from this gene; cDNA EST yk355e4.5 comes from this gene; cDNA EST yk224f4.5 comes fr... >gi 3924881 gnl PID e1354569 from this gene; cDNA EST yk249a6.5 comes from this gene; cDNA EST yk219a2.5 comes from this gene; cDNA EST yk355e4.5 comes from this gene; cDNA EST yk224f4.5 comes from...	0.35
1240	U67824	Human primary Alu transcript	6e-22	728832	!!!! ALU SUBFAMILY SB WARNING ENTRY	5e-07
1241	AF070636	Homo sapiens clone 24686 mRNA sequence	2e-22	98710	fatty-acid synthase (EC 2.3.1.85) - Brevibacterium ammoniagenes	2.5
1242	D14034	Human gene for Zn-alpha2-glycoprotein, complete cds	2e-22	4185939	(Y17832) pol protein [Human endogenous retrovirus K]	0.29
1243	M61835	Human lactase phlorizin hydrolase (LCT) gene, exon 2.	2e-22	728831	!!!! ALU SUBFAMILY J WARNING ENTRY	0.006
1244	AF100694	Mus musculus Pontin52 mRNA, complete cds	6e-23	1350828	RABPHILIN-3A >gi 477100 pir A48097 rabphilin-3A - bovine >gi 285646 gnl PID d1003285	0.14
1245	AF074985	Homo sapiens full length insert cDNA YH73H06	8e-24	3170548	(AF056116) unknown [Fugu rubripes]	0.24
1246	D14878	Human mRNA for protein D123, complete cds	7e-24	<NONE>	<NONE>	<NONE>
1247	D16917	Human HepG2 3' region cDNA, clone hmd3d07	6e-24	1397345	(U61955) contains multiple region of strong similarity to C2H2-type zinc fingers (PS:PS00028) [Caenorhabditis elegans]	2.4

444

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Human DNA				
1248	Z69654	sequence from cosmid L98A6. Huntington's Disease Region, chromosome 4p16.3.	3e-24	4240566	(AF123462) neurexin III [Homo sapiens]	4.5
1249	AB007914	Homo sapiens mRNA for KIAA0445 protein, complete cds	2e-24	3885949	(AF095568) amelogenin [Paleosuchus palpebrosus]	3.2
1250	AF088072	Homo sapiens full length insert cDNA clone ZD93D10	2e-24	323091	immunodominant microneme protein Etp100 - Eimeria tenella >gi 2707733 (AF032905) microneme protein precursor Etmic-1 [Eimeria tenella]	0.34
1251	AF069489	Homo sapiens cAMP specific phosphodiesterase 4A variant pde46 (PDE4A) gene, exons 2 through 13 and alternative splice exons 3a, 6a, 6b, and 9a	2e-24	728836	!!!! ALU SUBFAMILY SP WARNING ENTRY	1e-05
1252	Y12853	Homo sapiens P2X7 gene, exon 4-8	9e-25	728831	!!!! ALU SUBFAMILY J WARNING ENTRY	1e-05
1253	M27830	Human 28S ribosomal RNA gene, complete cds.	8e-25	<NONE>	<NONE>	<NONE>
1254	AB007953	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484	8e-25	<NONE>	<NONE>	<NONE>
1255	Z60212	H.sapiens CpG DNA, clone 195c8, forward read cpg195c8.ft1a.	8e-25	158154	(M81959) POU domain protein [Drosophila melanogaster]	3.3
1256	AF100694	Mus musculus Pontin52 mRNA, complete cds	7e-25	<NONE>	<NONE>	<NONE>
1257	AF100694	Mus musculus Pontin52 mRNA, complete cds	7e-25	<NONE>	<NONE>	<NONE>
1258	Y12851	Homo sapiens P2X7 gene, exon 1 and joined CDS	2e-25	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Mus musculus Tera				
1259	U64033	(Tera) mRNA, complete cds	9e-26	<NONE>	<NONE>	<NONE>
1260	U19181	Rattus norvegicus Rabin3 mRNA, complete cds.	9e-26	624225	(U19181) Rabin3 [Rattus norvegicus]	1e-13
1261	AF020788	Caenorhabditis elegans SEL-10 (sel-10) mRNA, complete cds	9e-26	3915881	SEL-10 PROTEIN Candida CDC4 gene (TR:E234056); cDNA EST EMBL:D27699 comes from this gene; cDNA EST EMBL:D27698 comes from this gene; cDNA EST EMBL:D32793 comes from this gene; cDNA EST EMBL:D33271 comes from this gen...	7e-32
1262	AB016930	Cricetulus griseus mRNA for Phosphatidylglycerophosphate synthase, complete cds	8e-26	4159682	(AB016930) Phosphatidylglycerophosphate synthase [Cricetulus griseus]	0.045
1263	AF100694	Mus musculus Pontin52 mRNA, complete cds	3e-26	3878629	(Z93385) predicted using Genefinder; Similarity to B.subtilis GTP-binding protein	2e-10
1264	X91195	H.sapiens SOM172 mRNA	1e-26	<NONE>	<NONE>	<NONE>
1265	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-26	1360637	(X95995) ENBP1 [Vicia sativa]	3.1
1266	L08237	Human MG21 mRNA, partial cds.	1e-26	950411	(L08237) located at OATL1 [Homo sapiens]	9e-09
1267	AF100694	Mus musculus Pontin52 mRNA, complete cds	9e-27	3881080	(AL032657) similar to EGF-like domain; cDNA EST yk299a12.3 comes from this gene; cDNA EST EMBL:D35398 comes from this gene; cDNA EST yk331h6.5 comes from this gene; cDNA EST yk299a12.5 comes from this gene; cDNA EST yk467g8....	0.001
1268	AF100694	Mus musculus Pontin52 mRNA, complete cds	8e-27	1731324	HYPOTHETICAL PROTEIN >gil166306	4.0

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1269	X89211	H.sapiens DNA for endogenous retroviral like element	8e-27	2065209	(Y12713) Gag polyprotein [Mus musculus]	0.005
1270	U73166	Homo sapiens cosmid clone LUCA15 from 3p21.3, complete sequence [Homo sapiens]	3e-27	728831	!!!! ALU SUBFAMILY J WARNING ENTRY	4e-04
1271	D78255	Mouse mRNA for PAP-1, complete cds	3e-27	1850098	(D78255) PAP-1 [Mus musculus]	2e-10
1272	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-27	2133579	spermatophorin Sp23 - yellow mealworm molitor]	0.39
1273	AB015202	Homo sapiens gene for hippocalcin, exon 2, 3 and complete cds	1e-27	3877698	(Z83318) predicted using Genefinder; cDNA EST yk369e7.5 comes from this gene [Caenorhabditis elegans]	0.37
1274	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-27	3328188	(AF074902) laminin alpha chain [Caenorhabditis elegans]	0.19
1275	Z29336	H.sapiens gene for Cu/Zn-superoxide dismutase	1e-27	728831	!!!! ALU SUBFAMILY J WARNING ENTRY	6e-05
1276	AF100694	Mus musculus Pontin52 mRNA, complete cds	9e-28	2133579	spermatophorin Sp23 - yellow mealworm molitor]	9.2
1277	AF100694	Mus musculus Pontin52 mRNA, complete cds	9e-28	2133579	spermatophorin Sp23 - yellow mealworm molitor]	0.054
1278	AB001636	Homo sapiens mRNA for ATP-dependent RNA helicase #46, complete cds	4e-28	3913425	PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE >gi 2275203 (AC002337) RNA helicase isolog [Arabidopsis thaliana]	3e-22
1279	AF100694	Mus musculus Pontin52 mRNA, complete cds	3e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	0.066

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	
1280	AF100694	Mus musculus Pontin52 mRNA, complete cds	3e-28	4056454		4e-05
1281	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	<NONE>	<NONE>	<NONE>
1282	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	<NONE>	<NONE>	<NONE>
1283	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	<NONE>	<NONE>	<NONE>
1284	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	<NONE>	<NONE>	<NONE>
1285	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	<NONE>	<NONE>	<NONE>
1286	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	<NONE>	<NONE>	<NONE>
1287	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	140505	PROBABLE INTRON MATURASE liverwort (Marchantia polymorpha) chloroplast >gi 11663	3.0
1288	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	140505	PROBABLE INTRON MATURASE liverwort (Marchantia polymorpha) chloroplast >gi 11663	1.8
1289	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	2133579	spermatophorin Sp23 - yellow mealworm molitor]	0.50
1290	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	0.087
1291	Z63029	H.sapiens CpG DNA, clone 77b3, forward read cpg77b3.ft1a .	1e-28	2493240	HYPOTHETICAL 29.3 KD PROTEIN pseudotsugata nuclear polyhedrosis virus]	0.014

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1292	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	118588	DEHYDRIN DHN3 >gi 100035 pir S18139 dehydrin DHN3 - garden pea >gi 20709 (X63063) pea dehydrin DHN3 [Pisum sativum]	0.010
1293	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	0.007
1294	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	0.002
1295	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	126363	LAMININ ALPHA-1 CHAIN PRECURSOR precursor - human	3e-04
1296	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	1e-04
1297	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	3e-05
1298	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	3157926	(AC002131) Strong similarity to extensin-like protein gb Z34465 from Zea mays. [Arabidopsis thaliana]	2e-05
1299	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	1e-05

449

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					kinetoplast-associated protein -	
1300	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	320919	Trypanosoma cruzi >gi 162142 (M25364) kinetoplast-associated protein	1e-07
1301	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	9e-08
1302	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	1e-09
1303	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	9e-10
1304	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	4e-10
1305	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	9e-11
1306	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	6e-11

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Mus musculus				
1307	AF100694	Pontin52 mRNA, complete cds	4e-29	<NONE>	<NONE>	<NONE>
1308	AF079529	Homo sapiens cAMP-specific phosphodiesterase 8B	4e-29	<NONE>	<NONE>	<NONE>
1309	X93334	H.sapiens mitochondrial DNA, complete genome	4e-29	116977	CYTOCHROME C OXIDASE POLYPEPTIDE I chain I - human mitochondrion (SGC1) >gi 13006 (V00662) cytochrome oxidase I [Homo sapiens] >gi 506829 (J01415) cytochrome oxidase subunit I [Homo sapiens] sapiens]	3e-09
1310	AF020760	Homo sapiens serine protease (Omi) mRNA, complete cds	4e-29	2738915	(AF020760) serine protease [Homo sapiens]	8e-12
1311	U95097	Xenopus laevis mitotic phosphoprotein 43 mRNA, partial cds	4e-29	2072294	(U95097) mitotic phosphoprotein 43 [Xenopus laevis]	1e-25
1312	L32162	Homo sapiens transcription factor mRNA, 5' end.	2e-29	2501706	RENAL TRANSCRIPTION FACTOR KID-1 finger protein [Mus musculus]	8e-15
1313	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-29	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	1e-04
1314	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-29	1169643	FMRFAMIDE-RELATED NEUROPEPTIDES PRECURSOR >gi 416208 (U03137) neuropeptide precursor FMRFamide-related peptide [Lymnaea stagnalis]	1e-05
1315	U50839	Homo sapiens g16 protein (g16) mRNA, complete cds	1e-29	3212101	(AF069517) RNA binding protein DEF-3 [Homo sapiens]	6e-10

Nearest Neighbor (BlastN vs. Genbank)				Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					intercellular adhesion molecule	
1316	X69711	H. sapiens mRNA for ICAM-R	5e-30	299356	3, ICAM-3=lymphocyte function-associated antigen 1 counter-receptor homolog [human, tonsil, Peptide Partial, 518 aa]	3e-08
1317	AF010227	Homo sapiens receptor-associated coactivator 3	5e-30	2331250	(AF012108) Amplified in Breast Cancer [Homo sapiens]	8e-09
1318	AF086395	Homo sapiens full length insert cDNA clone ZD75C01	2e-30	3861241	(AJ235273) CELL SURFACE ANTIGEN (sca5)	4.2
1319	M27830	Human 28S ribosomal RNA gene, complete cds.	2e-30	1730522	PHOSPHOGLYCERATE KINASE 2.7.2.3) - Pyrococcus woesei >gi 1054832 (X73527) phosphoglycerate kinase [Pyrococcus woesei]	3.8
1320	M79307	Mouse GTP-binding protein (Rab17) mRNA sequence.	2e-30	464564	RAS-RELATED PROTEIN RAB-17 Rab17 - mouse (fragment) >gi 297157 (X70804) rab17 [Mus musculus]	9e-11
1321	AL022168	Human DNA sequence from clone U247E12 on chromosome Xq22-23, complete sequence [Homo sapiens]	1e-30	2072967	(U93570) putative p150 [Homo sapiens]	3e-11
1322	X85124	M.musculus pacsin gene	1e-30	2217964	(Z50798) p52 [Gallus gallus]	1e-34
1323	U37408	Homo sapiens phosphoprotein CtBP mRNA, complete cds	5e-31	74518	structural polyprotein - Venezuelan equine encephalitis virus (strain TRD) >gi 323710. (J04332) poly-envelope protein [Venezuelan equine encephalitis virus]	1.1
1324	L04193	Human lens membrane protein (mp19) gene, exon 11.	2e-31	728831	!!!! ALU SUBFAMILY J WARNING ENTRY	7e-07
1325	M11167	Human 28S ribosomal RNA gene.	6e-32	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1326	M33336	Human cAMP-dependent protein kinase type I-alpha subunit (PRKAR1A) mRNA, complete cds	2e-32	<NONE>	<NONE>	<NONE>
1327	J03060	Human glucocerebrosidase pseudogene, complete cds	2e-32	2144479	glucosylceramidase (EC 3.2.1.45) precursor - human	1e-05
1328	U33053	Human lipid-activated protein kinase PRK1 mRNA, complete cds	7e-33	2137689	protein kinase (EC 2.7.1.37) - mouse	1e-14
1329	J04617	Human elongation factor EF-1-alpha gene, complete cds. > :: dbj E02629 E02629 DNA of human polypeptide chain elongation factor-1 alpha	6e-33	<NONE>	<NONE>	<NONE>
1330	L40396	Homo sapiens (clone s22i71) mRNA fragment	6e-33	124235	INTERMEDIATE FILAMENT PROTEIN B protein B - common roundworm	1.00
1331	Z72813	S.cerevisiae chromosome VII reading frame ORF YGR028w	6e-33	1709135	MSP1 PROTEIN HOMOLOG Yeast MSP1 protein (TAT-binding homolog 4)	8e-50
1332	AB007941	Homo sapiens mRNA for KIAA0472 protein, partial cds	2e-33	1150834	(U42471) Wiscott-Aldrich Syndrome protein homolog [Mus musculus]	2.0
1333	AF044574	Rattus norvegicus putative peroxisomal 2,4-dienoyl-CoA reductase (DCR-AKL) mRNA, complete cds	2e-34	4105269	(AF044574) putative peroxisomal 2,4-dienoyl-CoA reductase [Rattus norvegicus]	6e-15
1334	D14657	Human mRNA for KIAA0101 gene, complete cds	7e-35	<NONE>	<NONE>	<NONE>
1335	X69910	H.sapiens p63 mRNA for transmembrane protein	7e-35	2136323	trithorax homolog HTX - human (fragment) homolog=MLL {alternative splicing, clone 14p-18B}	0.94

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Homo sapiens				
1336	AF053455	tetraspan TM4SF (TSPAN-5) gene, complete cds	7e-35	3152703	(AF065389) tetraspan NET-4 [Homo sapiens]	1e-25
1337	X58374	D.melanogaster crn mRNA	3e-35	117478	CROOKED NECK PROTEIN	6e-41
1338	AF086492	Homo sapiens full length insert cDNA clone ZD95D11	9e-36	2909809	(AF031328) aminoglycoside 6'-N-acetyltransferase It	1.9
1339	Z96223	H.sapiens telomeric DNA sequence, clone 12PTEL120, read 12PTELOO120.seq	3e-36	2408068	(Z99165) hypothetical protein	0.61
1340	Z37986	H.sapiens mRNA for phenylalkylamine binding protein.	1e-36	1362793	emopamil-binding protein - human >gi 780263	5e-11
1341	U57847	Human ribosomal protein S27 mRNA, complete cds. end similar to similar to metallopanstimulin 1 >:: gb AA316327 AA316327 EST188061 HCC cell line (matatasis to liver in mouse) II Homo sapiens cDNA 5' end similar to similar to metallopanstimulin 1	3e-37	1171014	40S RIBOSOMAL PROTEIN S27 growth factor-inducible zinc finger protein MPS-1 - human >gi 431319 (L19739) metallopanstimulin [Homo sapiens] >gi 1373421 (U57847) ribosomal protein S27	1.4
1342	Y15054	Rattus norvegicus mRNA for 70 kDa tumor specific antigen, partial	3e-37	3123027	70 KD WD-REPEAT TUMOR-SPECIFIC ANTIGEN >gi 2505957 gnl PID e353992 (Y15054) 70 kD tumor-specific antigen [Rattus norvegicus]	2e-15
1343	AF084205	Rattus norvegicus serine/threonine protein kinase TAO1 mRNA, complete cds	3e-37	3452473	(AF084205) serine/threonine protein kinase TAO1 [Rattus norvegicus]	5e-47
1344	X78604	R.norvegicus (Sprague Dawley) ARL5 mRNA for ARF-like protein 5	1e-37	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1345	AJ236644	Homo sapiens chromosome 22 CpG island DNA, genomic MseI fragment, clone 22CGIB49A3, complete read	1e-37	2239219	(Z97210) hypothetical protein	6e-05
1346	U09367	Human zinc finger protein ZNF136	4e-39	2137269	DNA-binding protein - mouse >gij437444	7e-23
1347	Z69649	Human DNA sequence from cosmid L69F7B, Huntington's Disease Region, chromosome 4p16.3 contains Huntington Disease (HD) gene.	3e-39	3096918	(AL023094) putative cyclase associated protein CAP [Arabidopsis thaliana]	5.6
1348	AF065389	Homo sapiens tetraspan NET-4 mRNA, complete cds	1e-39	3152703	(AF065389) tetraspan NET-4 [Homo sapiens]	6e-29
1349	AF038172	Homo sapiens clone 23923 mRNA sequence	1e-40	1813464	(U60883) CapC [Bacillus firmus]	2.8
1350	Z83095	H.sapiens Fanconi anaemia group A gene, exons 39, 40, 41, 42 and 43	1e-40	2137870	zinc finger protein - mouse (fragment)	3e-23
1351	AF057734	Homo sapiens 17-beta-hydroxysteroid dehydrogenase IV (HSD17B4) gene, exon 16	1e-40	2842416	(AL008730) dJ487J7.1.1 (putative protein dJ487J7.1 isoform 1) [Homo sapiens]	6e-61
1352	AF070567	Homo sapiens clone 24544 beta-dystrobrevin mRNA, partial cds	4e-41	3133087	(Y15718) dystrobrevin B DTN-B2 [Homo sapiens]	7e-13
1353	AF006088	Homo sapiens Arp2/3 protein complex subunit p16-Arc (ARC16) mRNA, complete cds	2e-41	3121767	ARP2/3 COMPLEX 16 KD SUBUNIT	3e-36
1354	X69942	M.musculus mRNA of enhancer-trap-locus 1	6e-42	2291152	(AF016418) No definition line found [Caenorhabditis elegans]	6.4

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1355	X87838	H.sapiens mRNA for beta-catenin	5e-42	1373019	(U28811) cysteine-rich fibroblast growth factor receptor	8e-05
1356	AB018268	Homo sapiens mRNA for KIAA0725 protein, partial cds	5e-42	3882171	(AB018268) KIAA0725 protein [Homo sapiens]	2e-33
1357	M84424	Human cathepsin E (CTSE) gene, exon 9 and complete cds.	2e-42	<NONE>	<NONE>	<NONE>
1358	U80776	Human EST clone NIB1543 mariner transposon Hsmar1 orf gene, complete cds	2e-42	2231380	(U80776) ort; encodes putative chimeric protein with SET domain in N-terminus with similarity to several other human, Drosophila, nematode and yeast proteins [Homo sapiens]	3e-11
1359	U55184	Human G protein Golf alpha gene, exon 12 and complete cds	2e-42	3165531	(AF067608) No definition line found [Caenorhabditis elegans]	1e-16
1360	AC005190	Homo sapiens PAC clone DJ1152D16 from Xq23, complete sequence [Homo sapiens]	6e-43	2978255	(AB007407) myeloid zinc finger protein-2 [Mus musculus]	2.3
1361	AB018284	Homo sapiens mRNA for KIAA0741 protein, complete cds	5e-43	<NONE>	<NONE>	<NONE>
1362	AB011137	Homo sapiens mRNA for KIAA0565 protein, complete cds	5e-43	3043654	(AB011137) KIAA0565 protein [Homo sapiens]	1e-07
1363	M93651	Human set gene, complete cds.	2e-43	<NONE>	<NONE>	<NONE>
1364	Z47087	H.sapiens mRNA for RNA polymerase II elongation factor-like protein.	2e-43	1872514	(U84404) E6-associated protein E6-AP/ubiquitin-protein ligase [Homo sapiens] >gi 2361031 (AF016708) E6-AP ubiquitin-protein ligase [Homo sapiens]	7.2
1365	U27197	Drosophila melanogaster pelota (pelo) mRNA, complete cds	2e-43	1352736	PELOTA PROTEIN >gi 973224 (U27197) pelota [Drosophila melanogaster]	1e-46

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					RRP5 PROTEIN HOMOLOG	
1366	D80007	Human mRNA for KIAA0185 gene, partial cds	6e-44	2498864	(KIAA0185) hypothetical protein YM9959.11C of <i>S.cerevisiae</i> . [Homo sapiens]	6e-09
1367	AF005039	Homo sapiens secretory carrier membrane protein (SCAMP3) mRNA, complete cds	6e-44	2232243	(AF005039) secretory carrier membrane protein [Homo sapiens]	2e-09
1368	X68101	<i>R.norvegicus</i> trg mRNA	2e-44	550420	(X68101) trg gene product [Rattus norvegicus]	1e-37
1369	AF044206	Homo sapiens cyclooxygenase (COX-2) gene, promoter and exon 1	2e-45	2072953	(U93565) putative p150 [Homo sapiens]	5e-06
1370	L48708	Homo sapiens faciogenital dysplasia (FGD1) gene, 5' end of intron 17	8e-46	<NONE>	<NONE>	<NONE>
1371	X15822	Human COX VIIa-L mRNA for liver-specific cytochrome c oxidase (EC 1.9.3.1.)	3e-46	117121	CYTOCHROME C OXIDASE POLYPEPTIDE VIIA-LIVER PRECURSOR >gi 2144370 pir OSHU7L cytochrome-c oxidase (EC 1.9.3.1) chain VIIa precursor, hepatic - human >gi 30147 (X15822) precursor (AA -23 to 60) [Homo sapiens]	5e-13
1372	U47323	Mus musculus stromal cell protein mRNA, complete cds	3e-46	1493833	(U47323) stromal cell protein [Mus musculus]	1e-48
1373	AF059524	Homo sapiens reticulon gene family protein	7e-47	1731169	HYPOTHETICAL 113.1 KD PROTEIN T28D9.7 IN CHROMOSOME II >gi 861264 (U28738) coded for by <i>C. elegans</i> cDNA yk8h5.3; coded for by <i>C. elegans</i> cDNA yk8h5.5; similar to <i>C. elegans</i> deg-1 and mec-4 in exon 2 [Caenorhabditis elegans]	7.8
1374	AJ132583	Homo sapiens mRNA for puromycin sensitive aminopeptidase, partial	3e-47	1777519	(U39123) T cell receptor beta chain [Homo sapiens]	9.7

457

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1375	M97856	Homo sapiens histone binding protein mRNA, complete cds.	3e-47	2645327	(U83821) NADH dehydrogenase subunit 3 [Oryzomys palustris]	5.7
1376	U53220	Human retinoblastoma-related Rb2/p130 gene, 5' flanking region and partial cds	3e-47	2499225	CMP-SIALIC ACID TRANSPORTER CMP-sialic acid transporter [Cricetulus griseus]	5.3
1377	X87870	H.sapiens mRNA for hepatocyte nuclear factor 4a	1e-47	728832	!!!! ALU SUBFAMILY SB WARNING ENTRY	7.3
1378	AF060195	Mus musculus proteasome regulator PA28 beta subunit gene, complete cds	3e-48	478681	limb deformity protein - chicken	0.25
1379	AB018285	Homo sapiens mRNA for KIAA0742 protein, partial cds	1e-48	3122969	TESTIS SPECIFIC PROTEIN A (ZINC FINGER PROTEIN TSGA) >gi 281040 pir S28499 probable zinc finger protein - rat >gi 57504 (X59993) zinc finger protein	1e-30
1380	U35032	Human endogenous retrovirus clone c5.11, HERV-H multiply spliced subgenomic leader, protease and integrase region mRNA, partial cds	4e-49	88558	retroviral proteinase-like protein - human	6e-05
1381	AB007956	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487	1e-49	<NONE>	<NONE>	<NONE>
1382	D86987	Homo sapiens mRNA for KIAA0214 protein, complete cds	1e-49	2497944	ALPHA SCRUIIN >gi 633238 (Z38132) scruiin [Limulus polyphemus] >gi 1093326 prf 2103269A scrulin [Limulus sp.]	9.7
1383	U25826	Human transcription factor (SC1) gene, complete cds.	4e-50	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1384	U46690	Mus musculus ATP-dependent RNA helicase mRNA, partial cds.	4e-50	1335873	(U46690) ATP-dependent RNA helicase [Mus musculus]	3e-24
1385	AF072128	Mus musculus claudin-2 mRNA, complete cds	2e-50	3335184	(AF072128) claudin-2 [Mus musculus]	4e-24
1386	AF093593	Homo sapiens snRNA activating protein complex 19kDa subunit (SNAP19) mRNA, complete cds	1e-50	3668416	(AF093593) snRNA activating protein complex 19kDa subunit [Homo sapiens]	0.003
1387	U79745	Homo sapiens monocarboxylate transporter homologue MCT6 mRNA, complete cds	1e-50	1177607	(X92485) pva1 [Plasmodium vivax]	2e-07
1388	L09647	Rattus norvegicus hepatocyte nuclear factor 3a	1e-50	404764	(L10409) fork head related protein [Mus musculus]	2e-21
1389	X61506	Mouse E46 mRNA for E46 protein	4e-51	114909	BRAIN PROTEIN E46	1e-20
1390	M33387	Human debrisoquine 4-hydroxylase (CYP2D8P) and	1e-51	126296	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG protein [Nycticebus coucang]	5e-15
1391	AF019767	Homo sapiens zinc finger protein (ZPR1) mRNA, complete cds	4e-52	961507	(D63788) anchor protein, LCM	5.9
1392	Z37986	H.sapiens mRNA for phenylalkylamine binding protein.	2e-52	<NONE>	<NONE>	<NONE>
1393	U65416	Human MHC class I molecule (MICB) gene, complete cds	2e-52	3878637	(Z49128) weak similarity with SINR protein (Swiss Prot accession number P06533); cDNA EST EMBL:T00631 comes from this gene; cDNA EST yk293d10.5 comes from this gene [Caenorhabditis elegans]	8.7

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					beta-globin DNA-binding	
1394	Z57647	H.sapiens CpG DNA, clone 189a6. forward read cpg189a6.ft1a.	2e-52	111187	protein B1, transcription factor PU.1 - mouse >gi 200586 (M32370) PU.1 protein [Mus musculus] >gi 200972 (M38252) transcription factor Pu.1 [Mus musculus]	5.8
1395	L13738	Human activated p21cdc42Hs kinase (ack) mRNA, complete cds.	2e-52	2921447	(AF037260) non-receptor protein tyrosine kinase Ack [Mus musculus]	7e-23
1396	AF042379	Homo sapiens spindle pole body protein spc97 homolog GCP2 mRNA, complete cds	7e-53	2801701	(AF042379) spindle pole body protein spc97 homolog GCP2	1e-16
1397	AF047441	Homo sapiens RNA polymerase I 40kD subunit mRNA, complete cds	6e-53	3914807	DNA-DIRECTED RNA POLYMERASE I 40 KD POLYPEPTIDE (RPA40) (RPA39) >gi 2266929 (AF008442) RNA polymerase I subunit hRPA39 [Homo sapiens]	4e-19
1398	AF104670	Homo sapiens cell cycle protein (PA2G4) gene, exons 6 through 13, and complete cds	2e-53	<NONE>	<NONE>	<NONE>
1399	S60754	{ VNTR locus DXZ4, hypervariable tandem repeat cluster} [human, Genomic, 2991 nt] >:: gb L07935 HUMVNT RA Homo sapiens microsatellite VNTR DNA sequence.	2e-53	1209669	(U38810) CAGR1 [Homo sapiens] >gi 3098420 (AF040945) homeotic regulator homolog MAB21 [Mus musculus]	4.6
1400	D86972	Human mRNA for KIAA021S gene, complete cds	1e-53	3426041	(AC005168) unknown protein [Arabidopsis thaliana]	9.1

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1401	AJ236682	Homo sapiens chromosome 22 CpG island DNA, genomic MseI fragment, clone 22CGIB49E6, complete read	7e-54	3928721	(AL034355) putative cytochrome oxidase subunit I [Streptomyces coelicolor]	0.30
1402	AJ236682	Homo sapiens chromosome 22 CpG island DNA, genomic MseI fragment, clone 22CGIB49E6, complete read	6e-54	3928721	(AL034355) putative cytochrome oxidase subunit I [Streptomyces coelicolor]	0.28
1403	M37583	Human histone (H2A.Z) mRNA, complete cds.	6e-54	70711	histone H2A.F, embryonic - chicken	2e-16
1404	AJ009947	Homo sapiens mRNA for putative ATPase, partial	6e-54	3550295	(AJ009947) putative ATPase [Homo sapiens]	3e-18
1405	Y08459	B.taurus mRNA for novel cytoplasmic protein	2e-54	<NONE>	<NONE>	<NONE>
1406	AF042384	Homo sapiens BC-2 protein mRNA, complete cds	2e-54	2828147	(AF042384) BC-2 protein [Homo sapiens]	2e-14
1407	AF042379	Homo sapiens spindle pole body protein spc97 homolog GCP2 mRNA, complete cds	8e-55	2801701	(AF042379) spindle pole body protein spc97 homolog GCP2	2e-17
1408	AF005355	Oryctolagus cuniculus translation initiation factor eIF2C mRNA, complete cds	7e-55	3253159	(AF005355) translation initiation factor eIF2C	3e-53
1409	AF008442	Homo sapiens RNA polymerase I subunit hRPA39 mRNA, complete cds	3e-55	3335138	(AF047441) RNA polymerase I 40kD subunit [Homo sapiens]	3e-20
1410	AF047441	Homo sapiens RNA polymerase I 40kD subunit mRNA, complete cds	3e-55	3335138	(AF047441) RNA polymerase I 40kD subunit [Homo sapiens]	3e-20

461

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1411	X08004	Human mRNA for Rap1B protein > :: emb A08693 A08693 H.sapiens rap1b cDNA	2e-55	539995	transforming protein rap1b - rat (strain Copenhagen)	2e-18
1412	AF010403	Homo sapiens ALR mRNA, complete cds	2e-55	2358285	(AF010403) ALR [Homo sapiens]	1e-49
1413	M77016	Human tropomodulin mRNA, complete cds.	8e-56	262249	(S52010) orf1 5' of EpoR [mice, Peptide, 85 aa] [Mus sp.]	0.027
1414	AB020633	Homo sapiens mRNA for KIAA0826 protein, partial cds	2e-56	<NONE>	<NONE>	<NONE>
1415	X87489	H.sapiens genomic DNA (chromosome 3; clone NL1243D)	2e-56	1814029	(U84501) cuticle collagen [Caenorhabditis briggsae]	0.038
1416	AB007893	Homo sapiens KIAA0433 mRNA, partial cds	2e-56	2887437	(AB007893) KIAA0433 [Homo sapiens]	9e-21
1417	X78925	H.sapiens HZF2 mRNA for zinc finger protein	1e-56	3342002	(AF054180) hematopoietic cell derived zinc finger protein [Homo sapiens]	2e-21
1418	Z56281	H.sapiens mRNA for interferon regulatory factor 3	9e-57	2497442	INTERFERON REGULATORY FACTOR 3 factor 3 [Homo sapiens]	2e-21
1419	U78772	Homo sapiens nuclear VCP-like protein NVLP.1	8e-57	2406565	(U68140) nuclear VCP-like protein NVLP.2 [Homo sapiens]	5e-20
1420	D79994	Human mRNA for KIAA0172 gene, partial cds	3e-57	1136404	(D79994) similar to ankyrin of Chromatium vinosum. [Homo sapiens]	9e-38
1421	AB002342	Human mRNA for KIAA0344 gene, complete cds	1e-57	2224629	(AB002342) KIAA0344 [Homo sapiens]	4e-20
1422	L19437	Human transaldolase mRNA containing transposable element, complete cds	1e-57	1553119	(U63159) transaldolase [Mus musculus]	2e-20
1423	D17532	Human mRNA for RCK, complete cds	9e-58	129376	PROBABLE ATP-DEPENDENT RNA HELICASE P54 (ONCOGENE RCK) (DEAD BOX PROTEIN 6)	1e-10

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1424	X79568	H.sapiens BDP1 mRNA for protein-tyrosine-phosphatase	9e-58	1871531	(X79568) protein-tyrosine-phosphatase	1e-22
1425	X79568	H.sapiens BDP1 mRNA for protein-tyrosine-phosphatase	9e-58	1871531	(X79568) protein-tyrosine-phosphatase	9e-23
1426	AB012295	Homo sapiens HKE1.5 mRNA for GDS-related protein, complete cds	7e-58	2648021	(Z97184) RGL2 [Homo sapiens]	9e-19
1427	AF086040	Homo sapiens full length insert cDNA clone YX52E07	1e-58	543222	glutamine (Q)-rich factor 1, QRF-1 - mouse factor 1, QRF-1 [mice, B-cell leukemia, BCL1, Peptide Partial, 84 aa]	3e-36
1428	AB018195	Homo sapiens ca xi mRNA for carbonic anhydrase-related protein XI, complete cds	4e-59	<NONE>	<NONE>	<NONE>
1429	AF071777	Mus musculus IRE1 (Ire1) mRNA, complete cds	4e-59	3766209	(AF071777) IRE1 [Mus musculus]	7e-28
1430	AB000462	Homo sapiens mRNA for SH3 binding protein, complete cds, clone:RES4-23A	3e-59	<NONE>	<NONE>	<NONE>
1431	AF038172	Homo sapiens clone 23923 mRNA sequence	3e-59	3758855	(Z98551) MAL3P6.11 [Plasmodium falciparum]	1.3
1432	Z84812	Human DNA sequence from phage pTEL from a contig from the tip of the short arm of chromosome 16, spanning 2Mb of 16p13.3 Contains ESTs	1e-59	400927	RIBONUCLEOPROTEIN RB97D ribonucleoprotein [Drosophila melanogaster]	2.5
1433	U36484	Human laminin-binding protein gene, partial cds, and E2 small nucleolar RNA gene, complete sequence	1e-59	226005	protein 40kD [Mus musculus]	7e-05

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					DUAL SPECIFICITY	
1434	L11285	Homosapiens ERK activator kinase (MEK2) mRNA.	1e-59	2499630	MITOGEN-ACTIVATED PROTEIN KINASE KINASE 2 (MAP KINASE KINASE 2) (MAPKK 2) kinase type 2 [Gallus gallus]	3e-21
1435	AF086555	Homo sapiens full length insert cDNA clone ZE14E04	4e-60	3287674	(AC005239) F23149_1 [Homo sapiens]	2e-04
1436	M24766	Human (clone pHAIV2-12) alpha-2 collagen type IV	4e-60	29551	(X05610) alpha (2) chain. [Homo sapiens]	6e-15
1437	X65550	H.sapiens mki67a mRNA (long type) for antigen of monoclonal antibody Ki-67	4e-60	1170654	ANTIGEN KI-67 >gi 539555 pir A48666 cell proliferation antigen Ki-67, long form - human Ki-67 [Homo sapiens]	3e-15
1438	M27319	Human calmodulin mRNA. complete cds.	4e-60	1345451	(X05949) Calmodulin (AA 2 - 59) (449 is 1st base in codon) [Drosophila melanogaster]	7e-20
1439	Y12781	Homo sapiens mRNA for transducin (beta) like 1 protein	3e-60	62133	(X06172) put. 134 kD protein (AA 1 - 1187); put. replicase	7.4
1440	AB002383	Human mRNA for KIAA0385 gene. complete cds	1e-60	1001548	(D64000) hypothetical protein	4.4
1441	AF070614	Homo sapiens clone 24732 unknown mRNA. partial cds	2e-61	3283879	(AF070614) unknown [Homo sapiens]	3e-17
1442	AB002326	Human mRNA for KIAA0328 gene. partial cds	6e-62	547891	MICROTUBULE-ASSOCIATED PROTEIN 4 microtubule-associated protein-U [Bos taurus]	5.6
1443	AF086471	Homo sapiens full length insert cDNA clone ZD88A01	5e-62	<NONE>	<NONE>	<NONE>
1444	AB002311	Human mRNA for KIAA0313 gene. complete cds	2e-62	2506357	2,3-DIHYDROXYPHENYLPROPIONATE 1,2-DIOXYGENASE >gi 1657544 (U73857) similar to mcpl gene (catechol 2,3-dioxygenase) of A. eutrophus 3-(2,3-dihydroxyphenylpropionate)1, 2-dioxygenase 2,3-dihydroxyphenylpropionate 1,2-dioxygenase	3.4

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1445	AF069737	Xenopus laevis notchless (nle) mRNA, complete cds	2e-62	3687833	(AF069737) notchless [Xenopus laevis]	1e-55
1446	AF044209	Homo sapiens nuclear receptor co-repressor N-CoR mRNA, complete cds	5e-63	2137603	nuclear receptor co-repressor N-CoR - mouse musculus >gi 1583865 prf 2121436A thyroid hormone receptor co-repressor [Mus musculus]	2e-47
1447	M69238	Human aryl hydrocarbon receptor nuclear translocator (ARNT) mRNA, complete cds.	2e-63	2702319	(AF001307) aryl hydrocarbon receptor nuclear translocator; Arnt [Homo sapiens]	5e-19
1448	X80497	H.sapiens PHKLA mRNA	2e-63	1170685	PHOSPHORYLASE B KINASE ALPHA REGULATORY CHAIN, LIVER ISOFORM (PHOSPHORYLASE KINASE ALPHA L SUBUNIT) >gi 663010 (X80497) phosphorylase kinase phosphorylase kinase alpha subunit [Homo sapiens]	5e-22
1449	AF031141	Homo sapiens ubiquitin conjugating enzyme	2e-63	2623260	(AF031141) ubiquitin conjugating enzyme [Homo sapiens]	1e-23
1450	Z37166	H.sapiens BAT1 mRNA for nuclear RNA helicase	6e-64	2500529	PROBABLE ATP-DEPENDENT RNA HELICASE P47 >gi 2135840 pir I37201 nuclear RNA helicase (DEAD family) BAT1 - human >gi 587146 (Z37166) nuclear RNA helicase (DEAD family) [Homo sapiens]	9e-24
1451	M64240	Human helix-loop-helix zipper protein (max) mRNA, complete cds. >:: gb 141138 I41138 Sequence 1 from patent US 5624818 >:: gb 177062 I77062 Sequence 1 from patent US 5693487	5e-64	88175	Myc-binding factor Max, short form - human	8e-22

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1452	M98252	Homo sapiens lysyl hydroxylase (partial clone 2.2 Kb LH) RNA, complete mature peptide.	2e-64	400205	PROCOLLAGEN-LYSINE 2-OXOGLUTARATE 5-DIOXYGENASE PRECURSOR (LYSYL HYDROXYLASE) lysyl hydroxylase [Homo sapiens]	7e-22
1453	U09550	Human oviductal glycoprotein mRNA, complete cds.	8e-65	2493676	OVIDUCT-SPECIFIC GLYCOPROTEIN PRECURSOR (OVIDUCTAL GLYCOPROTEIN) (OVIDUCTIN)	2e-11
1454	X67877	R.norvegicus mRNA for cytosolic resiniferatoxin-binding protein	7e-65	423664	resiniferatoxin-binding protein RBP-26, cytosolic - rat >gi 311660 (X67877) cytosolic resiniferatoxin binding protein RBP-26 [Rattus norvegicus] >gi 1093373 prf 2103310A resiniferatoxin-binding protein [Rattus norvegicus]	2e-40
1455	AB018254	Homo sapiens mRNA for KIAA0711 protein, complete cds	6e-65	92298	glutamine/glutamic acid-rich protein	0.98
1456	J03607	Human 40-kDa keratin intermediate filament precursor gene.	3e-65	1070608	keratin 19, type I, cytoskeletal - human sapiens]	4e-07
1457	U65896	Human gamma-glutamyl carboxylase gene, complete cds	2e-65	<NONE>	<NONE>	<NONE>
1458	U07681	Human NAD(H)-specific isocitrate dehydrogenase alpha subunit precursor mRNA, complete cds.	2e-65	1708399	ISOCITRATE DEHYDROGENASE (NAD), MITOCHONDRIAL SUBUNIT ALPHA PRECURSOR (ISOCITRIC DEHYDROGENASE) (NAD+-SPECIFIC ICDH) dehydrogenase alpha chain precursor - human >gi 706839 subunit precursor [Homo sapiens]	4e-26
1459	U88080	Human zinc finger protein (LD5-1) gene, exons 4, 5 and 6, and complete cds	2e-65	1373394	(U57796) zinc finger protein [Homo sapiens] >gi 2306773	2e-39

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					tensin - chicken (fragment)	
1460	M96625	Gallus domesticus tensin mRNA sequence.	3e-66	2134419	>gi 63805 (Z18529) tensin [Gallus gallus] >gi 212755 (L06662) tensin [Gallus gallus]	1e-51
1461	U13262	Mus musculus myelin gene expression factor (MEF-2) mRNA, partial cds.	1e-70	536926	(U13262) myelin gene expression factor [Mus musculus]	9e-42
1462	U64033	Mus musculus Tera (Tera) mRNA, complete cds	5e-72	1575505	(U64033) Tera [Mus musculus]	9e-34
1463	X78989	M.musculus mRNA for testin	6e-74	1351218	TESTIN 2 (TES2) [CONTAINS: TESTIN 1]	8e-31
1464	U64033	Mus musculus Tera (Tera) mRNA, complete cds	2e-74	1575505	(U64033) Tera [Mus musculus]	5e-37
1465	AF057365	Canis familiaris UDP N-acetylglucosamine transporter mRNA, complete cds	9e-79	3298605	(AF057365) UDP N-acetylglucosamine transporter [Canis familiaris]	9e-10
1466	AJ006064	Rattus norvegicus mRNA for coronin-like protein	1e-82	3757680	(AJ006064) coronin-like protein [Rattus norvegicus]	3e-62
1467	U91582	Macaca fascicularis UDP-glucuronosyltransferase mRNA, complete cds	4e-89	140396	KARYOGAMY PROTEIN KAR4 yeast (Saccharomyces cerevisiae)	1e-08
1468	X06762	Mouse Hox2.3 mRNA	3e-92	123255	HOMEODOMAIN PROTEIN HOXB7 (HOX-2C)	9e-23
1469	AB016930	Cricetus griseus mRNA for Phosphatidylglycerophosphate synthase, complete cds	5e-94	4159682	(AB016930) Phosphatidylglycerophosphate synthase [Cricetus griseus]	7e-34
1470	X74504	M.musculus T10 mRNA	7e-97	1711658	SER/THR-RICH PROTEIN T10 IN DGCR REGION >gi 480900 pir S37488 gene T10 protein - mouse	3e-59

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1471	U13175	Rattus norvegicus clone ubc10a ubiquitin conjugating enzyme (E217kB) mRNA, complete cds.	3e-98	1351345	UBIQUITIN-CONJUGATING ENZYME E2-17 KD 3 (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (E2(17)KB 3) >gi 1085588 pir S53358 ubiquitin conjugating enzyme (E217kB) - rat >gi 595666 (U13175) ubiquitin conjugating enzyme [Rattus norvegicus] norvegicus] >gi 1145691 (U39318) UbcH5C [Homo sapiens]	5e-05
1472	S79873	h-lamp-2=lysosome-associated membrane protein-2 protein-2b (LAMP2) mRNA, alternatively spliced form h-lamp-2b, complete cds.	e-119	<NONE>	<NONE>	<NONE>
1473	D13623	Rat mRNA for p34 protein, complete cds	e-112	480379	ribosome-binding protein p34 - rat sp.]	2e-05
1474	AB013357	Mus musculus mRNA for 49 kDa zinc finger protein, complete cds	e-136	4153886	(AB013357) 49 kDa zinc finger protein	5e-08
1475	AB016930	Cricetus griseus mRNA for Phosphatidylglycerophosphate synthase, complete cds	e-117	4159682	(AB016930) Phosphatidylglycerophosphate synthase [Cricetus griseus]	4e-32
1476	U38253	Rattus norvegicus initiation factor eIF-2B gamma subunit (eIF-2B gamma) mRNA, complete cds	e-103	2494312	TRANSLATION INITIATION FACTOR EIF-2B GAMMA SUBUNIT (EIF-2B GDP-GTP EXCHANGE FACTOR) subunit [Rattus norvegicus]	3e-42

468

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1477	X73683	R.norvegicus mRNA for histone H3.3	e-117	122075	histone H3.3 (H3.3) (H3.3Q) histone H3.3 - fruit fly (Drosophila melanogaster) histone H3.3B - chicken >gi 2119023 pir S61218 histone H3.3 - fruit fly (Drosophila hydei) 1-136 [Oryctolagus cuniculus] >gi 8046 (X53822) Histone H3.3Q gene product [Drosophila melanogaster] >gi 51198 gallus] >gi 161190 (M17876) histone H3 [Spisula solidissima] >gi 211853 (M11393) histone 3.3 [Gallus gallus] >gi 306848 (M11354) H3.3 histone [Homo sapiens melanogaster] >gi 963031 (X81205) histone H3.3 H3.3A variant [Drosophila melanogaster] musculus]	1e-45
1478	U32498	Rattus norvegicus rsec8 mRNA, partial cds	e-108	2143962	rsec8 - rat (fragment) >gi 1019441 (U32498) rsec8 [Rattus norvegicus]	7e-48
1479	U41736	Mus musculus ancient ubiquitous 46 kDa protein AUP1 precursor (Aup1) mRNA, complete cds	e-146	1517822	(U41736) ancient ubiquitous 46 kDa protein AUP46 precursor [Mus musculus]	5e-49
1480	AF041338	Bos taurus vacuolar proton pump subunit SFD alpha isoform (SFD) mRNA, complete cds	e-119	2895578	(AF041338) vacuolar proton pump subunit SFD alpha isoform [Bos taurus]	3e-49
1481	AF064553	Mus musculus NSD1 protein mRNA, complete cds	e-121	3329465	(AF064553) NSD1 protein [Mus musculus]	2e-50
1482	AB000517	Rattus sp. mRNA for CDP-diacylglycerol synthase, complete cds	e-146	1517822	(U41736) ancient ubiquitous 46 kDa protein AUP46 precursor [Mus musculus]	2e-51
1483	D38517	Mouse mRNA for Dhml protein, complete cds	e-118	2137562	mouse Dhml protein - mouse musculus]	6e-54

469

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1484	X54352	M.domesticus MD6 mRNA	e-139	1085499	CDC4 repeat unit-containing protein - mouse	1e-55
1485	U57692	Mus musculus N-terminal asparagine amidohydrolase (Ntan1) mRNA, complete cds	e-118	2498797	PROTEIN N-TERMINAL ASPARAGINE AMIDOHYDROLASE (PROTEIN NH2-TERMINAL ASPARAGINE DEAMIDASE) (NTN-AMIDASE) (PNAD) (PROTEIN NH2-TERMINAL ASPARAGINE AMIDOHYDROLASE) (PNA) >gi 1373365 (U57691) N-terminal asparagine amidohydrolase [Mus musculus] amidohydrolase [Mus musculus]	5e-57
1486	X80169	M.musculus mRNA for 200 kD protein	e-119	1717793	PROTEIN TSG24 (MEIOTIC CHECK POINT REGULATOR) >gi 1083553 pir A55117 tsg24	9e-58
1487	U57692	Mus musculus N-terminal asparagine amidohydrolase (Ntan1) mRNA, complete cds	e-120	2498797	PROTEIN N-TERMINAL ASPARAGINE AMIDOHYDROLASE (PROTEIN NH2-TERMINAL ASPARAGINE DEAMIDASE) (NTN-AMIDASE) (PNAD) (PROTEIN NH2-TERMINAL ASPARAGINE AMIDOHYDROLASE) (PNA) >gi 1373365 (U57691) N-terminal asparagine amidohydrolase [Mus musculus] amidohydrolase [Mus musculus]	8e-58
1488	U08215	Mus musculus Hsp70-related NST-1 (hsr.1) mRNA, complete cds.	e-109	473407	(U08215) NST-1 [Mus musculus]	7e-58
1489	D85926	Mouse mRNA for Ray, complete cds	e-110	1944389	(D85926) Ray [Mus musculus] (L20427)	2e-58
1490	L20427	Rattus norvegicus dihydroxypolyprenylbenzoate methyltransferase mRNA, complete cds	e-123	457372	dihydroxypolyprenylbenzoate methyltransferase [Rattus norvegicus]	4e-59
1491	X56044	M.musculus mRNA for protein Htf9C	e-121	3183977	(X56044) protein Htf9C [Mus musculus]	1e-60

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					PROTO-ONCOGENE	
1492	S74774	p59fyn(T)=OKT3-induced calcium influx regulator	e-163	729896	TYROSINE-PROTEIN KINASE FYN (P59-FYN) >gi 420217 pir A44991 protein-tyrosine kinase (EC 2.7.1.112) fyn - mouse	8e-63
1493	U88873	Mus musculus BUB2-like protein 1 (HBLP1) mRNA, complete cds	e-123	4099611	(U88873) BUB2-like protein 1 [Mus musculus]	1e-63
1494	U48852	Cricetulus griseus HT protein mRNA, complete cds.	e-117	1216486	(U48852) HT protein [Cricetulus griseus]	7e-64
1495	AF032667	Rattus norvegicus rexo70 mRNA, complete cds	e-142	2827160	(AF032667) rexo70 [Rattus norvegicus]	5e-66
1496	M62722	Chinese hamster phosphatidylserine decarboxylase mRNA, 3' end.	e-114	118910	PHOSPHATIDYLSERINE DECARBOXYLASE PROENZYME >gi 109423 pir A38732 phosphatidylserine decarboxylase (EC 4.1.1.65) - Chinese hamster (fragment)	2e-67
1497	AF072758	Mus musculus fatty acid transport protein 3 mRNA, partial cds	e-130	3335567	(AF072758) fatty acid transport protein 3; FATP3 [Mus musculus]	1e-67
1498	AB005549	Rattus norvegicus mRNA for atypical PKC specific binding protein, complete cds	e-113	3868778	(AB005549) atypical PKC specific binding protein [Rattus norvegicus]	2e-69
1499	U57344	Mus musculus homeobox protein Meis3 mRNA, complete cds	e-143	3024124	HOMEBOX PROTEIN MEIS3	6e-72
1500	U09874	Mus musculus SKD3 mRNA, complete cds.	e-142	2493735	SKD3 PROTEIN SKD3 [Mus musculus]	1e-72
1501	U72194	Mus musculus muskelin mRNA, complete cds	e-148	3493462	(U72194) muskelin [Mus musculus]	2e-74
1502	XS0169	M.musculus mRNA for 200 kD protein	e-155	1717793	PROTEIN TSG24 (MEIOTIC CHECK POINT REGULATOR) >gi 1083553 pir A55117 tsg24	3e-77

Nearest Neighbor (BlastN vs. Genbank)				Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Mus musculus				
1503	U72194	muskelin mRNA, complete cds	e-154	3493462	(U72194) muskelin [Mus musculus]	2e-78
1504	Y12836	Cricetulus griseus mRNA for Zn finger factor	e-146	3150148	(Y12836) Zn finger factor [Cricetulus griseus]	3e-83

Table 5

SEQ ID	Start	Stop	Score	Direction	Description
29	295	421	5872	For	mkk like kinases
30	31	182	3943	For	Basic region plus leucine zipper transcription factors
31	298	397	5625	For	mkk like kinases
186	175	395	7660	For	SH2 Domain
187	358	432	4320	For	Ank repeat
196	37	322	6049	For	mkk like kinases
234	23	121	4607	For	SH3 Domain
308	110	172	4150	For	Zinc finger, C2H2 type
410	42	191	4036	For	Basic region plus leucine zipper transcription factors
431	71	428	5538	Rev	ATPases Associated with Various Cellular Activities
552	116	288	3930	Rev	Basic region plus leucine zipper transcription factors
639	157	561	5797	For	ATPases Associated with Various Cellular Activities
746	209	427	5379	For	Fibronectin type III domain
768	116	288	3930	For	Basic region plus leucine zipper transcription factors
807	339	392	3620	For	Zinc finger, C2H2 type
820	341	406	2930	Rev	EF-hand
822	108	262	4179	For	Basic region plus leucine zipper transcription factors
836	158	353	4430	For	Basic region plus leucine zipper transcription factors
1157	41	444	5279	Rev	protein kinase
1192	186	416	5469	For	Fibronectin type III domain
1268	238	315	3540	For	Ank repeat
1269	79	240	11640	For	LIM domain containing proteins
1288	73	234	3953	For	Basic region plus leucine zipper transcription factors

SEQ ID	Start	Stop	Score	Direction	Description
1309	248	404	8226	for	LIM domain containing proteins
1324	294	356	4690	for	Zinc finger, C2H2 type
1325	1	234	8981	for	C2 domain (prot. kinase C like)
1336	66	164	6390	for	WD domain, G-beta repeats
1360	222	377	8686	for	LIM domain containing proteins
1365	69	257	5221	for	Basic region plus leucine zipper transcription factors
1380	42	140	7130	for	WD domain, G-beta repeats
1386	243	398	8736	for	LIM domain containing proteins
1410	222	350	10553	for	Trypsin
1417	8	354	6073	for	Protein Tyrosine Phosphatase
1454	49	209	3996	for	Basic region plus leucine zipper transcription factors
1464	4	180	4978	for	RNA recognition motif. (aka RRM, RBD, or RNP domain)
1478	54	437	5176	for	protein kinase
1496	241	520	3929	for	Helicases conserved C-terminal domain
1496	40	612	5187	for	protein kinase
1503	154	216	4870	for	Zinc finger, C2H2 type
1514	2	252	4662	for	RNA recognition motif. (aka RRM, RBD, or RNP domain)
1527	156	212	3520	for	Zinc finger, C2H2 type
1538	9	635	11087	for	wnt family of developmental signaling proteins
1540	289	471	4107	for	Basic region plus leucine zipper transcription factors
1549	200	391	4118	for	Basic region plus leucine zipper transcription factors
1556	163	354	3958	for	Basic region plus leucine zipper transcription factors
1557	207	398	4038	for	Basic region plus leucine zipper transcription factors
1563	107	298	3978	for	Basic region plus leucine zipper transcription factors

SEQ ID	Start	Stop	Score	Direction	Description
1622	180	365	4022	for	Basic region plus leucine zipper transcription factors
1630	100	291	3998	for	Basic region plus leucine zipper transcription factors
1674	196	258	4880	for	Zinc finger, C2H2 type
1676	9	86	6610	for	Homeobox Domain
1677	316	369	5780	rev	Thioredoxins
1688	109	410	17414	for	Ras family
1704	184	372	3977	for	Basic region plus leucine zipper transcription factors
1707	92	439	24100	rev	Phosphatidylinositol-specific phospholipase C, Y domain
1711	263	361	6400	for	WD domain, G-beta repeats
1744	238	433	10572	rev	Serine carboxypeptidases
1755	281	367	2580	for	EF-hand
1762	236	334	5880	for	WD domain, G-beta repeats
1779	64	126	4790	for	Zinc finger, C2H2 type
1801	295	351	4030	for	Zinc finger, C2H2 type
1804	301	378	3460	for	Ank repeat
1808	36	161	4170	for	Basic region plus leucine zipper transcription factors
1811	184	315	8390	for	N-terminal homology in Ets domain
1814	127	294	10770	for	Bromodomain (conserved sequence found in human, Drosophila and yeast proteins.)
1818	9	146	4741	for	Double-stranded RNA binding motif
1819	278	355	3460	for	Ank repeat
1820	123	299	12150	for	Homeobox Domain
1821	127	303	12180	for	Homeobox Domain
1830	184	267	4270	for	Ank repeat
1832	18	173	8987	for	SH3 Domain
1835	51	206	8987	for	SH3 Domain
1839	224	307	4270	for	Ank repeat
1846	12	398	36700	for	G-protein alpha subunit

SEQ ID	Start	Stop	Score	Direction	Description
1909	160	258	6370	for	WD domain, G-beta repeats
1911	35	151	9335	for	Zinc finger, C3HC4 type (RING finger)
1980	60	197	7917	for	Zinc finger, C3HC4 type (RING finger)
2065	253	306	5410	for	Zinc finger, CCHC class
2135	2	401	10596	for	ATPases Associated with Various Cellular Activities
2216	90	179	5380	for	WW/rsp5/WWP domain containing proteins
2218	127	225	5500	for	WD domain, G-beta repeats
2281	20	387	6044	for	Protein Tyrosine Phosphatase
2282	183	353	5136	for	C2 domain (prot. kinase C like)
2286	12	382	5228	for	protein kinase
2310	20	371	5962	for	Protein Tyrosine Phosphatase
2363	48	211	4132	for	Basic region plus leucine zipper transcription factors
2424	43	194	3996	for	Basic region plus leucine zipper transcription factors
2428	25	350	4675	for	Dual specificity phosphatase, catalytic domain
2562	18	101	4560	for	Ank repeat
2577	0	311	10295	for	4 transmembrane segments integral membrane proteins
2591	60	165	4560	for	SH2 Domain
2684	9	461	5759	for	ATPases Associated with Various Cellular Activities
2826	116	400	16107	for	DEAD and DEAH box helicases
2859	100	320	5550	rev	ATPases Associated with Various Cellular Activities
2871	198	392	9384	for	DEAD and DEAH box helicases
2944	18	281	10480	for	Calpain large subunit, domain III
2969	5	387	5976	rev	protein kinase
3015	131	214	3600	for	Ank repeat
3047	191	292	5295	for	WD domain, G-beta repeats
3081	190	252	4360	for	Zinc finger, C2H2 type
3108	275	367	5791	for	WD domain, G-beta repeats
3147	190	369	4022	for	Basic region plus leucine zipper transcription factors
3152	129	320	3947	for	Basic region plus leucine zipper transcription factors
3158	167	334	4180	for	Basic region plus leucine zipper transcription factors
3175	14	164	5951	for	mkk like kinases

SEQ ID	Start	Stop	Score	Direction	Description
3175	8	112	5968	for	protein kinase
3178	45	386	19398	for	ATPases Associated with Various Cellular Activities
3183	14	215	9133	for	4 transmembrane segments integral membrane proteins
3190	229	390	6089	for	mkk like kinases
3190	118	390	8063	for	protein kinase
3193	293	355	3570	for	Zinc finger, C2H2 type
3195	0	215	10146	for	4 transmembrane segments integral membrane proteins
3197	281	343	4490	for	Zinc finger, C2H2 type
3208	34	256	4190	for	Basic region plus leucine zipper transcription factors
3258	138	394	9877	for	Ras family
3266	8	139	9328	for	ATPases Associated with Various Cellular Activities
3267	97	180	3820	for	Ank repeat
3274	11	187	15442	for	Fork head domain, eukaryotic transcription factors
3281	15	182	9681	for	mkk like kinases
3285	16	102	4680	for	EF-hand
3292	208	300	5585	for	WD domain, G-beta repeats
3297	7	153	6100	for	Helicases conserved C-terminal domain
3306	161	223	4900	for	Zinc finger, C2H2 type
3307	43	321	8740	for	SH2 Domain
3339	94	342	14970	for	SH2 Domain
3345	65	271	12512	for	PDZ domain
3351	124	270	6068	for	Phorbol esters/diacylglycerol binding

Example 4

DIFFERENTIAL EXPRESSION OF POLYNUCLEOTIDES OF THE INVENTION:
DESCRIPTION OF LIBRARIES AND DETECTION OF DIFFERENTIAL EXPRESSION

- 5 The relative expression levels of the polynucleotides of the invention was assessed in several libraries prepared from various sources, including cell lines and patient tissue samples. Table 6 provides a summary of these libraries, including the shortened library name (used hereafter), the mRNA source used to prepare the cDNA library, the abbreviated name of the library that is used in the tables below (in quotes),
10 and the approximate number of clones in the library.

Table 6
Description of cDNA Libraries

Library (lib #)	Description	Number of Clones in this Clustering
1	Km12 L4 Human Colon Cell Line, High Metastatic Potential (derived from Km12C) "High Colon"	307133
2	Km12C Human Colon Cell Line, Low Metastatic Potential "Low Colon"	284755
3	MDA-MB-231 Human Breast Cancer Cell Line, High Metastatic Potential; micro-metastases in lung "High Breast"	326937
4	MCF7 Human Breast Cancer Cell, Non Metastatic "Low Breast"	318979
8	MV-522 Human Lung Cancer Cell Line, High Metastatic Potential "High Lung"	223620
9	UCP-3 Human Lung Cancer Cell Line, Low Metastatic Potential "Low Lung"	312503

Library (lib #)	Description	Number of Clones in this Clustering
12	Human microvascular endothelial cells (HMEC) – Untreated PCR (OligodT) cDNA library	41938
13	Human microvascular endothelial cells (HMEC) – Basic fibroblast growth factor (bFGF) treated PCR (OligodT) cDNA library	42100
14	Human microvascular endothelial cells (HMEC) – Vascular endothelial growth factor (VEGF) treated PCR (OligodT) cDNA library	42825
15	Normal Colon – UC#2 Patient PCR (OligodT) cDNA library “Normal Colon Tumor Tissue”	34285
16	Colon Tumor – UC#2 Patient PCR (OligodT) cDNA library “Normal Colon Tumor Tissue”	35625
17	Liver Metastasis from Colon Tumor of UC#2 Patient PCR (OligodT) cDNA library “High Colon Metastasis Tissue”	36984
18	Normal Colon – UC#3 Patient PCR (OligodT) cDNA library “Normal Colon Tumor Tissue”	36216
19	Colon Tumor – UC#3 Patient PCR (OligodT) cDNA library “High Colon Tumor Tissue”	41388
20	Liver Metastasis from Colon Tumor of UC#3 Patient PCR (OligodT) cDNA library “High Colon Metastasis Tissue”	30956
21	G RRpz Human Prostate Cell Line	164801
22	WOca Human Prostate Cancer Cell Line	162088

The KM12L4 and KM12C cell lines are described in Example 1 above. The MDA-MB-231 cell line was originally isolated from pleural effusions (Cailleau, *J. Natl. Cancer. Inst.* (1974) 53:661), is of high metastatic potential, and forms poorly differentiated adenocarcinoma grade II in nude mice consistent with breast carcinoma.

The MCF7 cell line was derived from a pleural effusion of a breast adenocarcinoma and is non-metastatic. The MV-522 cell line is derived from a human lung carcinoma and is of high metastatic potential. The UCP-3 cell line is a low metastatic human lung carcinoma cell line; the MV-522 is a high metastatic variant of UCP-3. These cell lines are well-recognized in the art as models for the study of human breast and lung cancer (see, e.g., Chandrasekaran et al., *Cancer Res.* (1979) 39:870 (MDA-MB-231 and MCF-7); Gastpar et al., *J Med Chem* (1998) 41:4965 (MDA-MB-231 and MCF-7); Ranson et al., *Br J Cancer* (1998) 77:1586 (MDA-MB-231 and MCF-7); Kuang et al., *Nucleic Acids Res* (1998) 26:1116 (MDA-MB-231 and MCF-7); Varki et al., *Int J Cancer* (1987) 40:46 (UCP-3); Varki et al., *Tumour Biol.* (1990) 11:327; (MV-522 and UCP-3); Varki et al., *Anticancer Res.* (1990) 10:637; (MV-522); Kelner et al., *Anticancer Res* (1995) 15:867 (MV-522); and Zhang et al., *Anticancer Drugs* (1997) 8:696 (MV522)). The samples of libraries 15-20 are derived from two different patients (UC#2, and UC#3). The bFGF-treated HMEC were prepared by incubation with bFGF at 10ng/ml for 2 hrs; the VEGF-treated HMEC were prepared by incubation with 20ng/ml VEGF for 2 hrs. Following incubation with the respective growth factor, the cells were washed and lysis buffer added for RNA preparation. The GRRpz cell line refers to low passage (3 passages or fewer) human prostate cells, and the WOca cell line refers to low passage (3 passages or fewer) human prostate cancer cells.

Each of the libraries is composed of a collection of cDNA clones that in turn are representative of the mRNAs expressed in the indicated mRNA source. In order to facilitate the analysis of the millions of sequences in each library, the sequences were assigned to clusters. The concept of "cluster of clones" is derived from a sorting/grouping of cDNA clones based on their hybridization pattern to a panel of roughly 300 7bp oligonucleotide probes (see Drmanac et al., *Genomics* (1996) 37(1):29). Random cDNA clones from a tissue library are hybridized at moderate stringency to 300 7bp oligonucleotides. Each oligonucleotide has some measure of specific hybridization to that specific clone. The combination of 300 of these measures of hybridization for 300 probes equals the "hybridization signature" for a specific clone. Clones with similar sequence will have similar hybridization signatures. By developing a sorting/grouping algorithm to analyze these signatures, groups of clones in a library can be identified and brought together computationally. These groups of clones are termed "clusters". Depending on the stringency of the selection in the algorithm (similar to the stringency of hybridization in a classic library cDNA screening protocol), the "purity" of each cluster can be controlled. For example, artifacts of clustering may

occur in computational clustering just as artifacts can occur in "wet-lab" screening of a cDNA library with 400 bp cDNA fragments, at even the highest stringency. The stringency used in the implementation of cluster herein provides groups of clones that are in general from the same cDNA or closely related cDNAs. Closely related clones
5 can be a result of different length clones of the same cDNA, closely related clones from highly related gene families, or splice variants of the same cDNA.

Differential expression for a selected cluster was assessed by first determining the number of cDNA clones corresponding to the selected cluster in the first library (Clones in 1st), and the determining the number of cDNA clones
10 corresponding to the selected cluster in the second library (Clones in 2nd). Differential expression of the selected cluster in the first library relative to the second library is expressed as a "ratio" of percent expression between the two libraries. In general, the "ratio" is calculated by: 1) calculating the percent expression of the selected cluster in the first library by dividing the number of clones corresponding to a selected cluster in
15 the first library by the total number of clones analyzed from the first library; 2) calculating the percent expression of the selected cluster in the second library by dividing the number of clones corresponding to a selected cluster in a second library by the total number of clones analyzed from the second library; 3) dividing the calculated percent expression from the first library by the calculated percent expression from the
20 second library. If the "number of clones" corresponding to a selected cluster in a library is zero, the value is set at 1 to aid in calculation. The formula used in calculating the ratio takes into account the "depth" of each of the libraries being compared, *i.e.*, the total number of clones analyzed in each library.

In general, a polynucleotide is said to be significantly differentially
25 expressed between two samples when the ratio value is greater than at least about 2, preferably greater than at least about 3, more preferably greater than at least about 5, where the ratio value is calculated using the method described above. The significance of differential expression is determined using a z score test (Zar, Biostatistical Analysis, Prentice Hall, Inc., USA, "Differences between Proportions," pp 296-298 (1974)).

EXAMPLE 5

POLYNUCLEOTIDES DIFFERENTIALLY EXPRESSED IN HIGH METASTATIC POTENTIAL
BREAST CANCER CELLS VERSUS LOW METASTATIC BREAST CANCER CELLS

5 A number of polynucleotide sequences have been identified that are
differentially expressed between cells derived from high metastatic potential breast
cancer tissue and low metastatic breast cancer cells. Expression of these sequences in
breast cancer can be valuable in determining diagnostic, prognostic and/or treatment
information. For example, sequences that are highly expressed in the high metastatic
10 potential cells can be indicative of increased expression of genes or regulatory
sequences involved in the metastatic process. A patient sample displaying an increased
level of one or more of these polynucleotides may thus warrant more aggressive
treatment. In another example, sequences that display higher expression in the low
metastatic potential cells can be associated with genes or regulatory sequences that
15 inhibit metastasis, and thus the expression of these polynucleotides in a sample may
warrant a more positive prognosis than the gross pathology would suggest.

The differential expression of these polynucleotides can be used as a
diagnostic marker, a prognostic marker, for risk assessment, patient treatment and the
like. These polynucleotide sequences can also be used in combination with other
20 known molecular and/or biochemical markers.

The following tables summarize polynucleotides that are differentially
expressed between high metastatic potential breast cancer cells and low metastatic
potential breast cancer cells.

Table 7

25 Differentially expressed polynucleotides: Higher expression in
high metastatic potential breast cancer (lib3) relative to low metastatic
breast cancer cells (lib4)

SEQ ID NOs:	Lib3 clones	Lib4 clones	lib3/lib4
472	64	0	62
1851	6	0	6
1856	8	0	8
1867	6	0	6
1872	6	0	6
1875	12	3	4
1923	89	22	4

482

SEQ ID NOs:	Lib3 clones	Lib4 clones	lib3/lib4
2118	7	0	7
2119	7	0	7
2135	37	13	3
2190	19	0	19
2193	16	5	3
2232	12	2	6
2239	6	0	6
2338	21	2	10
2378	16	4	4
2394	6	0	6
2395	6	0	6
2490	13	3	4
2505	16	2	8
2540	8	1	8
2542	11	1	11
2607	11	2	5
2640	22	5	4
2674	8	0	8
2679	19	0	19
2684	14	4	3
2707	8	0	8
2724	9	0	9
2757	6	0	6
2776	10	0	10
2804	13	2	6
2818	6	0	6
2906	14	0	14
2959	26	8	3
2964	17	4	4
2968	6	0	6
2977	22	3	7
2980	13	1	13
3010	6	0	6
3043	10	1	10
3071	33	12	3
3072	9	1	9
3095	19	3	6
3097	11	2	5
3173	12	2	6
3203	8	1	8
3210	27	8	3

483

SEQ ID NOs:	Lib3 clones	Lib4 clones	lib3/lib4
3212	13	1	13
3284	8	0	8
3288	6	0	6
3331	14	3	5
3335	13	1	13

Table 8

Differentially expressed polynucleotides: Higher expression in low metastatic breast cancer cells (lib4) relative to high metastatic potential breast cancer (lib3)

5

SEQ ID NOs:	Lib 3 Clones	Lib 4 Clones	lib4/lib3
402	0	6	6
614	3	21	7
624	0	6	6
626	0	8	8
712	0	9	9
744	0	7	7
1325	2	29	15
1452	2	13	7
1880	0	9	9
1915	0	7	7
1951	0	6	6
1955	8	32	4
2015	0	7	7
2046	0	7	7
2076	1	22	23
2087	0	6	6
2124	0	9	9
2145	0	8	8
2162	0	6	6
2163	0	12	12
2164	5	19	4
2172	2	15	8
2192	5	16	3
2244	20	43	2
2266	3	18	6
2313	24	56	2
2346	1	13	13

484

SEQ ID NOs:	Lib 3 Clones	Lib 4 Clones	lib4/lib3
2355	0	10	10
2371	0	6	6
2393	1	17	17
2404	1	21	22
2443	0	6	6
2460	0	11	11
2523	0	6	6
2575	1	10	10
2578	0	6	6
2584	1	17	17
2590	0	6	6
2609	1	9	9
2632	5	24	5
2714	5	24	5
2728	0	6	6
2752	1	14	14
2794	4	15	4
2826	0	7	7
2987	5	15	3
3005	1	14	14
3009	20	58	3
3047	4	17	4
3057	2	17	9
3075	2	11	6
3076	0	6	6
3102	0	6	6
3128	15	52	4
3132	15	52	4
3142	0	6	6
3187	22	49	2
3253	23	96	4
3282	19	46	2
3285	20	40	2
3346	0	9	9

485

EXAMPLE 6

POLYNUCLEOTIDES DIFFERENTIALLY EXPRESSED IN HIGH METASTATIC POTENTIAL LUNG
CANCER CELLS VERSUS LOW METASTATIC LUNG CANCER CELLS

5 A number of polynucleotide sequences have been identified that are
differentially expressed between cells derived from high metastatic potential lung
cancer cells and low metastatic lung cancer cells. Expression of these sequences in lung
cancer tissue can be valuable in determining diagnostic, prognostic and/or treatment
information. For example, sequences that are highly expressed in the high metastatic
10 potential cells can be indicative of increased expression of genes or regulatory
sequences involved in the metastatic process. A patient sample displaying an increased
level of one or more of these polynucleotides may thus warrant more aggressive
treatment. In another example, sequences that display higher expression in the low
metastatic potential cells can be associated with genes or regulatory sequences that
15 inhibit metastasis, and thus the expression of these polynucleotides in a sample may
warrant a more positive prognosis than the gross pathology would suggest.

 The differential expression of these polynucleotides can be used as a
diagnostic marker, a prognostic marker, for risk assessment, patient treatment and the
like. These polynucleotide sequences can also be used in combination with other
20 known molecular and/or biochemical markers.

 The following tables summarize polynucleotides that are differentially
expressed between high metastatic potential lung cancer cells and low metastatic
potential lung cancer cells:

Table 9

Differentially expressed polynucleotides: Higher expression in high metastatic potential lung cancer cells (lib8) relative to low metastatic lung cancer cells (lib9)

SEQ ID NO:	Lib8 clones	Lib9 clones	lib8/lib9
14	10	0	10
137	5	0	5
151	5	0	7
152	9	0	13
171	6	0	8
200	10	0	14
254	5	0	7
262	5	0	7
271	5	0	7
348	6	1	8
412	5	0	7
507	5	0	7
520	6	0	8
530	5	0	7
588	5	0	7
623	7	0	10
637	7	0	10
660	5	0	7
678	8	0	11
680	5	0	7
700	9	2	6
714	28	13	3
774	11	0	15
812	5	0	7
834	8	2	6
901	11	2	8
1168	5	0	7
1333	6	0	8
1352	5	0	7
1524	11	1	15
1706	5	0	7
1752	17	9	3
1768	20	4	7
1769	5	0	7
1780	6	0	8

SEQ ID NO:	Lib8 clones	Lib9 clones	lib8/lib9
1781	40	3	19
1799	6	1	8
1803	6	1	8
1811	16	9	2
1884	6	0	8
1919	8	1	11
1939	6	0	8
1975	43	9	7
2024	12	1	17
2045	8	1	11
2060	20	13	2
2071	16	4	6
2128	5	0	7
2177	10	2	7
2181	44	13	5
2184	11	1	15
2185	10	4	3
2283	7	0	10
2311	10	4	3
2314	10	0	14
2393	14	6	3
2398	6	1	8
2460	10	4	3
2514	6	0	8
2597	5	0	7
2657	8	2	6
2669	6	1	8
2670	6	1	8
3047	21	3	10
3050	16	5	4
3092	7	1	10
3140	181	119	2
3157	5	0	7
3187	16	5	4
3210	5	0	7
3220	28	4	10
3236	7	1	10
3249	16	0	22
3264	8	2	6
3305	7	0	10
3309	20	0	28

SEQ ID NO:	Lib8 clones	Lib9 clones	lib8/lib9
3318	24	4	8
3330	5	0	7
3331	5	0	7

Table 10

Differentially expressed polynucleotides: Higher expression in low metastatic lung cancer cells (lib 9) relative to high metastatic potential lung cancer cells (lib 8)

SEQ ID NO:	Lib 8 clones	Lib 9 clones	lib 9/lib 8
24	3	20	5
53	0	18	13
64	0	8	6
70	0	11	8
105	10	66	5
129	0	16	11
214	1	14	10
233	4	35	6
237	0	13	9
264	0	29	21
329	2	17	6
368	1	37	26
370	0	11	8
418	0	8	6
450	0	9	6
461	0	9	6
484	0	26	19
494	0	41	29
517	1	12	9
522	1	11	8
581	1	17	12
614	3	23	5
706	0	11	8
726	5	23	3
806	0	14	10
824	0	9	6
836	1	14	10
874	0	12	9
900	5	21	3
1017	2	14	5

SEQ ID NO:	Lib 8 clones	Lib 9 clones	lib 9/lib 8
1144	0	8	6
1154	0	12	9
1166	2	45	16
1170	1	13	9
1302	2	13	5
1326	1	13	9
1327	1	13	9
1367	0	12	9
1377	0	12	9
1437	2	18	6
1442	1	14	10
1466	0	13	9
1476	0	13	9
1495	0	8	6
1496	1	13	9
1664	38	253	5
1682	1	17	12
1687	0	9	6
1758	0	8	6
1817	4	18	3
1837	3	16	4
1845	3	23	5
1856	2	17	6
1910	1	18	13
2146	2	16	9
2156	0	9	6
2463	0	12	9
2724	10	38	3
2749	403	2000	4
2801	6	25	3
2993	3	18	4
3080	0	10	7
3107	3	23	5
3292	0	20	14
3324	110	548	4

EXAMPLE 7

POLYNUCLEOTIDES DIFFERENTIALLY EXPRESSED IN HIGH METASTATIC POTENTIAL
COLON CANCER CELLS VERSUS LOW METASTATIC COLON CANCER CELLS

5 A number of polynucleotide sequences have been identified that are
differentially expressed between cells derived from high metastatic potential colon
cancer cells and low metastatic colon cancer cells. Expression of these sequences in
colon cancer tissue can provide diagnostic, prognostic and/or treatment information.
For example, sequences that are highly expressed in the high metastatic potential cells
10 can be indicative of increased expression of genes or regulatory sequences involved in
the metastatic process. A patient sample displaying an increased level of one or more of
these polynucleotides may thus warrant more aggressive treatment. In another example,
sequences that display higher expression in the low metastatic potential cells can be
associated with genes or regulatory sequences that inhibit metastasis, and thus the
15 expression of these polynucleotides in a sample may warrant a more positive prognosis
than the gross pathology would suggest.

The differential expression of these polynucleotides can be used as a
diagnostic marker, a prognostic marker, for risk assessment, patient treatment and the
like. These polynucleotide sequences can also be used in combination with other
20 known molecular and/or biochemical markers.

The following table summarizes identified polynucleotides with
differential expression between high metastatic potential colon cancer cells and low
metastatic potential colon cancer cells:

Table 11

25 Differentially expressed polynucleotides: Higher expression in low metastatic colon
cancer cells (lib 2) relative to high metastatic potential colon cancer cells (lib 1)

SEQ ID NOs:	Lib 1 clones	Lib 2 clones	lib 2/lib 1
429	0	9	10
1494	0	8	9
1923	34	114	4
1986	3	12	4
2018	0	9	10
2036	2	10	5
2049	8	25	3
2135	24	87	4

491

SEQ ID NOs:	Lib 1 clones	Lib 2 clones	lib 2/lib 1
2146	2	16	9
2208	6	27	5
2215	2	11	6
2239	1	10	11
2307	2	12	6
2313	28	62	2
2357	5	14	3
2360	3	21	8
2362	0	6	6
2378	3	12	4
2569	3	20	7
2571	0	6	6
2588	54	172	3
2592	15	41	3
2611	0	6	6
2636	0	9	10
2641	7	20	3
2650	0	9	10
2662	0	9	10
2674	4	13	4
2682	0	6	6
2702	9	25	3
2704	8	23	3
2715	2	12	6
2804	9	22	3
2821	13	29	2
2840	1	8	9
2846	2	15	8
2866	0	6	6
2906	0	6	6
2915	44	109	3
2933	0	6	6
2935	5	16	3
2957	1	11	12
2959	3	27	10
2977	16	30	2
2980	12	27	2
3000	2	13	7
3009	12	29	3
3115	0	7	8
3156	502	2170	5

1872

SEQ ID NOs:	Lib 1 clones	Lib 2 clones	lib 2/lib 1
3210	2	21	11
3211	0	9	10
3213	0	7	8
3235	2	12	6
3251	2	12	6
3296	3	12	4
3335	1	8	9

EXAMPLE 8

POLYNUCLEOTIDES DIFFERENTIALLY EXPRESSED IN HIGH METASTATIC POTENTIAL
COLON CANCER PATIENT TISSUE VERSUS NORMAL PATIENT TISSUE

5

A number of polynucleotide sequences have been identified that are differentially expressed between cells derived from high metastatic potential colon cancer tissue and normal tissue. Expression of these sequences in colon cancer tissue can provide diagnostic, prognostic and/or treatment information. For example, sequences that are highly expressed in the high metastatic potential cells can be indicative of increased expression of genes or regulatory sequences involved in the advanced disease state which involves processes such as angiogenesis, dedifferentiation, cell replication, and metastasis. A patient sample displaying an increased level of one or more of these polynucleotides may thus warrant more aggressive treatment.

15

The differential expression of these polynucleotides can be used as a diagnostic marker, a prognostic marker, for risk assessment, patient treatment and the like. These polynucleotide sequences can also be used in combination with other known molecular and/or biochemical markers.

20

The following tables summarize polynucleotides that are differentially expressed between high metastatic potential colon cancer tissue and normal colon tissue:

Table 12

Differentially expressed polynucleotides isolated from samples from two patients
(patient 2 and patient 3 and) : Lower expression in high metastatic potential colon tissue
(patient 2:lib 17; patient 3:lib 20) vs. normal colon tissue (patient 2:lib 15; patient
3:lib 18)

5

SEQ ID NO:	lib 15 clones	lib 17 clones	lib 15/lib 17
69	19	7	3
123	6	0	6
140	24	8	3
197	6	0	6
198	113	0	121
254	28	9	3
412	28	9	3
512	11	1	12
641	17	7	3
642	7	0	8
954	12	3	4
1011	209	16	14
1024	8	0	9
1040	12	3	4
1055	26	7	4
1106	31	15	2
1125	17	0	18
1129	17	0	18
1138	109	0	117
1244	14	1	15
1253	73	0	78
1283	34	7	5
1285	34	7	5
1339	13	4	3
1474	73	0	78
1505	18	3	6
1553	68	6	12
1554	2542	14	195
1605	2542	14	195
1628	6	0	6
1643	142	4	38
1753	12	0	10
1764	13	0	14

494

SEQ ID NO:	lib 15 clones	lib 17 clones	lib 15/lib 17
SEQ ID NO:	Lib18 Clones	Lib20 Clones	lib18/lib20
105	28	11	2
198	21	0	18
254	9	0	8
412	9	0	8
1011	11	1	9
1138	14	0	12
1253	23	0	20
1643	18	0	15
1764	12	0	10
3156	140	43	3

Table 13

- Differentially expressed polynucleotides isolated from samples from two patients (patient 2 and patient 3): Lower expression in normal colon tissue (patient 2:lib 15; patient 3:lib 18)vs. high metastatic potential colon tissue (patient 2:lib 17; patient 3:lib 20).

SEQ ID NO:	Lib 15 Clones	Lib 17 Clones	lib 17/lib 15
321	3	23	7
363	1	9	8
836	21	99	4
859	6	20	3
885	13	28	2
916	13	28	2
981	2	11	5
1226	8	70	8
1308	0	8	7
1317	29	84	3
1429	27	127	4
1442	0	9	8
1534	1	12	11
1540	12	43	3
1552	0	7	7
1556	1	9	8
1557	1	9	8
1569	2189	5122	2
1571	6	18	3
1576	3	25	8

495

SEQ ID NO:	Lib 15 Clones	Lib 17 Clones	lib 17/lib 15
1581	4	22	5
1601	25	157	6
1613	9	48	5
1616	15	61	4
1620	2	17	8
1622	4	99	23
1626	6	35	5
1647	4	22	5
1664	4	28	7
1683	2	18	8
1704	3	15	5
1800	0	7	7
2749	23	60	2
2784	4	14	3
2805	1	9	8
2976	3	14	4
3128	18	57	3
3129	26	124	4
3146	64	210	3
3150	940	2267	2
3151	2	15	7
SEQ ID NO:	lib 18 clones	lib 20 clones	lib 20/lib 18
865	0	5	6
1569	1	7	8
1580	1	7	8
1590	1	7	8
2790	0	5	6

EXAMPLE 9

POLYNUCLEOTIDES DIFFERENTIALLY EXPRESSED IN HIGH COLON TUMOR POTENTIAL
PATIENT TISSUE VERSUS METASTASIZED COLON CANCER PATIENT TISSUE

- 5 A number of polynucleotide sequences have been identified that are differentially expressed between cells derived from colon cancer tissue and cells derived from colon cancer tissue metastases to liver. Expression of these sequences in colon cancer tissue can provide diagnostic, prognostic and/or treatment information associated with the transformation of precancerous tissue to malignant tissue. This information

496

can be useful in the prevention of achieving the advanced malignant state in these tissues, and can be important in risk assessment for a patient.

The following table summarizes identified polynucleotides with differential expression between high tumor potential colon cancer tissue and cells
5 derived from high metastatic potential colon cancer cells:

Table 14

Differentially expressed polynucleotides:

Greater expression in metastatic colon tumor tissue (lib 20) vs.
10 colon tumor tissue (lib 19)

SEQ ID NO:	lib 19 clones	lib 20 clones	lib 20/lib 19
937	0	6	8
976	0	5	7
1520	1	8	11
1546	1	11	15
1550	1	11	15
1574	1	8	11
1580	0	7	9
1590	0	7	9
1599	8	21	4
1607	158	632	5
1622	1	7	9

Table 15

Greater expression in colon tumor tissue (lib 19) than metastatic colon tissue (lib 20)

SEQ ID NO:	lib 19 clones	lib 20 clones	lib 19/lib 20
105	64	11	4
1011	53	1	40
1226	18	4	3
1571	8	0	6
1726	15	3	4
1811	17	2	6
2749	47	6	6
3146	19	2	7
3324	20	1	15

447

EXAMPLE 10

POLYNUCLEOTIDES DIFFERENTIALLY EXPRESSED IN HIGH TUMOR POTENTIAL
COLON CANCER PATIENT TISSUE VERSUS NORMAL PATIENT TISSUE

5 A number of polynucleotide sequences have been identified that are differentially expressed between cells derived from high tumor potential colon cancer tissue and normal tissue. Expression of these sequences in colon cancer tissue can provide diagnostic, prognostic and/or treatment information associated with the prevention of the malignant state in these tissues, and can be important in risk
10 assessment for a patient. For example, sequences that are highly expressed in the potential colon cancer cells are associated with or can be indicative of increased expression of genes or regulatory sequences involved in early tumor progression. A patient sample displaying an increased level of one or more of these polynucleotides may thus warrant closer attention or more frequent screening procedures to catch the
15 malignant state as early as possible.

The following tables summarize polynucleotides that are differentially expressed between high metastatic potential colon cancer cells and normal colon cells:

Table 16

Differentially expressed polynucleotides detected in samples from patient (patient 2)
20 Higher expression in normal colon tissue (patient 2, lib 15)
vs. tumor potential colon tissue (patient 2:lib16)

SEQ ID NO:	lib 15 clones	lib 16 clones	lib 16/lib 15
69	19	7	3
105	116	54	2
140	24	4	6
197	6	0	6
198	113	3	40
254	28	6	5
412	28	6	5
642	7	0	7
830	10	2	5
938	31	13	3
1011	209	37	6
1095	12	3	4
1125	17	0	18

SEQ ID NO:	lib 15 clones	lib 16 clones	lib 16/lib 15
1129	17	0	18
1138	109	1	115
1253	73	1	77
1283	34	13	3
1285	34	13	3
1339	13	3	5
1453	11	3	4
1474	73	1	77
1505	18	6	3
1554	2542	448	6
1605	2542	448	6
1614	36	14	3
1630	24	9	3
1643	142	2	75
1646	39	14	3
1649	24	8	3
1677	19	6	3
1753	13	0	14
1764	13	0	14
1766	177	65	3
1772	24	8	3

Table 17

Differentially expressed polypeptides detected in samples from patient. Lower expression in normal colon tissue (lib 18) than colon tumor tissue (lib 19)

SEQ ID NO:	lib 18 clones	lib 19 clones	lib 19/lib 18
3146	3	19	6
3150	21	228	10
3324	3	20	6

Table 18

Differentially expressed polypeptides detected in samples from patient. Higher expression in normal colon tissue (lib 18) than colon tumor tissue (lib 19)

SEQ ID NO:	lib 18 clones	lib 19 clones	lib 18/lib 19
198	21	2	12
465	6	0	7
489	6	0	7
745	6	0	7
859	11	2	6
976	7	0	8
1011	209	37	6
1045	8	1	9
1138	14	0	16
1253	23	0	26
1392	16	4	5
1474	23	0	26
1589	6	0	7
1591	22	11	2
1607	386	158	3
1643	18	0	21
1753	12	0	14
1764	12	0	14
SEQ ID NO:	lib 18 clones	lib 19 clones	lib 19/lib 18
105	28	64	2
1011	11	53	4
1226	2	18	8
1251	6	19	3
1559	1	9	8
1571	0	8	7
1608	1	9	8
1766	2	13	6
1782	1	9	8
1811	1	17	15

Table 19

Differentially expressed polynucleotides:

Higher expression in colon tumor tissue

(patient 2, lib 16) vs. normal colon tissue (patient 2, lib 15)

SEQ ID NO:	lib 15 clones	lib 16 clones	lib 16/lib 15
7	1	9	9
164	6	19	3
734	4	15	4
836	21	53	2
928	2	11	5
965	2	11	5
987	2	11	5
1026	7	19	3
1044	4	16	4
1119	4	16	4
1226	8	46	5
1227	0	9	9
1251	7	95	13
1316	0	6	6
1429	27	81	3
1442	0	9	9
1540	12	28	2
1553	68	590	8
1560	4	24	6
1577	1	10	9
1588	5	20	4
1610	3	13	4
1620	2	23	11
1626	6	23	4
1673	2	15	7
2416	0	7	7
2749	23	54	2
2976	3	14	4
3129	26	64	2
3132	18	54	3

EXAMPLE 11

POLYNUCLEOTIDES DIFFERENTIALLY EXPRESSED IN GROWTH FACTOR-STIMULATED
HUMAN MICROVASCULAR ENDOTHELIAL CELLS (HMEC) RELATIVE TO UNTREATED
HMEC

5 A number of polynucleotide sequences have been identified that are differentially expressed between human microvascular endothelial cells (HMEC) that have been treated with growth factors relative to untreated HMEC.

Sequences that are differentially expressed between growth factor-treated HMEC and untreated HMEC can represent sequences encoding gene products involved
10 in angiogenesis, metastasis (cell migration), and other developmental and oncogenic processes. For example, sequences that are more highly expressed in HMEC treated with growth factors (such as bFGF or VEGF) relative to untreated HMEC can serve as markers of cancer cells of higher metastatic potential. Detection of expression of these
15 sequences in colon cancer tissue can provide diagnostic, prognostic and/or treatment information associated with the prevention of achieving the malignant state in these tissues, and can be important in risk assessment for a patient. A patient sample displaying an increased level of one or more of these polynucleotides may thus warrant closer attention or more frequent screening procedures to catch the malignant state as early as possible.

20 The following table summarizes identified polynucleotides with differential expression between growth factor-treated and untreated HMEC.

Table 20

Differentially expressed polynucleotides:

25 Higher expression in untreated HMEC (lib 12) vs. bFGF treated HMEC (lib 13)

SEQ ID NO:	lib 12 clones	lib 13 clones	lib 12/lib 13
849	6	0	6
1059	6	0	6
1206	12	2	6
3208	12	0	12

Lower expression in untreated HMEC (lib 12) vs. bFGF treated HMEC (lib 13)

2748	3	12	4
3325	0	6	6

Table 21

Differentially expressed polynucleotides:

Higher expression in untreated HMEC (lib 12) VEGF treated HMEC (lib14)

SEQ ID NO:	lib 12 clones	lib 14 clones	lib 12/lib 14
1150	9	0	9

5

Lower expression in untreated HMEC (lib 12) vs. VEGF treated HMEC (lib14)

3324	22	50	2
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EXAMPLE 12

10 POLYNUCLEOTIDES DIFFERENTIALLY EXPRESSED IN NORMAL PROSTATE CELLS RELATIVE TO PROSTATE CANCER CELLS

A number of polynucleotide sequences have been identified that are differentially expressed between cells derived from normal prostate cells and prostate cancer cells. Expression of these sequences prostate tissue suspected of being cancerous can provide diagnostic, prognostic and/or treatment information. These polynucleotide sequences can also be used in combination with other known molecular and/or biochemical markers. The following table summarizes identified polynucleotides with differential expression between high metastatic potential colon cancer cells and low metastatic potential colon cancer cells:

20

Table 22

Differentially expressed polynucleotides: normal prostate cell line (lib 21)
vs. prostate cancer cell line (lib 22)

Higher in lib 21

SEQ ID NO:	lib 21 clones	lib 22 clones	lib 21/lib 22
53	17	2	8
1754	22	8	3
1801	7	0	7
1845	22	6	4
446	8	0	8
1410	6	0	6
2060	18	6	3
2143	12	3	4
2632	13	1	13
2899	16	2	8
3338	12	2	6

5

Higher in lib 22

86	2	13	7
93	0	9	9
687	0	9	9
1269	1	15	15
1581	25	74	3
1647	25	74	3
1649	12	27	2
1710	5	16	3
1717	5	16	3
1772	12	27	2
1960	0	6	6
2987	0	6	6
3128	13	42	3
3132	13	42	3
3150	263	962	4
3222	0	6	6
3268	0	6	6

504

EXAMPLE 13

POLYNUCLEOTIDES DIFFERENTIALLY EXPRESSED ACROSS MULTIPLE LIBRARIES

A number of polynucleotide sequences have been identified that are differentially expressed between cancerous cells and normal cells across two or more tissue types tested (*i.e.*, breast, colon, lung, and prostate). Expression of these sequences in a tissue of any origin can provide diagnostic, prognostic and/or treatment information associated with the prevention of achieving the malignant state in these tissues, and can be important in risk assessment for a patient. These polynucleotides can also serve as non-tissue specific markers of, for example, risk of metastasis of a tumor. The following polynucleotides were differentially expressed but without tissue type-specificity in at least two of the breast, colon, lung, and prostate libraries tested: 53, 105, 355, 412, 614, 836, 1442, 1581, 1647, 1649, 1664, 1772, 1782, 1811, 1845, 1856, 1875, 1923, 2060, 2071, 2135, 2146, 2239, 2313, 2378, 2393, 2416, 2460, 2490, 2632, 2674, 2704, 2724, 2749, 2784, 2804, 2959, 2976, 2977, 2980, 2987, 3009, 3047, 3128, 3129, 3132, 3146, 3150, 3156, 3210, 3324, 3331, and 3335.

Those skilled in the art will recognize, or be able to ascertain, using not more than routine experimentation, many equivalents to the specific embodiments of the invention described herein. Such specific embodiments and equivalents are intended to be encompassed by the following claims.

All publications and patent applications cited in this specification are herein incorporated by reference as if each individual publication or patent application were specifically and individually indicated to be incorporated by reference. The citation of any publication is for its disclosure prior to the filing date and should not be construed as an admission that the present invention is not entitled to antedate such publication by virtue of prior invention.

Although the foregoing invention has been described in some detail by way of illustration and example for purposes of clarity of understanding, it is readily apparent to those of ordinary skill in the art in light of the teachings of this invention that certain changes and modifications may be made thereto without departing from the spirit or scope of the appended claims.

Deposit Information:

The following materials were deposited with the American Type Culture Collection (ATCC); CMCC = Chiron Master Culture Collection:

cDNA Libraries Deposited with ATCC

Tube Number	Deposit Date	ATCC Accession No.	CMCC Accession No.
ES137	May 30, 2000		
ES138	May 30, 2000		
ES139	May 30, 2000		
ES140	May 30, 2000		
ES141	May 30, 2000		
ES142	May 30, 2000		
ES143	May 30, 2000		
ES144	May 30, 2000		
ES145	May 30, 2000		
ES146	May 30, 2000		
ES147	May 30, 2000		
ES148	May 30, 2000		
ES149	May 30, 2000		
ES150	May 30, 2000		
ES151	May 30, 2000		
ES152	May 30, 2000		
ES153	May 30, 2000		
ES154	May 30, 2000		
ES155	May 30, 2000		
ES156	May 30, 2000		
ES157	May 30, 2000		
ES158	May 30, 2000		
ES159	May 30, 2000		
ES160	May 30, 2000		
ES161	May 30, 2000		
ES162	May 30, 2000		
ES163	May 30, 2000		
ES164	May 30, 2000		
ES165	May 30, 2000		
ES166	May 30, 2000		
ES167	May 30, 2000		

Table 23 lists the clones for each deposit, designated as "tube" number.

- 5 This deposit is provided merely as convenience to those of skill in the art, and is not an admission that a deposit is required under 35 U.S.C. §112. The sequence of the polynucleotides contained within the deposited material, as well as the amino acid sequence of the polypeptides encoded thereby, are incorporated herein by reference and are controlling in the event of any conflict with the written description of sequences

herein. A license may be required to make, use, or sell the deposited material, and no such license is granted hereby.

Retrieval of Individual Clones from Deposit of Pooled Clones

Where the ATCC deposit is composed of a pool of cDNA clones, the deposit was prepared by first transfecting each of the clones into separate bacterial cells. The clones were then deposited as a pool of equal mixtures in the composite deposit. Particular clones can be obtained from the composite deposit using methods well known in the art. For example, a bacterial cell containing a particular clone can be identified by isolating single colonies, and identifying colonies containing the specific clone through standard colony hybridization techniques, using an oligonucleotide probe or probes designed to specifically hybridize to a sequence of the clone insert (e.g., a probe based upon unmasked sequence of the encoded polynucleotide having the indicated SEQ ID NO). The probe should be designed to have a T_m of approximately 80°C (assuming 2°C for each A or T and 4°C for each G or C). Positive colonies can then be picked, grown in culture, and the recombinant clone isolated. Alternatively, probes designed in this manner can be used to PCR to isolate a nucleic acid molecule from the pooled clones according to methods well known in the art, e.g., by purifying the cDNA from the deposited culture pool, and using the probes in PCR reactions to produce an amplified product having the corresponding desired polynucleotide sequence.

Table 23

Clone Name	Tube
M00001351A:B02	ES 137
M00001356A:H11	ES 137
M00001363D:D09	ES 137
M00001395D:H02	ES 137
M00001439C:H06	ES 137
M00001476B:G10	ES 137
M00001582A:E02	ES 137
M00003750D:E06	ES 137
M00003761C:F02	ES 137
M00003770A:E05	ES 137
M00003786A:A11	ES 137
M00003800A:F09	ES 137
M00003816D:E11	ES 137
M00003902A:C03	ES 137
M00003991C:F06	ES 137

Clone Name	Tube
M00003995B:E03	ES 137
M00004046C:A08	ES 137
M00004105D:D05	ES 137
M00004139B:B10	ES 137
M00004140D:C03	ES 137
M00004144A:H05	ES 137
M00004152A:C12	ES 137
M00004155D:A10	ES 137
M00004168A:G11	ES 137
M00004197B:H10	ES 137
M00004222C:E03	ES 137
M00004234A:E07	ES 137
M00004239B:F11	ES 137
M00004241B:H07	ES 137
M00004264B:A05	ES 137

Clone Name	Tube
M00004278A:F09	ES 137
M00004282D:C11	ES 137
M00004308C:C06	ES 137
M00004340C:C07	ES 137
M00004354D:E05	ES 137
M00004361A:H02	ES 137
M00004372B:F07	ES 137
M00004378A:B10	ES 137
M00004393B:E07	ES 137
M00023282A:C02	ES 137
M00023300D:C11	ES 137
M00023316C:G08	ES 137
M00023333D:C12	ES 137
M00023352B:F03	ES 137
M00023352D:H03	ES 137
M00023376B:G04	ES 137
M00023377B:F01	ES 137
M00023398B:D12	ES 137
M00023399C:E10	ES 137
M00026803A:F08	ES 137
M00026843B:D10	ES 137
M00026850D:F09	ES 137
M00026851B:F01	ES 137
M00026856D:F02	ES 137
M00026857D:G12	ES 137
M00026859D:D01	ES 137
M00026860B:C05	ES 137
M00026865B:A06	ES 137
M00026868C:E11	ES 137
M00026878A:F05	ES 137
M00026882D:G09	ES 137
M00026885A:H09	ES 137
M00026901A:G07	ES 137
M00026914A:H10	ES 137
M00026915B:C06	ES 137
M00026918B:D01	ES 137
M00026922C:B02	ES 137
M00026922C:G03	ES 137
M00026926A:E10	ES 137
M00026927D:F02	ES 137
M00026928D:A03	ES 137
M00026935C:B04	ES 137
M00026941D:A04	ES 137
M00026944B:E03	ES 137
M00026946A:F12	ES 137

Clone Name	Tube
M00026980A:D09	ES 137
M00027016A:B06	ES 137
M00027018A:C09	ES 137
M00027021A:G02	ES 137
M00027022D:G11	ES 137
M00027030C:H06	ES 137
M00027035D:C06	ES 137
M00027049B:F05	ES 137
M00027078A:B02	ES 137
M00027080A:B01	ES 137
M00027085C:E11	ES 137
M00027094A:B03	ES 137
M00027103B:A09	ES 137
M00027108C:B03	ES 137
M00027121D:C05	ES 137
M00027135A:B11	ES 137
M00027136C:C09	ES 137
M00027141C:H03	ES 137
M00027159D:F03	ES 137
M00027162B:F05	ES 137
M00027178B:G09	ES 137
M00027179D:E06	ES 138
M00027181D:A05	ES 138
M00027195C:E04	ES 138
M00027198B:B08	ES 138
M00027200A:F02	ES 138
M00027207B:F07	ES 138
M00027212D:E03	ES 138
M00027228D:A01	ES 138
M00027232D:B08	ES 138
M00027233B:C01	ES 138
M00027236A:E04	ES 138
M00027237C:B08	ES 138
M00027248A:C02	ES 138
M00027256B:H09	ES 138
M00027258A:A07	ES 138
M00027263A:F10	ES 138
M00027292D:F10	ES 138
M00027297A:C04	ES 138
M00027299B:B12	ES 138
M00027301A:G05	ES 138
M00027301B:B08	ES 138
M00027314C:D09	ES 138
M00027319D:B11	ES 138
M00027324D:C05	ES 138

Clone Name	Tube
M00027347C:G07	ES 138
M00027355A:B07	ES 138
M00027359B:G05	ES 138
M00027366A:F11	ES 138
M00027379C:B07	ES 138
M00027392B:H02	ES 138
M00027396D:G08	ES 138
M00027398C:F07	ES 138
M00027438C:G07	ES 138
M00027462A:D07	ES 138
M00027462B:H07	ES 138
M00027468A:C09	ES 138
M00027475B:E10	ES 138
M00027476A:C09	ES 138
M00027486A:F06	ES 138
M00027520A:C05	ES 138
M00027525B:D06	ES 138
M00027526D:F03	ES 138
M00027528C:B10	ES 138
M00027537C:B01	ES 138
M00027546C:B10	ES 138
M00027591B:C04	ES 138
M00027596A:A10	ES 138
M00027596C:E06	ES 138
M00027602B:C01	ES 138
M00027615A:F10	ES 138
M00027617B:C12	ES 138
M00027620D:F11	ES 138
M00027625A:H01	ES 138
M00027634A:D11	ES 138
M00027641C:A03	ES 138
M00027647C:D03	ES 138
M00027652B:F11	ES 138
M00027668C:H12	ES 138
M00027729D:H06	ES 138
M00027733A:A02	ES 138
M00027741B:F09	ES 138
M00027743A:C03	ES 138
M00027801C:C11	ES 138
M00027813C:F01	ES 138
M00027818C:C07	ES 138
M00027836D:F12	ES 138
M00027837C:D09	ES 138
M00028120D:F12	ES 138
M00028066C:D07	ES 138

Clone Name	Tube
M00028184D:G10	ES 138
M00028185B:A06	ES 138
M00028196D:A03	ES 138
M00028201B:H12	ES 138
M00028207D:E09	ES 138
M00028210B:D02	ES 138
M00028212C:B08	ES 138
M00028215D:F03	ES 138
M00028220A:B04	ES 138
M00028314D:F05	ES 138
M00028316B:H12	ES 138
M00028354A:B12	ES 138
M00028354D:A03	ES 138
M00028357A:G10	ES 138
M00028362A:G11	ES 138
M00028364C:G08	ES 138
M00028369D:E08	ES 138
M00028617C:A12	ES 138
M00028768C:D05	ES 138
M00028770A:D04	ES 138
M00028772C:B09	ES 138
M00028775D:F03	ES 138
M00028777B:G12	ES 138
M00031368A:E10	ES 138
M00031417C:G09	ES 138
M00031419D:C04	ES 138
M00031485D:G02	ES 138
M00032480B:E10	ES 139
M00032492A:C01	ES 139
M00032495B:D02	ES 139
M00032499C:A01	ES 139
M00032508B:H03	ES 139
M00032510D:F12	ES 139
M00032510D:G06	ES 139
M00032513D:F01	ES 139
M00032530D:C02	ES 139
M00032535D:H01	ES 139
M00032539B:C11	ES 139
M00032540A:A09	ES 139
M00032541D:H08	ES 139
M00032545B:H09	ES 139
M00032545D:G05	ES 139
M00032550D:C02	ES 139
M00032551B:G05	ES 139
M00032577A:C04	ES 139

Clone Name	Tube
M00032578A:G06	ES 139
M00032584A:H08	ES 139
M00032592A:H11	ES 139
M00032597C:B01	ES 139
M00032638C:G08	ES 139
M00032638D:A06	ES 139
M00032668D:G12	ES 139
M00032678C:D06	ES 139
M00032688D:D11	ES 139
M00032712B:G02	ES 139
M00032724A:C05	ES 139
M00032725C:F06	ES 139
M00032726C:C01	ES 139
M00032731B:C10	ES 139
M00032731C:C07	ES 139
M00032737B:E09	ES 139
M00032739A:A06	ES 139
M00032744B:F10	ES 139
M00032766B:D12	ES 139
M00032766C:A04	ES 139
M00032790B:A07	ES 139
M00032793A:F06	ES 139
M00032797B:G02	ES 139
M00032808B:G10	ES 139
M00032811B:D02	ES 139
M00032829B:E06	ES 139
M00032830D:G03	ES 139
M00032831C:G07	ES 139
M00032853D:G12	ES 139
M00032864B:B09	ES 139
M00032871D:E11	ES 139
M00032876C:D06	ES 139
M00032907A:G04	ES 139
M00032909A:B06	ES 139
M00032917D:G09	ES 139
M00032918B:D08	ES 139
M00032918B:E06	ES 139
M00032918C:B10	ES 139
M00032921B:H08	ES 139
M00032933A:C10	ES 139
M00032939B:E07	ES 139
M00032940A:C02	ES 139
M00032942D:C12	ES 139
M00032944B:B02	ES 139
M00032984C:G05	ES 139

Clone Name	Tube
M00032990B:A11	ES 139
M00032994A:A08	ES 139
M00032995C:C05	ES 139
M00033007C:E01	ES 139
M00033019B:E10	ES 139
M00033033C:H01	ES 139
M00033034C:A06	ES 139
M00033034C:F02	ES 139
M00033037D:C11	ES 139
M00033074A:C08	ES 139
M00033130B:F06	ES 139
M00033140D:F06	ES 139
M00033173D:C01	ES 139
M00033176B:E12	ES 139
M00033186C:D11	ES 139
M00033189D:F08	ES 139
M00033202D:G06	ES 139
M00033204B:A07	ES 139
M00033205A:F03	ES 139
M00033217B:H07	ES 139
M00033218A:C04	ES 139
M00033223B:H07	ES 139
M00033226A:A11	ES 139
M00033231D:B09	ES 139
M00033231D:G10	ES 139
M00033243B:A05	ES 139
M00033246C:E08	ES 139
M00033248A:B02	ES 139
M00033261C:D12	ES 139
M00033262D:A11	ES 139
M00033263B:G04	ES 139
M00033276B:G08	ES 139
M00033185C:D01	ES 139
M00033288B:D12	ES 140
M00033300D:H12	ES 140
M00033306D:G08	ES 140
M00033306D:H09	ES 140
M00033308B:G05	ES 140
M00033343C:H08	ES 140
M00033345D:A09	ES 140
M00033346C:A05	ES 140
M00033347C:F02	ES 140
M00033349D:F05	ES 140
M00033358A:H12	ES 140
M00033362C:C05	ES 140

Clone Name	Tube
M00033375A:G04	ES 140
M00033376A:C12	ES 140
M00033377D:A05	ES 140
M00033410B:C09	ES 140
M00033424B:A04	ES 140
M00033424D:H12	ES 140
M00033425A:C10	ES 140
M00033427D:F01	ES 140
M00033432B:H10	ES 140
M00033437C:A07	ES 140
M00033437C:C03	ES 140
M00033442A:D06	ES 140
M00033446C:G08	ES 140
M00033446D:B02	ES 140
M00033450C:A02	ES 140
M00033451A:H01	ES 140
M00033454A:D09	ES 140
M00033457D:A05	ES 140
M00033560D:G07	ES 140
M00033561C:A02	ES 140
M00033566C:E08	ES 140
M00033570B:C08	ES 140
M00033570B:E06	ES 140
M00033570C:C10	ES 140
M00033578D:G02	ES 140
M00033581C:H10	ES 140
M00033581D:D08	ES 140
M00033583B:E06	ES 140
M00033583D:B05	ES 140
M00033584D:G11	ES 140
M00033585D:A02	ES 140
M00033588C:G04	ES 140
M00033594C:B03	ES 140
M00033595A:C11	ES 140
M00038259A:G08	ES 140
M00038259B:A02	ES 140
M00038259B:G08	ES 140
M00038259C:H09	ES 140
M00038272A:G01	ES 140
M00038272D:F11	ES 140
M00038279C:A11	ES 140
M00038284B:H04	ES 140
M00038303A:C03	ES 140
M00038303C:D02	ES 140
M00038303D:E07	ES 140

Clone Name	Tube
M00038315C:G11	ES 140
M00038325D:F12	ES 140
M00038326B:D04	ES 140
M00038327A:C11	ES 140
M00038327D:A05	ES 140
M00038328D:A03	ES 140
M00038329A:E08	ES 140
M00038387B:A07	ES 140
M00038614C:H11	ES 140
M00038615A:H12	ES 140
M00038616D:B12	ES 140
M00038618C:C08	ES 140
M00038619B:A03	ES 140
M00038620B:E09	ES 140
M00038631C:B10	ES 140
M00038631D:B02	ES 140
M00038632C:B09	ES 140
M00038633A:D07	ES 140
M00038633B:G02	ES 140
M00038635A:G09	ES 140
M00038635B:C08	ES 140
M00038638D:H03	ES 140
M00038639B:C03	ES 140
M00038639D:F07	ES 140
M00038661A:A07	ES 140
M00038662B:A12	ES 140
M00038663B:H06	ES 140
M00038663D:H10	ES 140
M00038664C:E04	ES 140
M00038991A:D01	ES 140
M00038994A:A10	ES 140
M00038995C:G08	ES 140
M00038995D:E05	ES 140
M00038999B:G11	ES 140
M00038999D:C11	ES 140
M00039002D:G11	ES 140
M00039004B:A06	ES 140
M00039004B:C11	ES 140
M00039005C:H01	ES 141
M00039006D:B01	ES 141
M00039011D:C10	ES 141
M00039013A:C09	ES 141
M00039013D:F02	ES 141
M00039014A:H10	ES 141
M00039014B:C04	ES 141

Clone Name	Tube
M00039015A:D07	ES 141
M00039015B:G10	ES 141
M00039015B:H09	ES 141
M00039015D:H04	ES 141
M00039016A:A02	ES 141
M00039016D:G06	ES 141
M00039024B:B10	ES 141
M00039025A:H09	ES 141
M00039026D:F05	ES 141
M00039028C:B11	ES 141
M00039030B:E02	ES 141
M00039036C:B05	ES 141
M00039039B:E03	ES 141
M00039039B:F09	ES 141
M00039042B:B02	ES 141
M00039043B:E01	ES 141
M00039049D:G07	ES 141
M00039050A:H10	ES 141
M00039052C:F07	ES 141
M00039058A:A04	ES 141
M00039058C:H02	ES 141
M00039059C:G08	ES 141
M00039061B:F08	ES 141
M00039063B:D08	ES 141
M00039064D:H09	ES 141
M00039066D:G08	ES 141
M00039068B:B04	ES 141
M00039068C:E06	ES 141
M00039070D:C02	ES 141
M00039072C:C03	ES 141
M00039072C:E02	ES 141
M00039079A:A05	ES 141
M00039080C:H06	ES 141
M00039081B:G06	ES 141
M00039082B:A05	ES 141
M00039084C:G07	ES 141
M00039084C:H03	ES 141
M00039084C:H04	ES 141
M00039084D:D07	ES 141
M00039096A:A05	ES 141
M00039096A:E07	ES 141
M00039097D:D06	ES 141
M00039099A:H08	ES 141
M00039104D:C09	ES 141
M00039105C:B08	ES 141

Clone Name	Tube
M00039107C:E04	ES 141
M00039108D:B06	ES 141
M00039112B:C05	ES 141
M00039118B:C05	ES 141
M00039118D:A06	ES 141
M00039120C:C09	ES 141
M00039120C:H03	ES 141
M00039123A:B10	ES 141
M00039124C:F03	ES 141
M00039124C:H02	ES 141
M00039124C:H08	ES 141
M00039126D:A08	ES 141
M00039127A:G11	ES 141
M00039127D:E10	ES 141
M00039129C:D04	ES 141
M00039133B:F08	ES 141
M00039135D:F05	ES 141
M00039135D:G02	ES 141
M00039135D:H02	ES 141
M00039139A:C09	ES 141
M00039139C:G12	ES 141
M00039140A:B08	ES 141
M00039140D:A04	ES 141
M00039140D:D09	ES 141
M00039141C:E01	ES 141
M00039142D:B11	ES 141
M00039144C:E06	ES 141
M00039147A:F10	ES 141
M00039156A:B11	ES 141
M00039158B:G12	ES 141
M00039166B:G06	ES 141
M00039167B:H09	ES 141
M00039168C:A04	ES 141
M00039169A:E12	ES 141
M00039170A:B10	ES 141
M00039170C:F05	ES 141
M00039171B:D11	ES 141
M00039177B:D03	ES 141
M00039179A:G09	ES 141
M00039180A:A07	ES 141
M00039196B:H06	ES 141
M00039196D:A07	ES 141
M00039200A:C10	ES 141
M00039211A:C12	ES 141
M00039212C:C12	ES 142

Clone Name	Tube
M00039213A:D01	ES 142
M00039213B:F05	ES 142
M00039218A:F03	ES 142
M00039221A:H03	ES 142
M00039224A:E12	ES 142
M00039228A:B05	ES 142
M00039230A:A10	ES 142
M00039230D:D09	ES 142
M00039230D:G12	ES 142
M00039233A:A03	ES 142
M00039238A:B12	ES 142
M00039238D:A08	ES 142
M00039241A:E11	ES 142
M00039249A:C12	ES 142
M00039249C:G11	ES 142
M00039255C:E12	ES 142
M00039257D:C03	ES 142
M00039258B:E06	ES 142
M00039258D:B08	ES 142
M00039260C:G03	ES 142
M00039263D:A12	ES 142
M00039266A:B02	ES 142
M00039266D:F12	ES 142
M00039266D:H04	ES 142
M00039273B:F02	ES 142
M00039273D:B02	ES 142
M00039274B:G07	ES 142
M00039276B:H09	ES 142
M00039277D:G10	ES 142
M00039279B:C11	ES 142
M00039279B:H02	ES 142
M00039279C:B08	ES 142
M00039281D:B04	ES 142
M00039284D:B12	ES 142
M00039286A:C06	ES 142
M00039287C:A06	ES 142
M00039288C:B11	ES 142
M00039293A:H04	ES 142
M00039293B:C11	ES 142
M00039295B:D03	ES 142
M00039297C:H08	ES 142
M00039298B:B06	ES 142
M00039298B:D03	ES 142
M00039298D:B04	ES 142
M00039299B:G12	ES 142

Clone Name	Tube
M00039300C:C09	ES 142
M00039300C:G04	ES 142
M00039301B:F06	ES 142
M00039303C:F11	ES 142
M00039304D:B09	ES 142
M00039308B:G08	ES 142
M00039310A:C07	ES 142
M00039313D:G04	ES 142
M00039316A:C01	ES 142
M00039318B:B09	ES 142
M00039319B:H12	ES 142
M00039319C:A04	ES 142
M00039322A:F04	ES 142
M00039328D:D07	ES 142
M00039329A:C01	ES 142
M00039329C:B10	ES 142
M00039333D:D09	ES 142
M00039334B:E03	ES 142
M00039335A:E08	ES 142
M00039339A:H07	ES 142
M00039339C:F03	ES 142
M00039340A:D05	ES 142
M00039340B:E07	ES 142
M00039340B:G08	ES 142
M00039341C:H11	ES 142
M00039341D:D07	ES 142
M00039343B:F12	ES 142
M00039344B:G07	ES 142
M00039345A:D09	ES 142
M00039345C:C12	ES 142
M00039381C:H08	ES 142
M00039381D:C02	ES 142
M00039384C:E02	ES 142
M00039384C:F08	ES 142
M00039385B:E09	ES 142
M00039391D:F08	ES 142
M00039396D:B04	ES 142
M00039397B:H09	ES 142
M00039398A:B10	ES 142
M00039401B:D02	ES 142
M00039402B:E03	ES 142
M00039403A:G12	ES 142
M00039404B:A05	ES 142
M00039407B:G02	ES 142
M00039411C:E07	ES 142

Clone Name	Tube
M00039412D:G06	ES 142
M00039414D:G03	ES 142
M00039415D:E01	ES 142
M00039417A:D03	ES 142
M00039417A:E12	ES 142
M00039417B:F01	ES 143
M00039417C:A01	ES 143
M00039417C:G01	ES 143
M00039418B:D08	ES 143
M00039420D:D03	ES 143
M00039422D:F04	ES 143
M00039425C:G01	ES 143
M00039425D:E12	ES 143
M00039428C:E01	ES 143
M00039430B:F12	ES 143
M00039431B:F04	ES 143
M00039432C:A01	ES 143
M00039444C:H02	ES 143
M00039452C:G09	ES 143
M00039454B:A11	ES 143
M00039455D:H04	ES 143
M00039456A:C08	ES 143
M00039458B:H11	ES 143
M00039461A:F04	ES 143
M00039465A:A08	ES 143
M00039472C:B08	ES 143
M00039475C:E10	ES 143
M00039476B:A02	ES 143
M00039477A:B03	ES 143
M00039477D:A10	ES 143
M00039611D:D11	ES 143
M00039612B:B10	ES 143
M00039612B:G05	ES 143
M00039616A:B10	ES 143
M00039616B:C01	ES 143
M00039619B:D02	ES 143
M00039631A:C10	ES 143
M00039633D:D05	ES 143
M00039636C:D11	ES 143
M00039637C:A10	ES 143
M00039652B:D05	ES 143
M00039655B:H09	ES 143
M00039655C:C07	ES 143
M00039655C:E08	ES 143
M00039660C:C10	ES 143

Clone Name	Tube
M00039663C:G09	ES 143
M00039664D:G07	ES 143
M00039672D:D10	ES 143
M00039673A:F09	ES 143
M00039675D:B03	ES 143
M00039675D:H05	ES 143
M00039677A:B08	ES 143
M00039681B:H09	ES 143
M00039682A:C08	ES 143
M00039682C:H11	ES 143
M00039684D:B08	ES 143
M00039685A:A08	ES 143
M00039686C:C05	ES 143
M00039686C:E06	ES 143
M00039688C:G06	ES 143
M00039689C:E08	ES 143
M00039696A:E05	ES 143
M00039697B:F11	ES 143
M00039700B:D02	ES 143
M00039702A:B12	ES 143
M00039702A:B02	ES 143
M00039705D:F02	ES 143
M00039707A:D02	ES 143
M00039710C:G03	ES 143
M00039720D:D02	ES 143
M00039727C:B09	ES 143
M00039729A:A10	ES 143
M00039771C:E11	ES 143
M00039773D:A09	ES 143
M00039773D:F11	ES 143
M00039774C:A03	ES 143
M00039774C:C09	ES 143
M00039775A:A09	ES 143
M00039777C:E05	ES 143
M00039778B:G03	ES 143
M00039778C:A04	ES 143
M00039781D:D10	ES 143
M00039782A:H10	ES 143
M00039785D:G05	ES 143
M00039788A:E03	ES 143
M00039788B:A06	ES 143
M00039788C:A01	ES 143
M00039790B:D03	ES 143
M00039792A:B04	ES 143
M00039793D:C05	ES 143

Clone Name	Tube
M00039794A:E04	ES 143
M00039795B:H10	ES 143
M00039795D:E10	ES 143
M00039795D:G06	ES 143
M00039797C:G05	ES 143
M00039798B:B02	ES 143
M00039799A:D10	ES 143
M00039801A:H11	ES 143
M00039807A:D01	ES 143
M00039808D:H02	ES 143
M00039810A:H10	ES 143
M00039813B:B01	ES 144
M00039813B:D11	ES 144
M00039815C:F09	ES 144
M00039816B:D04	ES 144
M00039816C:D05	ES 144
M00039820A:F11	ES 144
M00039820A:H11	ES 144
M00039820B:B06	ES 144
M00039827B:F07	ES 144
M00039828B:C05	ES 144
M00039832A:B12	ES 144
M00039835A:F07	ES 144
M00039838A:F05	ES 144
M00039839B:B01	ES 144
M00039839C:E05	ES 144
M00039847A:F06	ES 144
M00039851B:G11	ES 144
M00039851C:D12	ES 144
M00039854B:F09	ES 144
M00039855C:F01	ES 144
M00039857B:G10	ES 144
M00039859A:F06	ES 144
M00039859C:G10	ES 144
M00039864A:A07	ES 144
M00039866B:A08	ES 144
M00039869B:F06	ES 144
M00039875D:A10	ES 144
M00039876D:H09	ES 144
M00039877C:C03	ES 144
M00039879C:F05	ES 144
M00039879D:B11	ES 144
M00039880A:H11	ES 144
M00039884A:H11	ES 144
M00039885C:D01	ES 144

Clone Name	Tube
M00039887C:E07	ES 144
M00039887D:C04	ES 144
M00039888B:D03	ES 144
M00039890A:H05	ES 144
M00039894C:H07	ES 144
M00039896C:H01	ES 144
M00039897D:C10	ES 144
M00039898A:A08	ES 144
M00039898D:C06	ES 144
M00039903A:H07	ES 144
M00039903C:D01	ES 144
M00039903C:F03	ES 144
M00039909C:G05	ES 144
M00039909D:C02	ES 144
M00039910C:G10	ES 144
M00039914D:G12	ES 144
M00039915D:C11	ES 144
M00039927A:F04	ES 144
M00039928B:G05	ES 144
M00039936C:C05	ES 144
M00039938C:A08	ES 144
M00039938C:E11	ES 144
M00039940A:D07	ES 144
M00039940D:G08	ES 144
M00039973D:C08	ES 144
M00039973D:D12	ES 144
M00039975C:C11	ES 144
M00039976D:A12	ES 144
M00039978A:G03	ES 144
M00039981A:E08	ES 144
M00039982C:H04	ES 144
M00039983D:A06	ES 144
M00039984A:C02	ES 144
M00039984B:G12	ES 144
M00039984D:G12	ES 144
M00039987A:F09	ES 144
M00039987C:E12	ES 144
M00039987C:G08	ES 144
M00039988A:E06	ES 144
M00039990C:D10	ES 144
M00040004D:B03	ES 144
M00040005B:C11	ES 144
M00040005D:B07	ES 144
M00040007D:A06	ES 144
M00040009D:B07	ES 144

Clone Name	Tube
M00040010A:F10	ES 144
M00040014B:D01	ES 144
M00040014D:D10	ES 144
M00040014D:F03	ES 144
M00040015C:F08	ES 144
M00040016C:H12	ES 144
M00040017A:C06	ES 144
M00040017D:G03	ES 144
M00040019A:E01	ES 144
M00040021A:F09	ES 144
M00040022C:D06	ES 144
M00040026B:F06	ES 144
M00040029A:B03	ES 144
M00040029A:G04	ES 144
M00040031A:E06	ES 144
M00040032A:B03	ES 144
M00040032A:D09	ES 144
M00040037A:E11	ES 145
M00040038D:G04	ES 145
M00040039D:D06	ES 145
M00040040A:A06	ES 145
M00040041C:C09	ES 145
M00040042B:A10	ES 145
M00040047C:F05	ES 145
M00040052D:F12	ES 145
M00040055D:A06	ES 145
M00040055D:B01	ES 145
M00040060C:H10	ES 145
M00040062B:B05	ES 145
M00040070B:B07	ES 145
M00040071B:A10	ES 145
M00040072C:G09	ES 145
M00040076C:D06	ES 145
M00040077D:C11	ES 145
M00040080C:C06	ES 145
M00040081C:E01	ES 145
M00040085D:A10	ES 145
M00040085D:E04	ES 145
M00040087D:F08	ES 145
M00040088C:E10	ES 145
M00040089A:G08	ES 145
M00040089B:E04	ES 145
M00040089C:E06	ES 145
M00040090B:G09	ES 145
M00040092B:F05	ES 145

Clone Name	Tube
M00040093B:C02	ES 145
M00040093D:D03	ES 145
M00040097A:C12	ES 145
M00040098C:B01	ES 145
M00040098D:E04	ES 145
M00040098D:G12	ES 145
M00040100C:E05	ES 145
M00040100D:B06	ES 145
M00040103B:H10	ES 145
M00040105C:F11	ES 145
M00040106B:B09	ES 145
M00040107B:H07	ES 145
M00040111C:D05	ES 145
M00040115B:A04	ES 145
M00040115B:H12	ES 145
M00040118D:G10	ES 145
M00040121B:C05	ES 145
M00040122D:A02	ES 145
M00040123A:A09	ES 145
M00040124D:H01	ES 145
M00040129D:E10	ES 145
M00040302C:A04	ES 145
M00040304B:F06	ES 145
M00040305A:D11	ES 145
M00040305C:H06	ES 145
M00040307B:F01	ES 145
M00040307C:F10	ES 145
M00040309A:E11	ES 145
M00004825D:D05	ES 145
M00004832D:H02	ES 145
M00004839C:H02	ES 145
M00005018A:B05	ES 145
M00005297D:H08	ES 145
M00005308A:D06	ES 145
M00005351C:G05	ES 145
M00005352C:A02	ES 145
M00005358B:B06	ES 145
M00005359A:D04	ES 145
M00005379A:E04	ES 145
M00005382B:F08	ES 145
M00005384A:C11	ES 145
M00005402B:F08	ES 145
M00005445D:B01	ES 145
M00005449B:B10	ES 145
M00005449B:D01	ES 145

Clone Name	Tube
M00005457C:A03	ES 145
M00005458A:F11	ES 145
M00005498A:H06	ES 145
M00005531D:F06	ES 145
M00005539D:G01	ES 145
M00005555A:A10	ES 145
M00005556B:D02	ES 145
M00005601D:D08	ES 145
M00005614B:B01	ES 145
M00005623A:G02	ES 145
M00005623D:G12	ES 145
M00005625A:C02	ES 145
M00005673B:B12	ES 145
M00005778B:F09	ES 145
M00005805D:D12	ES 145
M00005820C:E04	ES 145
M00006581D:F08	ES 145
M00006599D:B02	ES 145
M00006657C:G05	ES 145
M00006680B:D02	ES 145
M00006712C:H09	ES 145
M00006809B:B09	ES 145
M00006861B:F09	ES 145
M00006866A:D07	ES 146
M00006886D:H02	ES 146
M00006893C:E07	ES 146
M00006897A:H02	ES 146
M00006928D:D07	ES 146
M00006935C:F06	ES 146
M00006968A:G08	ES 146
M00006977C:G04	ES 146
M00006977D:A03	ES 146
M00007012D:H08	ES 146
M00007013A:D09	ES 146
M00007026B:H09	ES 146
M00007108B:A02	ES 146
M00007112C:B10	ES 146
M00007116C:G02	ES 146
M00007124D:H10	ES 146
M00007136A:A03	ES 146
M00007149A:G02	ES 146
M00007157C:F11	ES 146
M00007165B:G11	ES 146
M00007194A:B09	ES 146
M00007929C:B08	ES 146

Clone Name	Tube
M00007941D:C09	ES 146
M00007943D:C09	ES 146
M00007972B:H12	ES 146
M00007976A:C10	ES 146
M00007992C:F06	ES 146
M00007994A:G02	ES 146
M00008006B:B03	ES 146
M00008026B:C11	ES 146
M00008045A:H02	ES 146
M00008053A:F10	ES 146
M00008063B:A06	ES 146
M00021665B:F12	ES 146
M00021671D:F12	ES 146
M00021852D:A05	ES 146
M00021866D:A03	ES 146
M00021908D:G12	ES 146
M00021919C:A10	ES 146
M00021923C:D11	ES 146
M00021955A:H02	ES 146
M00021964C:E10	ES 146
M00021972D:C11	ES 146
M00022005C:C06	ES 146
M00022015B:B07	ES 146
M00022054A:H03	ES 146
M00022084D:B01	ES 146
M00022099B:D06	ES 146
M00022105C:C12	ES 146
M00022127C:H03	ES 146
M00022135C:B05	ES 146
M00022138A:E05	ES 146
M00022175D:D12	ES 146
M00022178B:D06	ES 146
M00022181C:D01	ES 146
M00022183B:C02	ES 146
M00022184C:C11	ES 146
M00022233C:A12	ES 146
M00022234C:D06	ES 146
M00022247A:E02	ES 146
M00022257A:B09	ES 146
M00022262D:G03	ES 146
M00022264B:G10	ES 146
M00022363C:G12	ES 146
M00022365D:A03	ES 146
M00022373A:B05	ES 146
M00022373C:B07	ES 146

Clone Name	Tube
M00022391B:E01	ES 146
M00022391D:F10	ES 146
M00022416A:A07	ES 146
M00022421B:C11	ES 146
M00022433A:E02	ES 146
M00022434D:D06	ES 146
M00022440B:E01	ES 146
M00022444D:G01	ES 146
M00022467C:B12	ES 146
M00022489C:G04	ES 146
M00022492C:A02	ES 146
M00022495D:H08	ES 146
M00022496B:E12	ES 146
M00022499A:B02	ES 146
M00022533A:A08	ES 146
M00022579C:C11	ES 146
M00022597D:A06	ES 146
M00022602A:E09	ES 146
M00022615D:G05	ES 146
M00022634D:C08	ES 146
M00022640C:C12	ES 146
M00022641C:H05	ES 146
M00022646A:H10	ES 146
M00022662D:G11	ES 146
M00022667D:B02	ES 146
M00022668B:B12	ES 146
M00022670D:H11	ES 146
M00022671B:A08	ES 146
M00022684A:C02	ES 146
M00022731A:D02	ES 147
M00022739A:B03	ES 147
M00022747D:E03	ES 147
M00022767B:G11	ES 147
M00022785C:G06	ES 147
M00022793D:B01	ES 147
M00022795B:G06	ES 147
M00022797B:G08	ES 147
M00022817A:H02	ES 147
M00022821C:C09	ES 147
M00022823C:C01	ES 147
M00022830D:D01	ES 147
M00022834B:G11	ES 147
M00022854A:B03	ES 147
M00022856C:A07	ES 147
M00022860C:G04	ES 147

Clone Name	Tube
M00022885C:H05	ES 147
M00022895A:H08	ES 147
M00022910A:A06	ES 147
M00022925C:A08	ES 147
M00022928B:C01	ES 147
M00022930C:E02	ES 147
M00022938B:F07	ES 147
M00022968B:E02	ES 147
M00022976C:F04	ES 147
M00022979A:D05	ES 147
M00022986D:H09	ES 147
M00022997A:F06	ES 147
M00023001C:C08	ES 147
M00023003C:D07	ES 147
M00023007A:H04	ES 147
M00023007C:E10	ES 147
M00023020C:G08	ES 147
M00023024D:F12	ES 147
M00023032A:B05	ES 147
M00023039D:B05	ES 147
M00023042D:D02	ES 147
M00023044B:D02	ES 147
M00023094A:B11	ES 147
M00023100A:E12	ES 147
M00039181D:E05	ES 147
M00039184A:D03	ES 147
M00039184B:B09	ES 147
M00039361B:E01	ES 147
M00039363A:C09	ES 147
M00039366C:B07	ES 147
M00039367B:H02	ES 147
M00039371B:H06	ES 147
M00039372C:D12	ES 147
M00039374B:B07	ES 147
M00039374C:H12	ES 147
M00039374C:H02	ES 147
M00039376D:H07	ES 147
M00039377D:E12	ES 147
M00039378D:H07	ES 147
M00039379A:B03	ES 147
M00039380C:C09	ES 147
M00039482B:G02	ES 147
M00039493A:C04	ES 147
M00039496B:D08	ES 147
M00039496B:H09	ES 147

Clone Name	Tube
M00039497C:C06	ES 147
M00039499C:A04	ES 147
M00039500C:C04	ES 147
M00039505C:E03	ES 147
M00039508A:C12	ES 147
M00039508C:G01	ES 147
M00039510C:G02	ES 147
M00039512C:D06	ES 147
M00039515A:A06	ES 147
M00039515D:C11	ES 147
M00039517B:G12	ES 147
M00039521A:A02	ES 147
M00039521D:H03	ES 147
M00039528B:B12	ES 147
M00039529C:D07	ES 147
M00039530B:E02	ES 147
M00039533A:C12	ES 147
M00039533B:G08	ES 147
M00039533D:F04	ES 147
M00039535D:D10	ES 147
M00039536C:C10	ES 147
M00039536C:H11	ES 147
M00039561A:B07	ES 147
M00039561B:A09	ES 147
M00039562B:G02	ES 147
M00039564B:C01	ES 147
M00039570A:D10	ES 147
M00039570B:D10	ES 147
M00039584C:C01	ES 147
M00039584C:C11	ES 147
M00039587C:F12	ES 147
M00039590D:D02	ES 147
M00039591C:D06	ES 147
M00039595C:E05	ES 147
M00039597D:F04	ES 147
M00039600A:A11	ES 148
M00039604B:E05	ES 148
M00039604D:G03	ES 148
M00039606B:D08	ES 148
M00039607D:E08	ES 148
M00039608D:H01	ES 148
M00039609D:F07	ES 148
M00039624A:H09	ES 148
M00039624B:F12	ES 148
M00039625B:G08	ES 148

Clone Name	Tube
M00039626D:F04	ES 148
M00039629B:F01	ES 148
M00039629D:B04	ES 148
M00039630A:C08	ES 148
M00039630C:H04	ES 148
M00039641A:A05	ES 148
M00039641C:D07	ES 148
M00039642D:B12	ES 148
M00039642D:H09	ES 148
M00039643C:B04	ES 148
M00039645C:E01	ES 148
M00039647A:H11	ES 148
M00039736D:G08	ES 148
M00039740B:F10	ES 148
M00039752B:G08	ES 148
M00039755A:B08	ES 148
M00039756B:H06	ES 148
M00039760B:B08	ES 148
M00040131B:D11	ES 148
M00040131C:F03	ES 148
M00040131D:G08	ES 148
M00040133B:B03	ES 148
M00040136C:F08	ES 148
M00040138B:H03	ES 148
M00040141D:F05	ES 148
M00040143A:H05	ES 148
M00040145D:D03	ES 148
M00040147D:H11	ES 148
M00040160B:A10	ES 148
M00040162A:E01	ES 148
M00040169B:F08	ES 148
M00040173D:B05	ES 148
M00040174C:E10	ES 148
M00040174D:G03	ES 148
M00040181B:H09	ES 148
M00040181D:H10	ES 148
M00040182D:D06	ES 148
M00040183A:F07	ES 148
M00040184C:A11	ES 148
M00040191A:B09	ES 148
M00040221A:G11	ES 148
M00040222D:G02	ES 148
M00040223A:C05	ES 148
M00040226A:H10	ES 148
M00040230A:H02	ES 148

Clone Name	Tube
M00040231B:C08	ES 148
M00040232D:B07	ES 148
M00040233A:H02	ES 148
M00040233C:G05	ES 148
M00040252C:C06	ES 148
M00040253C:A05	ES 148
M00040254B:C10	ES 148
M00040256A:A06	ES 148
M00040257D:H10	ES 148
M00040260B:D02	ES 148
M00040260C:D04	ES 148
M00040261C:F01	ES 148
M00040262B:B06	ES 148
M00040264D:G05	ES 148
M00040265D:B07	ES 148
M00040265D:C08	ES 148
M00040267A:E06	ES 148
M00040267C:C04	ES 148
M00040271B:E12	ES 148
M00040271C:D08	ES 148
M00040273B:H12	ES 148
M00040274A:D07	ES 148
M00040274A:H11	ES 148
M00040280C:H05	ES 148
M00040281D:B01	ES 148
M00040282A:A03	ES 148
M00040286C:C02	ES 148
M00040287C:B09	ES 148
M00040287D:D07	ES 148
M00039746C:A08	ES 148
M00039746C:G09	ES 148
M00039746C:H05	ES 148
M00039746C:H06	ES 148
M00039746D:D11	ES 148
M00039748A:F11	ES 148
M00039748C:F11	ES 148
M00039749D:D05	ES 148
M00039761D:E10	ES 148
M00039762B:F07	ES 148
M00039764C:D07	ES 148
M00039766A:G07	ES 148
M00039766D:H01	ES 149
M00039767B:A04	ES 149
M00039767C:E12	ES 149
M00039770A:G11	ES 149

Clone Name	Tube
M00039770C:E04	ES 149
M00039942D:C01	ES 149
M00039943B:F10	ES 149
M00039945C:F09	ES 149
M00039946B:F08	ES 149
M00039947A:D06	ES 149
M00039947C:G03	ES 149
M00039948A:E03	ES 149
M00039948D:D11	ES 149
M00039951A:B07	ES 149
M00039951B:B12	ES 149
M00039951B:C03	ES 149
M00039955C:C04	ES 149
M00039957C:C09	ES 149
M00039957D:A12	ES 149
M00039958A:A08	ES 149
M00039958C:B09	ES 149
M00040201C:G11	ES 149
M00040202A:F05	ES 149
M00040203A:H06	ES 149
M00040203B:A05	ES 149
M00040203D:H11	ES 149
M00040206A:A07	ES 149
M00040207B:D08	ES 149
M00040208A:C03	ES 149
M00040208B:A07	ES 149
M00040208D:G09	ES 149
M00040217D:B07	ES 149
M00040218C:C02	ES 149
M00040219B:D02	ES 149
M00040219D:E08	ES 149
M00040291D:C05	ES 149
M00040293D:G04	ES 149
M00040294D:D12	ES 149
M00040296D:E09	ES 149
M00040298B:G02	ES 149
M00040299B:F10	ES 149
M00040313C:D05	ES 149
M00040313D:E04	ES 149
M00040314D:H05	ES 149
M00040317A:H03	ES 149
M00040317D:F02	ES 149
M00040318A:B02	ES 149
M00040318C:H11	ES 149
M00040320D:F02	ES 149

Clone Name	Tube
M00040323B:C12	ES 149
M00040323C:G11	ES 149
M00040326A:F04	ES 149
M00040327B:G06	ES 149
M00040332D:B05	ES 149
M00040333D:G05	ES 149
M00040334D:B02	ES 149
M00040334D:C07	ES 149
M00040342B:D12	ES 149
M00040345D:A09	ES 149
M00040346A:C11	ES 149
M00040347D:F09	ES 149
M00040349D:B09	ES 149
M00040351B:F02	ES 149
M00040351D:A11	ES 149
M00040364A:E05	ES 149
M00040366A:B01	ES 149
M00040368A:A12	ES 149
M00040368A:F01	ES 149
M00040368D:E09	ES 149
M00040371C:H05	ES 149
M00040375C:B06	ES 149
M00040376C:G02	ES 149
M00040377C:G07	ES 149
M00040383A:H02	ES 149
M00040383D:C04	ES 149
M00040385C:D02	ES 149
M00040386A:A02	ES 149
M00040387C:E07	ES 149
M00040387D:H05	ES 149
M00040390A:H02	ES 149
M00040390B:F02	ES 149
M00040391A:D10	ES 149
M00040392B:H01	ES 149
M00040392C:B12	ES 149
M00040394A:D04	ES 149
M00040395B:D11	ES 149
M00042534A:A05	ES 149
M00042538B:E06	ES 149
M00042543C:G04	ES 149
M00042558A:F03	ES 149
M00042560A:F12	ES 149
M00042565C:A08	ES 149
M00042566C:C05	ES 149
M00042567B:H10	ES 149

Clone Name	Tube
M00042693D:E04	ES 149
M00042696B:E05	ES 149
M00042697D:C07	ES 150
M00042698D:D10	ES 150
M00042698D:E01	ES 150
M00042702B:G02	ES 150
M00042704A:F09	ES 150
M00042711B:A11	ES 150
M00042717A:C07	ES 150
M00042737C:H04	ES 150
M00042740A:E09	ES 150
M00042742D:D05	ES 150
M00042887C:D07	ES 150
M00042895A:D10	ES 150
M00042895C:G01	ES 150
M00042902D:B08	ES 150
M00042904B:E07	ES 150
M00042905A:F11	ES 150
M00042905B:C03	ES 150
M00042905D:D02	ES 150
M00042347D:H11	ES 150
M00042348B:E05	ES 150
M00042349D:D07	ES 150
M00042431B:G08	ES 150
M00042431C:F01	ES 150
M00042431D:C10	ES 150
M00042432D:E02	ES 150
M00042435A:A11	ES 150
M00042436B:H09	ES 150
M00042437A:D04	ES 150
M00042439B:B03	ES 150
M00042439B:D03	ES 150
M00042440B:E09	ES 150
M00042463A:F09	ES 150
M00042470C:E05	ES 150
M00042511A:H04	ES 150
M00042515C:F08	ES 150
M00042751C:C12	ES 150
M00042752A:E11	ES 150
M00042756B:F11	ES 150
M00042756D:A10	ES 150
M00042759B:G11	ES 150
M00042760A:C12	ES 150
M00042765C:D04	ES 150
M00042767B:G10	ES 150

Clone Name	Tube
M00042769C:E09	ES 150
M00042770B:B12	ES 150
M00042770C:C04	ES 150
M00042771C:F06	ES 150
M00042774C:C05	ES 150
M00042781A:A07	ES 150
M00042784A:H06	ES 150
M00042788C:F11	ES 150
M00042790C:C07	ES 150
M00042792A:H01	ES 150
M00042797D:D10	ES 150
M00042799D:F08	ES 150
M00042800A:A03	ES 150
M00042802C:C04	ES 150
M00042806C:F07	ES 150
M00042807D:D05	ES 150
M00042823C:C02	ES 150
M00042830B:E02	ES 150
M00042839B:B11	ES 150
M00042841D:H07	ES 150
M00042849D:F11	ES 150
M00042852B:A03	ES 150
M00042852C:A01	ES 150
M00042856B:H02	ES 150
M00042352C:H03	ES 150
M00042352D:C01	ES 150
M00042352D:G09	ES 150
M00042448A:C09	ES 150
M00042448C:H12	ES 150
M00042453B:G09	ES 150
M00042518D:A06	ES 150
M00042518D:D04	ES 150
M00043296B:G09	ES 150
M00043304B:D05	ES 150
M00043304C:D02	ES 150
M00043305B:G02	ES 150
M00043306C:B03	ES 150
M00043306D:B07	ES 150
M00043310C:G06	ES 150
M00043311C:E03	ES 150
M00043312C:E08	ES 150
M00043320B:A07	ES 150
M00043324D:H11	ES 150
M00043328D:H02	ES 150
M00043332C:G04	ES 150

Clone Name	Tube
M00043334B:A10	ES 150
M00043338B:A03	ES 150
M00043338B:C11	ES 150
M00043339A:F11	ES 150
M00043340B:H08	ES 150
M00043344D:E04	ES 150
M00043345C:A06	ES 150
M00043346A:G01	ES 150
M00043350D:B11	ES 151
M00043351D:A11	ES 151
M00043352D:B05	ES 151
M00043352D:C03	ES 151
M00043359B:D10	ES 151
M00043359C:G01	ES 151
M00043361B:A01	ES 151
M00043366A:A02	ES 151
M00043366C:H05	ES 151
M00043367B:A08	ES 151
M00043368C:F09	ES 151
M00043370B:C08	ES 151
M00043372C:G05	ES 151
M00043377A:C03	ES 151
M00043378A:H10	ES 151
M00043379D:H02	ES 151
M00043383C:F12	ES 151
M00043383D:A02	ES 151
M00043384B:B02	ES 151
M00043386A:B08	ES 151
M00043389C:E03	ES 151
M00043389D:D07	ES 151
M00043391A:C10	ES 151
M00043391A:G08	ES 151
M00043392D:C11	ES 151
M00043393A:B08	ES 151
M00043401D:G08	ES 151
M00043402C:D08	ES 151
M00043405A:D11	ES 151
M00043405C:G12	ES 151
M00043405C:G02	ES 151
M00043406B:G12	ES 151
M00043407C:E05	ES 151
M00043408B:D11	ES 151
M00043409B:B03	ES 151
M00043410C:A09	ES 151
M00043411B:D08	ES 151

Clone Name	Tube
M00043411D:H06	ES 151
M00042584B:C10	ES 151
M00042623D:D07	ES 151
M00042625C:B04	ES 151
M00042626B:D08	ES 151
M00042627C:D01	ES 151
M00042630A:C05	ES 151
M00042955C:D05	ES 151
M00042956C:B06	ES 151
M00042960D:H08	ES 151
M00042962D:C05	ES 151
M00042964D:A03	ES 151
M00042966B:F07	ES 151
M00042966C:E06	ES 151
M00042970C:A04	ES 151
M00042970C:H10	ES 151
M00042976A:H04	ES 151
M00042979B:E02	ES 151
M00042981B:D11	ES 151
M00042983C:A11	ES 151
M00042983C:G06	ES 151
M00042986C:G12	ES 151
M00042988A:F06	ES 151
M00042997B:D06	ES 151
M00042998A:E03	ES 151
M00042998A:G04	ES 151
M00043001B:H10	ES 151
M00043001D:D03	ES 151
M00043002A:E05	ES 151
M00043003C:D08	ES 151
M00043011A:H12	ES 151
M00043015A:H10	ES 151
M00043022A:E12	ES 151
M00043026C:D07	ES 151
M00043028A:G05	ES 151
M00043029C:A06	ES 151
M00043032C:A10	ES 151
M00043034D:C01	ES 151
M00043036C:E05	ES 151
M00043036D:C09	ES 151
M00043040B:B07	ES 151
M00043044B:A12	ES 151
M00043044D:A09	ES 151
M00043045D:G12	ES 151
M00043046D:B11	ES 151

Clone Name	Tube
M00043060D:G12	ES 151
M00043066B:H11	ES 151
M00043067D:D10	ES 151
M00043125A:B11	ES 151
M00043125C:A11	ES 151
M00042611A:A06	ES 151
M00042611D:B12	ES 151
M00042612D:F06	ES 151
M00042614B:B05	ES 151
M00043073A:C12	ES 151
M00043078D:D04	ES 151
M00043081D:F05	ES 151
M00043087B:G07	ES 151
M00043093C:G11	ES 151
M00043095A:F09	ES 152
M00043096A:G04	ES 152
M00043108A:F06	ES 152
M00043109C:G01	ES 152
M00043131B:A09	ES 152
M00043133B:C11	ES 152
M00043138D:B11	ES 152
M00043143B:A10	ES 152
M00043148C:A09	ES 152
M00043154A:B07	ES 152
M00043162A:B08	ES 152
M00043162D:C12	ES 152
M00043164C:E12	ES 152
M00043165B:G01	ES 152
M00043173D:G03	ES 152
M00043184A:H08	ES 152
M00043187A:C04	ES 152
M00043191A:A07	ES 152
M00043192C:B12	ES 152
M00043200A:H09	ES 152
M00043200B:C08	ES 152
M00043202B:F01	ES 152
M00043203A:B09	ES 152
M00043210C:E05	ES 152
M00043211A:F01	ES 152
M00043213B:B12	ES 152
M00043215A:D02	ES 152
M00043220B:C04	ES 152
M00042591D:H03	ES 152
M00042592A:H10	ES 152
M00042593A:C02	ES 152

Clone Name	Tube
M00042593C:G06	ES 152
M00042595A:A11	ES 152
M00042595A:B01	ES 152
M00042596B:F06	ES 152
M00042596C:D07	ES 152
M00042597B:E12	ES 152
M00043416C:A02	ES 152
M00043417C:D05	ES 152
M00043418A:H10	ES 152
M00043419D:A10	ES 152
M00043428D:G08	ES 152
M00043430B:C02	ES 152
M00043431D:B08	ES 152
M00043433B:G09	ES 152
M00043433C:G07	ES 152
M00043437D:D04	ES 152
M00043440C:B07	ES 152
M00043446C:E12	ES 152
M00043447A:C07	ES 152
M00043449A:E12	ES 152
M00043450C:C06	ES 152
M00043453B:B09	ES 152
M00043458A:B12	ES 152
M00043461D:C02	ES 152
M00043461D:E06	ES 152
M00043465B:H02	ES 152
M00043465C:A03	ES 152
M00043465C:C09	ES 152
M00043476A:F07	ES 152
M00043483B:G10	ES 152
M00043491C:F04	ES 152
M00043492A:E01	ES 152
M00043513D:G08	ES 152
M00043516B:H09	ES 152
M00043518B:D06	ES 152
M00043526B:D10	ES 152
M00043527C:E09	ES 152
M00043528C:A02	ES 152
M00043616B:F02	ES 152
M00043616C:A05	ES 152
M00043632D:F09	ES 152
M00043634A:C10	ES 152
M00043635C:C11	ES 152
M00043636B:C06	ES 152
M00043637C:H01	ES 152

Clone Name	Tube
M00043638A:D06	ES 152
M00043640C:E03	ES 152
M00043648A:G07	ES 152
M00043649B:E07	ES 152
M00001338C:B02	ES 153
M00001338C:F05	ES 153
M00001338D:D01	ES 153
M00001340D:F07	ES 153
M00001344D:E08	ES 153
M00001346B:G11	ES 153
M00001348B:B03	ES 153
M00001349C:B04	ES 153
M00001351B:E11	ES 153
M00001352B:B02	ES 153
M00001353A:H07	ES 153
M00001353C:A05	ES 153
M00001353D:E05	ES 153
M00001356D:E06	ES 153
M00001358A:E08	ES 153
M00001359A:H10	ES 153
M00001361A:C12	ES 153
M00001361B:A12	ES 153
M00001362A:F09	ES 153
M00001364A:C09	ES 153
M00001364C:H10	ES 153
M00001368A:A08	ES 153
M00001368A:B07	ES 153
M00001368A:C02	ES 153
M00001369A:G06	ES 153
M00001374A:B02	ES 153
M00001374C:B10	ES 153
M00001375B:D04	ES 153
M00001378C:E10	ES 153
M00001379A:F09	ES 153
M00001382D:A07	ES 153
M00001382D:H08	ES 153
M00001384A:A07	ES 153
M00001385A:E07	ES 153
M00001386B:F11	ES 153
M00001387A:C12	ES 153
M00001387B:A11	ES 153
M00001389B:E10	ES 153
M00001389D:D06	ES 153
M00001390D:E02	ES 153
M00001391D:D03	ES 153

Clone Name	Tube
M00001393B:C03	ES 153
M00001393C:E08	ES 153
M00001393C:F04	ES 153
M00001393D:E02	ES 153
M00001396B:B01	ES 153
M00001396B:B12	ES 153
M00001396D:H02	ES 153
M00001397C:H08	ES 153
M00001399B:B01	ES 153
M00001399C:A01	ES 153
M00001403C:B03	ES 153
M00001403D:C12	ES 153
M00001406B:H09	ES 153
M00001406D:F06	ES 153
M00001410A:G10	ES 153
M00001416B:A05	ES 153
M00001421B:E07	ES 153
M00001422B:D06	ES 153
M00001424B:H06	ES 153
M00001424D:D02	ES 153
M00001426C:F06	ES 153
M00001428B:C10	ES 153
M00001429B:G05	ES 153
M00001430B:C01	ES 153
M00001433B:E02	ES 153
M00001442A:F08	ES 153
M00001442C:G12	ES 153
M00001444B:E04	ES 153
M00001444C:D11	ES 153
M00001445B:F06	ES 153
M00001449B:H10	ES 153
M00001451C:E10	ES 153
M00001460C:E10	ES 153
M00001461D:B10	ES 153
M00001461D:C10	ES 153
M00001465C:A02	ES 153
M00001466B:F03	ES 153
M00001467C:D04	ES 153
M00001477D:G09	ES 153
M00001485C:F06	ES 153
M00001488C:A03	ES 153
M00001497C:F10	ES 153
M00001503B:H10	ES 153
M00001506B:D11	ES 153
M00001512D:F08	ES 153

Clone Name	Tube
M00001518B:D10	ES 153
M00001528C:C03	ES 153
M00001532A:G08	ES 153
M00001533C:G11	ES 153
M00001533D:A01	ES 153
M00001534C:E07	ES 153
M00001535B:B10	ES 153
M00001535B:E02	ES 153
M00001537B:H10	ES 153
M00001538B:A07	ES 153
M00001539C:F12	ES 154
M00001542B:F09	ES 154
M00001543C:A08	ES 154
M00001544B:B05	ES 154
M00001544B:E06	ES 154
M00001546B:C11	ES 154
M00001548B:D06	ES 154
M00001550A:H06	ES 154
M00001550D:B11	ES 154
M00001551D:D01	ES 154
M00001551D:H09	ES 154
M00001554C:G10	ES 154
M00001558A:E06	ES 154
M00001559A:H09	ES 154
M00001561D:H04	ES 154
M00001562B:B02	ES 154
M00001562D:B07	ES 154
M00001565A:H05	ES 154
M00001568C:A03	ES 154
M00001570A:B07	ES 154
M00001591B:H05	ES 154
M00001596A:D02	ES 154
M00001600B:G01	ES 154
M00001605B:B05	ES 154
M00001606B:A10	ES 154
M00001606D:D06	ES 154
M00001607A:E04	ES 154
M00001607D:H09	ES 154
M00001609D:C11	ES 154
M00001616D:F03	ES 154
M00001617C:F10	ES 154
M00001618C:D01	ES 154
M00001619C:H09	ES 154
M00001620B:A03	ES 154
M00001623D:A10	ES 154

Clone Name	Tube
M00001623D:E12	ES 154
M00001624A:C01	ES 154
M00001625D:B04	ES 154
M00001626A:D07	ES 154
M00001632C:A10	ES 154
M00001633D:C11	ES 154
M00001637D:C12	ES 154
M00001648A:D10	ES 154
M00001661D:F06	ES 154
M00001663A:A12	ES 154
M00001671A:H10	ES 154
M00001671C:F03	ES 154
M00001675B:D06	ES 154
M00001677B:H08	ES 154
M00001680A:A01	ES 154
M00001683B:F11	ES 154
M00001684D:E04	ES 154
M00001686B:H01	ES 154
M00001686D:F06	ES 154
M00001688B:B11	ES 154
M00001692C:C04	ES 154
M00001771B:E06	ES 154
M00003746C:E11	ES 154
M00003749C:C08	ES 154
M00003753A:C11	ES 154
M00003758B:D07	ES 154
M00003758B:F06	ES 154
M00003760C:G10	ES 154
M00003761B:B02	ES 154
M00003763A:B02	ES 154
M00003763B:B10	ES 154
M00003764A:H09	ES 154
M00003764B:F11	ES 154
M00003764B:H11	ES 154
M00003764D:F07	ES 154
M00003768D:D08	ES 154
M00003770C:A10	ES 154
M00003771D:A03	ES 154
M00003773A:F10	ES 154
M00003780A:G01	ES 154
M00003782A:B02	ES 154
M00003785D:F07	ES 154
M00003787D:A10	ES 154
M00003808A:F11	ES 154
M00003808B:E07	ES 154

Clone Name	Tube
M00003812C:A03	ES 154
M00003814A:G05	ES 154
M00003819B:B01	ES 154
M00003820B:F11	ES 154
M00003821C:E12	ES 154
M00003822C:A09	ES 154
M00003822D:A02	ES 154
M00003823B:A06	ES 154
M00003825A:H10	ES 154
M00003828A:D11	ES 154
M00003830B:C06	ES 154
M00003830C:D02	ES 154
M00003837C:D10	ES 154
M00003839C:H10	ES 154
M00003842D:D11	ES 154
M00003842D:H09	ES 154
M00003845A:C07	ES 155
M00003845D:G03	ES 155
M00003847A:H04	ES 155
M00003848C:G09	ES 155
M00003851B:A01	ES 155
M00003854B:F07	ES 155
M00003855C:F02	ES 155
M00003884A:E12	ES 155
M00003887C:E09	ES 155
M00003888B:F09	ES 155
M00003891B:H02	ES 155
M00003898C:A01	ES 155
M00003900C:D12	ES 155
M00003906A:C02	ES 155
M00003911C:A09	ES 155
M00003914A:A08	ES 155
M00003915C:D10	ES 155
M00003915C:G08	ES 155
M00003916A:E04	ES 155
M00003926A:F11	ES 155
M00003935B:B01	ES 155
M00003938C:A05	ES 155
M00003942A:D01	ES 155
M00003958C:H08	ES 155
M00003959D:A05	ES 155
M00003960D:C12	ES 155
M00003963D:F01	ES 155
M00003965D:D11	ES 155
M00003968C:G03	ES 155

Clone Name	Tube
M00003970D:H07	ES 155
M00003972C:F07	ES 155
M00003974C:E11	ES 155
M00003974D:E02	ES 155
M00003979B:A04	ES 155
M00003980D:C06	ES 155
M00003985D:B02	ES 155
M00003988D:B01	ES 155
M00003991A:C11	ES 155
M00003993C:D07	ES 155
M00003993D:B03	ES 155
M00003994A:B10	ES 155
M00003996B:H07	ES 155
M00003998B:G10	ES 155
M00004028B:F10	ES 155
M00004029D:A01	ES 155
M00004031C:G06	ES 155
M00004036B:A11	ES 155
M00004036D:C12	ES 155
M00004038A:A04	ES 155
M00004042B:A11	ES 155
M00004047C:B09	ES 155
M00004047D:F12	ES 155
M00004053D:F09	ES 155
M00004054A:D03	ES 155
M00004055C:B10	ES 155
M00004055D:D05	ES 155
M00004057D:G01	ES 155
M00004061B:E05	ES 155
M00004062D:A02	ES 155
M00004066D:G10	ES 155
M00004067B:D03	ES 155
M00004080C:C04	ES 155
M00004085A:H01	ES 155
M00004085B:H02	ES 155
M00004087C:E02	ES 155
M00004093A:C03	ES 155
M00004096D:F02	ES 155
M00004102A:E03	ES 155
M00004103C:E10	ES 155
M00004104A:A12	ES 155
M00004110D:F09	ES 155
M00004114C:D11	ES 155
M00004115A:G12	ES 155
M00004118C:D12	ES 155

Clone Name	Tube
M00004122C:D01	ES 155
M00004134A:A08	ES 155
M00004136C:B12	ES 155
M00004139B:F01	ES 155
M00004141A:D01	ES 155
M00004141B:B01	ES 155
M00004141B:F08	ES 155
M00004143B:B04	ES 155
M00004144D:B02	ES 155
M00004146A:C11	ES 155
M00004146B:E08	ES 155
M00004146C:B04	ES 155
M00004147C:E01	ES 155
M00004151B:A07	ES 155
M00004155A:H03	ES 155
M00004155C:A10	ES 155
M00004158B:E03	ES 155
M00004158D:E08	ES 155
M00004159C:D10	ES 155
M00004159D:F12	ES 155
M00004160D:F06	ES 155
M00004160D:G05	ES 155
M00004162D:F02	ES 156
M00004163B:C03	ES 156
M00004163C:A03	ES 156
M00004164B:E12	ES 156
M00004165C:A11	ES 156
M00004166C:B10	ES 156
M00004169A:E04	ES 156
M00004170A:F03	ES 156
M00004171B:B03	ES 156
M00004172C:A08	ES 156
M00004172D:B12	ES 156
M00004172D:F04	ES 156
M00004175D:E06	ES 156
M00004176C:A09	ES 156
M00004179C:B06	ES 156
M00004179D:A12	ES 156
M00004187B:C02	ES 156
M00004189A:C12	ES 156
M00004192C:B06	ES 156
M00004195A:F07	ES 156
M00004200C:A04	ES 156
M00004201D:C01	ES 156
M00004201D:C03	ES 156

Clone Name	Tube
M00004204C:H08	ES 156
M00004207C:A04	ES 156
M00004208A:D08	ES 156
M00004210A:A03	ES 156
M00004212D:C03	ES 156
M00004214A:E05	ES 156
M00004214D:A05	ES 156
M00004215B:C05	ES 156
M00004220D:C11	ES 156
M00004225D:E03	ES 156
M00004229B:B06	ES 156
M00004230D:B05	ES 156
M00004237C:D10	ES 156
M00004242D:H01	ES 156
M00004245C:G10	ES 156
M00004246B:H07	ES 156
M00004251D:D03	ES 156
M00004263C:D03	ES 156
M00004266B:F07	ES 156
M00004269A:F11	ES 156
M00004269A:G11	ES 156
M00004269B:B04	ES 156
M00004270A:E09	ES 156
M00004276C:A08	ES 156
M00004277D:B02	ES 156
M00004278A:G06	ES 156
M00004278C:B10	ES 156
M00004281A:C04	ES 156
M00004282A:D01	ES 156
M00004282B:D07	ES 156
M00004282C:A12	ES 156
M00004284A:F08	ES 156
M00004295D:C07	ES 156
M00004296B:D03	ES 156
M00004303C:C05	ES 156
M00004310B:E02	ES 156
M00004316A:B03	ES 156
M00004320C:E07	ES 156
M00004321C:C11	ES 156
M00004322B:D03	ES 156
M00004324A:B03	ES 156
M00004324A:D10	ES 156
M00004324A:D05	ES 156
M00004328A:D01	ES 156
M00004330A:A01	ES 156

Clone Name	Tube
M00004336A:A01	ES 156
M00004341C:A09	ES 156
M00004341C:E05	ES 156
M00004344A:G11	ES 156
M00004344D:C12	ES 156
M00004347B:E04	ES 156
M00004347C:A05	ES 156
M00004350A:A04	ES 156
M00004351B:G07	ES 156
M00004352A:D08	ES 156
M00004357B:B06	ES 156
M00004358B:G02	ES 156
M00004359A:E01	ES 156
M00004360C:D09	ES 156
M00004365C:C09	ES 156
M00004365C:G11	ES 156
M00004366D:C11	ES 156
M00004368A:B11	ES 156
M00004372A:E12	ES 156
M00004376D:A12	ES 156
M00004385C:H12	ES 156
M00004393C:D06	ES 156
M00004406A:G09	ES 156
M00004416B:G10	ES 156
M00004418B:A11	ES 156
M00004419A:G02	ES 156
M00004420D:E05	ES 156
M00004430A:A05	ES 156
M00004430B:B10	ES 157
M00004443C:F07	ES 157
M00004462D:D12	ES 157
M00004502A:D12	ES 157
M00004507D:E03	ES 157
M00004509B:B10	ES 157
M00004509D:C06	ES 157
M00004603B:E02	ES 157
M00004603C:C10	ES 157
M00004606D:H09	ES 157
M00004608A:C10	ES 157
M00004608A:H04	ES 157
M00004609A:E09	ES 157
M00023389A:G04	ES 157
M00023394D:D10	ES 157
M00026809A:H08	ES 157
M00026818C:E01	ES 157

Clone Name	Tube
M00026836B:H03	ES 157
M00026842B:A01	ES 157
M00026842D:C02	ES 157
M00026850B:C09	ES 157
M00026856B:G03	ES 157
M00026900A:H07	ES 157
M00026907D:E07	ES 157
M00026910B:G06	ES 157
M00026914C:H09	ES 157
M00026936D:C07	ES 157
M00026961A:B06	ES 157
M00026994D:D07	ES 157
M00027004C:C11	ES 157
M00027017A:B09	ES 157
M00027036A:B06	ES 157
M00027050A:B02	ES 157
M00027052A:E10	ES 157
M00027057C:D10	ES 157
M00027064B:D06	ES 157
M00027081A:A08	ES 157
M00027093A:H02	ES 157
M00027131A:B03	ES 157
M00027159C:F07	ES 157
M00027167C:B10	ES 157
M00027168B:H08	ES 157
M00027170D:C07	ES 157
M00027173C:E11	ES 157
M00027177B:D04	ES 157
M00027178B:A11	ES 157
M00027182B:G06	ES 157
M00027189C:B10	ES 157
M00027193C:A07	ES 157
M00027215A:F06	ES 157
M00027215B:B12	ES 157
M00027244C:B06	ES 157
M00027247C:D02	ES 157
M00027262A:A07	ES 157
M00027270A:D04	ES 157
M00027274A:A09	ES 157
M00027290C:F06	ES 157
M00027291A:G08	ES 157
M00027311A:H09	ES 157
M00027313C:E01	ES 157
M00027314D:E02	ES 157
M00027316C:C03	ES 157

Clone Name	Tube
M00027319C:C03	ES 157
M00027319D:F07	ES 157
M00027332B:H09	ES 157
M00027359B:A06	ES 157
M00027363D:G04	ES 157
M00027364B:E12	ES 157
M00027376C:A02	ES 157
M00027381B:B04	ES 157
M00027400D:H02	ES 157
M00027433B:D12	ES 157
M00027457B:E11	ES 157
M00027459C:B10	ES 157
M00027467A:C07	ES 157
M00027475D:A01	ES 157
M00027480C:E09	ES 157
M00027485C:F07	ES 157
M00027506B:G01	ES 157
M00027513D:F06	ES 157
M00027523A:H05	ES 157
M00027527B:C05	ES 157
M00027549C:G03	ES 157
M00027569A:E05	ES 157
M00027586A:C09	ES 157
M00027589B:G07	ES 157
M00027591A:E04	ES 157
M00027600B:C07	ES 157
M00027605B:D09	ES 157
M00027688C:C01	ES 157
M00027717C:C06	ES 157
M00027724D:D04	ES 157
M00027734D:C03	ES 157
M00027746A:D06	ES 157
M00027801B:D07	ES 157
M00027806C:H05	ES 157
M00028055B:G07	ES 158
M00028063C:H01	ES 158
M00028067A:C11	ES 158
M00028069D:H02	ES 158
M00028070A:H09	ES 158
M00028070D:C03	ES 158
M00028188C:H11	ES 158
M00028193B:E07	ES 158
M00028196A:G03	ES 158
M00028210B:H03	ES 158
M00028211A:F10	ES 158

Clone Name	Tube
M00028212D:C05	ES 158
M00028219B:H05	ES 158
M00028361B:H08	ES 158
M00028366B:B08	ES 158
M00028616C:D09	ES 158
M00028620C:C07	ES 158
M00028763A:G11	ES 158
M00028764B:D03	ES 158
M00028771A:E02	ES 158
M00028773C:C05	ES 158
M00028774D:E10	ES 158
M00028777B:G04	ES 158
M00028782A:F01	ES 158
M00028784A:D12	ES 158
M00028786B:A04	ES 158
M00031370B:C01	ES 158
M00031416D:H05	ES 158
M00031484A:D03	ES 158
M00031485B:G05	ES 158
M00032471D:A05	ES 158
M00032473B:A03	ES 158
M00032474A:G03	ES 158
M00032475A:A06	ES 158
M00032489B:G12	ES 158
M00032490D:E08	ES 158
M00032494C:H08	ES 158
M00032497D:B10	ES 158
M00032504B:B10	ES 158
M00032507D:G08	ES 158
M00032508A:E03	ES 158
M00032515A:B12	ES 158
M00032517C:E10	ES 158
M00032519D:F08	ES 158
M00032534B:E12	ES 158
M00032541C:G03	ES 158
M00032553A:A07	ES 158
M00032556D:A03	ES 158
M00032562C:F01	ES 158
M00032567B:G05	ES 158
M00032568B:F08	ES 158
M00032577D:F01	ES 158
M00032580D:A09	ES 158
M00032581B:A09	ES 158
M00032584A:D06	ES 158
M00032586C:B04	ES 158

Clone Name	Tube
M00032590B:H01	ES 158
M00032594C:F05	ES 158
M00032597A:H02	ES 158
M00032605B:D09	ES 158
M00032613A:E11	ES 158
M00032614C:B10	ES 158
M00032614D:D08	ES 158
M00032620B:F06	ES 158
M00032621A:F11	ES 158
M00032628C:B06	ES 158
M00032634B:D09	ES 158
M00032637A:F09	ES 158
M00032638B:F02	ES 158
M00032644C:B05	ES 158
M00032645D:C01	ES 158
M00032647B:F06	ES 158
M00032652C:C07	ES 158
M00032666A:C02	ES 158
M00032671B:D06	ES 158
M00032671B:D08	ES 158
M00032676C:C10	ES 158
M00032688C:A03	ES 158
M00032700A:E09	ES 158
M00032707D:F08	ES 158
M00032711B:F01	ES 158
M00032723D:H02	ES 158
M00032727A:E04	ES 158
M00032728D:F01	ES 158
M00032729A:F10	ES 158
M00032733B:F12	ES 158
M00032734B:E12	ES 158
M00032734C:C05	ES 158
M00032749D:G03	ES 158
M00032753A:C07	ES 158
M00032759A:A03	ES 158
M00032765A:C05	ES 158
M00032770C:G11	ES 158
M00032772D:D03	ES 158
M00032773D:F08	ES 158
M00032774C:C04	ES 158
M00032787D:C05	ES 159
M00032791B:H11	ES 159
M00032791D:F01	ES 159
M00032792C:B01	ES 159
M00032793A:G06	ES 159

Clone Name	Tube
M00032795C:A03	ES 159
M00032797D:D08	ES 159
M00032825B:F08	ES 159
M00032826C:D10	ES 159
M00032828A:A06	ES 159
M00032829D:A05	ES 159
M00032830D:D02	ES 159
M00032831A:C07	ES 159
M00032831A:E09	ES 159
M00032835D:G04	ES 159
M00032836B:A07	ES 159
M00032848D:B10	ES 159
M00032892C:C12	ES 159
M00032908A:D08	ES 159
M00032918D:B04	ES 159
M00032928C:D02	ES 159
M00032944A:B07	ES 159
M00032945D:B07	ES 159
M00032979D:C11	ES 159
M00032979D:H07	ES 159
M00032985D:G09	ES 159
M00032987B:F01	ES 159
M00032988B:G01	ES 159
M00033006A:F10	ES 159
M00033028C:A02	ES 159
M00033028D:C10	ES 159
M00033037B:F04	ES 159
M00033041A:B11	ES 159
M00033055D:D02	ES 159
M00033071C:G05	ES 159
M00033071D:E08	ES 159
M00033072A:A09	ES 159
M00033080C:A07	ES 159
M00033081D:D11	ES 159
M00033144A:D02	ES 159
M00033146D:A03	ES 159
M00033147C:B08	ES 159
M00033149B:E10	ES 159
M00033150B:E02	ES 159
M00033150C:A11	ES 159
M00033183B:F10	ES 159
M00033218C:F07	ES 159
M00033223C:G04	ES 159
M00033230C:G10	ES 159
M00033232B:C08	ES 159

Clone Name	Tube
M00033246A:H12	ES 159
M00033248D:H11	ES 159
M00033264B:E06	ES 159
M00033274D:F03	ES 159
M00033311B:G10	ES 159
M00033324B:F04	ES 159
M00033326B:B05	ES 159
M00033329C:C02	ES 159
M00033296C:C11	ES 159
M00033302A:E11	ES 159
M00033302B:F10	ES 159
M00033303C:F09	ES 159
M00033342B:F03	ES 159
M00033344A:B06	ES 159
M00033359C:H05	ES 159
M00033360C:A03	ES 159
M00033374D:C07	ES 159
M00033413A:A08	ES 159
M00033420B:E08	ES 159
M00033434D:F05	ES 159
M00033441A:B12	ES 159
M00033445D:G03	ES 159
M00038290A:D12	ES 159
M00038304B:E02	ES 159
M00038389D:D10	ES 159
M00038390B:F02	ES 159
M00038616C:C09	ES 159
M00038616D:B07	ES 159
M00038618D:D08	ES 159
M00038619B:F09	ES 159
M00038619D:C12	ES 159
M00039001A:B10	ES 159
M00039024D:E12	ES 159
M00039055C:A01	ES 159
M00039056B:G01	ES 159
M00039063C:H09	ES 159
M00039067A:C05	ES 159
M00039067B:F07	ES 159
M00039076D:G04	ES 159
M00039078B:B03	ES 159
M00039078D:C10	ES 159
M00039081B:C04	ES 159
M00039081B:G07	ES 159
M00039100A:G04	ES 159
M00039105D:A08	ES 159

Clone Name	Tube
M00039107A:E12	ES 159
M00039111A:C12	ES 160
M00039121D:E07	ES 160
M00039124D:H01	ES 160
M00039125D:H12	ES 160
M00039131C:B09	ES 160
M00039133B:D06	ES 160
M00039133C:F12	ES 160
M00039134D:F08	ES 160
M00039138B:G05	ES 160
M00039140A:F05	ES 160
M00039143A:F04	ES 160
M00039143D:C10	ES 160
M00039146B:G04	ES 160
M00039162D:C04	ES 160
M00039165D:C04	ES 160
M00039175A:F01	ES 160
M00039204A:E09	ES 160
M00039207A:F07	ES 160
M00039219B:C08	ES 160
M00039222B:A04	ES 160
M00039225A:D11	ES 160
M00039246B:A08	ES 160
M00039248C:A08	ES 160
M00039251C:H12	ES 160
M00039251D:B08	ES 160
M00039255D:B01	ES 160
M00039258C:C01	ES 160
M00039270D:D02	ES 160
M00039275B:E02	ES 160
M00039278C:D03	ES 160
M00039284D:H07	ES 160
M00039285B:G04	ES 160
M00039291D:F02	ES 160
M00039294C:B09	ES 160
M00039302B:E10	ES 160
M00039326A:G07	ES 160
M00039326C:B08	ES 160
M00039331B:F09	ES 160
M00039338B:F07	ES 160
M00039344C:A11	ES 160
M00039349D:B11	ES 160
M00039381C:C07	ES 160
M00039383A:H07	ES 160
M00039411D:D09	ES 160

Clone Name	Tube
M00039413C:E06	ES 160
M00039430A:E04	ES 160
M00039433B:D06	ES 160
M00039433C:E03	ES 160
M00039438B:D08	ES 160
M00039440C:G06	ES 160
M00039457D:C02	ES 160
M00039471D:G10	ES 160
M00039472B:E05	ES 160
M00039478C:B02	ES 160
M00039554D:B09	ES 160
M00039556C:G05	ES 160
M00039559B:C07	ES 160
M00039560B:G09	ES 160
M00039560C:G06	ES 160
M00039617C:A10	ES 160
M00039654C:C11	ES 160
M00039668C:F01	ES 160
M00039672C:D05	ES 160
M00039686C:C01	ES 160
M00039694C:H01	ES 160
M00039698C:B03	ES 160
M00039710B:A01	ES 160
M00039710B:E01	ES 160
M00039785C:H12	ES 160
M00039786D:A10	ES 160
M00039805B:B06	ES 160
M00039806B:D05	ES 160
M00039820B:F06	ES 160
M00039822A:H02	ES 160
M00039826B:F09	ES 160
M00039826D:E04	ES 160
M00039828B:H06	ES 160
M00039829B:E01	ES 160
M00039860B:E01	ES 160
M00039860D:B02	ES 160
M00039861C:B12	ES 160
M00039865A:C09	ES 160
M00039869A:H01	ES 160
M00039871C:G05	ES 160
M00039873B:H04	ES 160
M00039874A:B06	ES 160
M00039885C:D11	ES 160
M00039894C:D09	ES 160
M00039895D:C04	ES 160

Clone Name	Tube
M00039900B:G04	ES 160
M00039915B:E08	ES 160
M00039921A:B10	ES 160
M00004824A:D12	ES 160
M00004824D:H05	ES 160
M00004831C:G11	ES 160
M00004832D:G04	ES 160
M00004836B:C02	ES 161
M00004839B:C12	ES 161
M00004843A:G12	ES 161
M00004846A:A10	ES 161
M00004850A:B02	ES 161
M00004852D:C06	ES 161
M00004856D:F09	ES 161
M00004873B:G04	ES 161
M00004876B:A06	ES 161
M00005002A:C03	ES 161
M00005003D:C02	ES 161
M00005013D:H05	ES 161
M00005014B:F02	ES 161
M00005016C:E04	ES 161
M00005309B:A11	ES 161
M00005314A:G10	ES 161
M00005332A:C06	ES 161
M00005333D:D08	ES 161
M00005346D:A03	ES 161
M00005349C:C02	ES 161
M00005359B:B08	ES 161
M00005359B:D09	ES 161
M00005364B:E10	ES 161
M00005365A:F05	ES 161
M00005366D:F08	ES 161
M00005367D:A11	ES 161
M00005375D:A10	ES 161
M00005379A:D10	ES 161
M00005380B:H10	ES 161
M00005383A:C11	ES 161
M00005385A:B12	ES 161
M00005385D:F07	ES 161
M00005387A:B03	ES 161
M00005392A:G06	ES 161
M00005401D:F09	ES 161
M00005403C:A01	ES 161
M00005405C:D01	ES 161
M00005409D:B02	ES 161

Clone Name	Tube
M00005413D:A05	ES 161
M00005422B:B08	ES 161
M00005422D:H02	ES 161
M00005422D:H10	ES 161
M00005423A:C11	ES 161
M00005423C:A10	ES 161
M00005423C:D07	ES 161
M00005434A:C03	ES 161
M00005442A:B10	ES 161
M00005445A:E07	ES 161
M00005445D:D04	ES 161
M00005445D:F11	ES 161
M00005452B:G03	ES 161
M00005452D:E05	ES 161
M00005460D:C11	ES 161
M00005461A:D12	ES 161
M00005463A:G02	ES 161
M00005466C:B01	ES 161
M00005468A:C04	ES 161
M00005468D:C01	ES 161
M00005474C:H09	ES 161
M00005485C:H04	ES 161
M00005489B:C08	ES 161
M00005500A:D04	ES 161
M00005504C:F12	ES 161
M00005504D:F06	ES 161
M00005505A:F01	ES 161
M00005505B:E01	ES 161
M00005506C:E09	ES 161
M00005506D:E11	ES 161
M00005507B:A03	ES 161
M00005511A:F05	ES 161
M00005512B:H01	ES 161
M00005515D:F02	ES 161
M00005520B:E01	ES 161
M00005520B:H05	ES 161
M00005524C:H04	ES 161
M00005535B:B01	ES 161
M00005540A:F09	ES 161
M00005557D:H10	ES 161
M00005569D:G09	ES 161
M00005570A:B08	ES 161
M00005570A:D05	ES 161
M00005603B:H03	ES 161
M00005606D:B12	ES 161

Clone Name	Tube
M00005607B:C04	ES 161
M00005616B:F07	ES 161
M00005622A:H02	ES 161
M00005623B:G01	ES 161
M00005626D:G11	ES 161
M00005634A:F07	ES 161
M00005641B:E09	ES 161
M00005643D:A05	ES 161
M00005674C:F04	ES 161
M00005675D:D09	ES 161
M00005689C:B02	ES 161
M00005703B:E03	ES 161
M00005703D:G10	ES 161
M00005710B:H03	ES 162
M00005743D:A12	ES 162
M00005763D:A01	ES 162
M00005766D:D12	ES 162
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M00005819D:F09	ES 162
M00005822C:A04	ES 162
M00006576D:C02	ES 162
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M00006582D:A09	ES 162
M00006585A:D07	ES 162
M00006585A:F09	ES 162
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M00006592A:A12	ES 162
M00006595B:C10	ES 162
M00006601D:G05	ES 162
M00006631C:A04	ES 162
M00006631D:D02	ES 162
M00006636B:E04	ES 162
M00006641B:F05	ES 162
M00006646A:A07	ES 162
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M00006678C:C02	ES 162
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M00006714C:D06	ES 162
M00006738A:F12	ES 162
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M00006740B:A09	ES 162
M00006743A:D04	ES 162
M00006743A:H11	ES 162
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M00006756C:A02	ES 162

Clone Name	Tube
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M00006885A:F07	ES 162
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M00006994C:F06	ES 162
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M00007006C:C12	ES 162
M00007007A:E04	ES 162
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M00007032A:B05	ES 162
M00007032C:A12	ES 162
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M00007048B:E11	ES 162
M00007048C:A12	ES 162
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M00007103D:C02	ES 162
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M00007117A:C11	ES 162
M00007126A:A02	ES 162
M00007141C:B05	ES 162
M00007154A:E06	ES 162
M00007155C:D07	ES 162
M00007155D:C09	ES 162
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M00007953D:F07	ES 162

Clone Name	Tube
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M00021958B:E08	ES 163

Clone Name	Tube
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M00022224A:C07	ES 163
M00022224A:G07	ES 163
M00022228B:B11	ES 163

Clone Name	Tube
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M00022237D:D06	ES 163
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M00022240B:C12	ES 163
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M00022472D:B01	ES 164
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M00022475D:C07	ES 164

Clone Name	Tube
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M00022487B:A08	ES 164
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M00022696B:C11	ES 164
M00039921C:H11	ES 164

Clone Name	Tube
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M00039932B:A07	ES 164
M00039976C:F11	ES 164
M00039977B:D12	ES 164
M00039981D:B01	ES 164
M00040003A:G10	ES 164
M00040016C:E07	ES 164
M00040023B:B10	ES 164
M00040025A:B04	ES 164
M00040034A:E06	ES 164
M00040034B:G02	ES 164
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M00040079B:F06	ES 164
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M00040081C:E02	ES 164
M00040094B:C08	ES 164
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M00040127C:D02	ES 164
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M00022703D:B11	ES 164
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M00022924B:A05	ES 165

Clone Name	Tube
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M00022947B:D02	ES 165
M00022952A:B02	ES 165
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M00023007D:D03	ES 165
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M00023097D:B08	ES 165
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M00039377B:E05	ES 165
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M00039647B:A02	ES 165
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M00040173D:A04	ES 165
M00040174D:G06	ES 165
M00040198A:F12	ES 165
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M00040267D:A12	ES 165
M00040287A:C11	ES 165
M00040287C:F10	ES 165
M00040289D:C06	ES 165

Clone Name	Tube
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M00040219B:B07	ES 165
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M00040351D:G07	ES 165
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M00042528C:H01	ES 165
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M00042743D:G10	ES 165
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M00055456C:H06	ES 166
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M00055468A:A08	ES 166

Clone Name	Tube
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M00055676A:G02	ES 166
M00055724B:E04	ES 166
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M00055980C:B04	ES 166
M00056004B:C05	ES 166
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M00056035D:A08	ES 166
M00056057C:F06	ES 166
M00056105A:D06	ES 166
M00056133A:E11	ES 166
M00056215D:F02	ES 166
M00056217D:E10	ES 166
M00056220D:G02	ES 166
M00056230D:E07	ES 166
M00056244A:B06	ES 166
M00056244C:H05	ES 166
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M00056320B:A03	ES 166
M00056342A:C03	ES 166
M00056345D:A04	ES 166
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M00056458C:E01	ES 166
M00042350A:A05	ES 166
M00042433A:E11	ES 166
M00042462B:C02	ES 166
M00042512D:D10	ES 166
M00042766C:D05	ES 166

Clone Name	Tube
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M00042801C:D01	ES 166
M00042822A:H04	ES 166
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M00042858C:G11	ES 166
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Clone Name	Tube
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M00054744C:F12	ES 167
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M00054781D:A11	ES 167
M00054786C:D08	ES 167
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M00054818B:F10	ES 167
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M00055423C:H10	ES 167
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M00055424D:G05	ES 167

Clone Name	Tube
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M00042585D:D03	ES 167
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M00042967D:C01	ES 167
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M00043017C:D08	ES 167
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M00043113C:G09	ES 167

Clone Name	Tube
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M00043077B:F11	ES 167
M00043077C:D12	ES 167
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M00043465C:H11	ES 167
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M00043485C:C03	ES 167
M00043490C:F02	ES 167
M00043495C:H05	ES 167
M00043528A:E11	ES 167
M00043529A:B08	ES 167
M00043640A:B01	ES 167

CLAIMS

We claim:

1. A library of polynucleotides, the library comprising the sequence information of at least one of SEQ ID NO:1-3351.
2. The library of claim 1, wherein the library is provided on a nucleic acid array.
3. The library of claim 1, wherein the library is provided in a computer-readable format.
4. The library of claim 1, wherein the library comprises a polynucleotide corresponding to a gene differentially expressed in a cancer cell of high metastatic potential relative to a control cell, wherein the control cell is a normal cell or a cell of low metastatic potential, wherein the expression is greater in the metastatic tissue, and wherein the sequence is selected from the group consisting of SEQ ID NOs:14, 137, 151, 152, 171, 200, 254, 262, 271, 348, 412, 472, 507, 520, 530, 588, 623, 637, 660, 678, 680, 700, 714, 774, 812, 834, 901, 937, 976, 1168, 1333, 1352, 1520, 1524, 1546, 1550, 1574, 1580, 1590, 1599, 1607, 1622, 1706, 1752, 1768, 1769, 1780, 1781, 1799, 1803, 1811, 1851, 1856, 1867, 1872, 1875, 1884, 1919, 1923, 1939, 1975, 2024, 2045, 2060, 2071, 2118, 2119, 2128, 2135, 2177, 2181, 2184, 2185, 2190, 2193, 2232, 2239, 2283, 2311, 2314, 2338, 2378, 2393, 2394, 2395, 2398, 2460, 2490, 2505, 2514, 2540, 2542, 2597, 2607, 2640, 2657, 2669, 2670, 2674, 2679, 2684, 2707, 2724, 2757, 2776, 2804, 2818, 2906, 2959, 2964, 2968, 2976, 2980, 2987, 3010, 3043, 3047, 3050, 3071, 3072, 3092, 3095, 3097, 3140, 3157, 3173, 3187, 3203, 3210, 3212, 3220, 3236, 3249, 3264, 3284, 3288, 3305, 3309, 3318, 3330, 3331, and 3335.
5. The library of claim 1, wherein the library comprises a polynucleotide corresponding to a gene differentially expressed in normal colon tissue relative to colon cancer tissue, wherein the expression is greater in the cancer tissue, and wherein the sequence is selected from the group consisting of SEQ ID NOs:7, 164, 734, 836, 928, 965, 987, 1026, 1044, 1119, 1226, 1227, 1251, 1316, 1429, 1442, 1540, 1553, 1560, 1577, 1588, 1610, 1620, 1626, 1673, 2416, 2749, 2976, 3129 and 3132.

6. The library of claim 1, wherein the library comprises a polynucleotide corresponding to a gene differentially expressed in normal colon tissue relative to colon cancer tissue, wherein the expression is greater in normal tissue than cancer tissue, and wherein the sequence is selected from the group consisting of SEQ ID NOs:105, 198, 465, 489, 745, 859, 976, 1011, 1045, 1138, 1226, 1251, 1253, 1392, 1474, 1559, 1571, 1589, 1591, 1607, 1608, 1643, 1753, 1764, 1766, 1782, 1811, 2749, 2784, 2790, 2805, 2976, 3128, 3129, 3146, 3150, and 3151.

7. The library of claim 1, wherein the library comprises a polynucleotide corresponding to a gene differentially expressed in normal human prostate cells relative to human prostate cancer cells, wherein the expression is greater in normal cells than cancer cells, and wherein the sequence is selected from the group consisting of SEQ ID NOs:53, 446, 1410, 1754, 1801, 1845, 2060, 2143, 2632, 2899, and 3338.

8. The library of claim 1, wherein the library comprises a polynucleotide corresponding to a gene differentially expressed in normal human prostate cells relative to human prostate cancer cells, wherein the expression is greater in cancer cells than normal cells, and wherein the sequence is selected from the group consisting of SEQ ID NOs:86, 93, 687, 1269, 1581, 1647, 1649, 1710, 1717, 1772, 1960, 2987, 3128, 3132, 3150, 3222, and 3268.

9. An isolated polynucleotide comprising a nucleotide sequence having at least 90% sequence identity to an identifying sequence of SEQ ID NOs:1-3351 or a degenerate variant or fragment thereof.

10. A recombinant host cell containing the polynucleotide of claim 9.

11. An isolated polypeptide encoded by the polynucleotide of claim 9.

12. An antibody that specifically binds a polypeptide of claim 11.

13. A vector comprising the polynucleotide of claim 9.

14. A method of detecting differentially expressed genes correlated with a cancerous state of a mammalian cell, the method comprising the step of:
detecting at least one differentially expressed gene product in a test sample derived from a cell suspected of being cancerous, wherein the gene product is encoded by a

gene corresponding to a sequence of at least one of SEQ ID NOs: 14, 137, 151, 152, 171, 200, 254, 262, 271, 348, 412, 472, 507, 520, 530, 588, 623, 637, 660, 678, 680, 700, 714, 774, 812, 834, 901, 937, 976, 1168, 1333, 1352, 1520, 1524, 1546, 1550, 1574, 1580, 1590, 1599, 1607, 1622, 1706, 1752, 1768, 1769, 1780, 1781, 1799, 1803, 1811, 1851, 1856, 1867, 1872, 1875, 1884, 1919, 1923, 1939, 1975, 2024, 2045, 2060, 2071, 2118, 2119, 2128, 2135, 2177, 2181, 2184, 2185, 2190, 2193, 2232, 2239, 2283, 2311, 2314, 2338, 2378, 2393, 2394, 2395, 2398, 2460, 2490, 2505, 2514, 2540, 2542, 2597, 2607, 2640, 2657, 2669, 2670, 2674, 2679, 2684, 2707, 2724, 2757, 2776, 2804, 2818, 2906, 2959, 2964, 2968, 2976, 2980, 2987, 3010, 3043, 3047, 3050, 3071, 3072, 3092, 3095, 3097, 3140, 3157, 3173, 3187, 3203, 3210, 3212, 3220, 3236, 3249, 3264, 3284, 3288, 3305, 3309, 3318, 3330, 3331, and 3335.

wherein detection of the differentially expressed gene product is correlated with a cancerous state of the cell from which the test sample was derived.

15. A method of detecting differentially expressed genes correlated with a cancerous state of a mammalian cell, the method comprising the step of:

detecting at least one differentially expressed gene product in a test sample derived from a cell suspected of being cancerous, wherein the gene product is encoded by a gene corresponding to a sequence of at least one of SEQ ID NOs: 7, 164, 734, 836, 928, 965, 987, 1026, 1044, 1119, 1226, 1227, 1251, 1316, 1429, 1442, 1540, 1553, 1560, 1577, 1588, 1610, 1620, 1626, 1673, 1960, 2416, 2749, 2976, 2987, 3128, 3129, 3132, 3150, 3222, and 3268.

wherein detection of the differentially expressed gene product is correlated with a cancerous state of the cell from which the test sample was derived.

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an						362
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gctagcagaa	gaagagaaat	aactaaaata	agagcacagc	tgaatgaagt	tgagaccag 300
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395

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405

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406

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408

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396

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402

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394

<210> 1858<211> 402<212> DNA<213> Homo sapien

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159

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403

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402

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440

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413

<210> 1864<211> 408<212> DNA<213> Homo sapien
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408
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389
<210> 1866<211> 398<212> DNA<213> Homo sapien
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398
<210> 1867<211> 410<212> DNA<213> Homo sapien
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410
<210> 1868<211> 387<212> DNA<213> Homo sapien
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387
<210> 1869<211> 405<212> DNA<213> Homo sapien
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405
<210> 1870<211> 403<212> DNA<213> Homo sapien
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300cttctggtga gtttggctac tgtgattttt gttgcaagtc ataaggcatt gtctgtggaa
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403

<210> 1871<211> 401<212> DNA<213> Homo sapien
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180gtagacaaaa agtcagttaa cagaacggag cagcggggag aggaagggaa aagcttcata
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401

<210> 1872<211> 385<212> DNA<213> Homo sapien
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385

<210> 1873<211> 404<212> DNA<213> Homo sapien
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120atgccttttt ataaagcctg tgcatttagg taggttgaag ctaggaggat tttctttata
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404

<210> 1874<211> 401<212> DNA<213> Homo sapien
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401

<210> 1875<211> 397<212> DNA<213> Homo sapien
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120aagaagggaa gctagtaagc aacttatagg gggcagtgtg agaaatgtca catgtttacat
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397

<210> 1876<211> 465<212> DNA<213> Homo sapien
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180tttttaata gagacggggt ttcactgtgt tggccagggt ggtctcgaac acctgacctc
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360gctagataaa tgtgctcttc tggttacccc accctgacag agtgcatttt tacacggcta
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465

<210> 1877<211> 388<212> DNA<213> Homo sapien

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120agcaaacata agacattttt agcacacctc tcttttaata gtactattct tgtgtggcaa
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360gacgattaag agttaatata gaacttag
388

<210> 1878<211> 429<212> DNA<213> Homo sapien

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429

<210> 1879<211> 433<212> DNA<213> Homo sapien

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433

<210> 1880<211> 422<212> DNA<213> Homo sapien

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420ag
422

<210> 1881<211> 418<212> DNA<213> Homo sapien

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360tcaaaaacca aaaaggtaaa aaaaaattgg gtacgggggc ccagccctgg aaacccaa
418

<210> 1882<211> 417<212> DNA<213> Homo sapien

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240taatttttaa aaaagggggc ccaggggtgg caaggcaata aaattggaaa tgaccctttt
300gagaactttc gtttttgctt aaaaaacagc ggggtgatga gaactcaaaa acctaaaaaa
360gatttttagtc aaagggaggg ctctttttct caccggacct ttaaaaaaa aatggcg
417

<210> 1883<211> 393<212> DNA<213> Homo sapien

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300ctgaaacacc atgtaaaaac ttgccatgta tggccggggc cggtgggtca cgctgtaat
360cccagcgctt tgggaggcca aggtggggcg atc
393

<210> 1884<211> 185<212> DNA<213> Homo sapien

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60aaagtccagg aattatcttc atccctggct atctttctta tatgaatgg acaaaagcgt
120tggcgattga ggagttttgc aaatctctag gtcacgctg cataaggttt gattactcan
180gagtt
185

<210> 1885<211> 392<212> DNA<213> Homo sapien

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392

<210> 1886<211> 413<212> DNA<213> Homo sapien

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360aatcaagggtg gtggcagcaa acttctagta gttttgatat gtccttgata gan
413

<210> 1887<211> 387<212> DNA<213> Homo sapien

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387

<210> 1888<211> 422<212> DNA<213> Homo sapien

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120gagagagaga gcgagcgaga gagagagaga gagagagaga gagagagtga gcccccccc
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360gtctagaccc acgctctctc tccttgatt ccctgcgttg ggctgaggac accccgcacc
420ct

422

<210> 1889<211> 410<212> DNA<213> Homo sapien

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120gttgccttat ttcctttgaa atgaacaagt aattgtgggg cgattttttc ggactatatt
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300tctgcgcccc tcaattggca ttctacgaaa atatggagcc gtcgtgagct tgcacacct
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410

<210> 1890<211> 402<212> DNA<213> Homo sapien

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120gcaagaggct gtacctaata ttcctcaacc taagaggcag tccaccatgg tcaacagcag
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240ctcggcagca attgactgtt tagaatacct tccagaccaa atggtgggtg aaataagcag
300aagctttcct gagcaaccag accgaacaga cttagtga aaacttctgt ttgatgccat
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402

<210> 1891<211> 412<212> DNA<213> Homo sapien

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412

<210> 1892<211> 399<212> DNA<213> Homo sapien

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240agtgcacaca gcctgtttgt tttagtatcc aaggaagaga ccaaggagcc agctggcggg
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399

<210> 1893<211> 394<212> DNA<213> Homo sapien

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240tcctggttg cagagcaaaa aggcaaacgt gaatcacata gtgtagacga agaataaac
300acttcttgct catgggggtcc atccagagcc tcacaatgtt tacagatgtg tctgactcat
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394

<210> 1894<211> 162<212> DNA<213> Homo sapien

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60tggaaatggc agttaaccac tgggagagca tccggacaga cgtttcgcca agatgggttg
120gatggccagt taaccactgg gagagcatcc ggacagacgt tt

162

<210> 1895<211> 396<212> DNA<213> Homo sapien

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60ggttctcatt agcaaccaat ttaagaacta cgagcgtcag aaggtgttcc tagaggagct

120gatggcacca gtggccagca tctggctttc tcaagacatg cacagagtgc tgtcagatgt
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240tccgtgtggc ttaaaccgtg cacgaatgag cttttgtgta tacagcattc tgggtgtggt
300gaaacgaact tgctggccca ctgacctaga agaggccaaa gctgggggat ttgtggtggg
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396

<210> 1896<211> 409<212> DNA<213> Homo sapien

ggcacgagaa tgactctgtt attaaagggtg gcatggagac tgtggaggga atatttttta
60aagcactact catatccttt aaactaaatt ttgccaaagc ccgagacaac attaaggaga
120aattgtacct taagttagta attccaaatc tatctgagtt gtatacccat caaagacaat
180acagctatta tcatagatga aggtatgcta taggcagatg tcattatctc tatattgaat
240aggtgaaaga taactgtagt cagggtgaaag gcattcatta tttttaagct gaaaagggga
300tccttgaaaa cactgaaaac ctctacaaca atcttcagga agcctgctat cttgggattc
360actaataata ggccaagaac aaaggcgagc atccattcct cactccacg
409

<210> 1897<211> 433<212> DNA<213> Homo sapien

ggcacgaggg gcaaaccctgg agaaccctcc taaatccata gagttttcaa aatgtgaatc
60tttgggaagcc ttgagttcag aatctgctgc tctggaatat ttcccttcga tcttatctca
120gtcacttcgt ttttgagaag agtgatgcct tgggcagct ttttttttt tcttttttaa
180aaaacagggg gttgaagccc accctattta aaaaccccc catttggaga attacaaggg
240ttttgtcctg aattggaggg tgggcaagcc caagccactc gggctaactg gttttgtct
300cggnggctat tccaagaaca aaaggaggaa gttggcccat taccgggggt gtcctggat
360gttgtttggg ggcgcgtgcc tttcaaaaac cccgccaaa aacaacccgg gaagggggag
420ggccccgctt ccn
433

<210> 1898<211> 399<212> DNA<213> Homo sapien

ggcacgagga aggcctaccg acttacttta tcattgaggg cttactgata caatgaaatg
60agtttcatga cttttttttt ttttaacccc tttttgaaaa aaaggggggt gggttaaaac
120ccaaaaatat cttgttgc tttgaaaaga aggcattgaa acaaaccttt ttgtagccag
180ggttaaaaaa acggaccggg ttgggcccct cttggttaagg ggggacttca gggccccggg
240aaggccggtt tgggggtaac ctgaggggga cacaggccct ggggggggag ggttttttta
300actggttacc cgggccata ggcagacttt ttaaaaaaag gtccttgaag ggggatgtgc
360aaagacatgc gggcccgctt aaaagcgcg attaaaaan
399

<210> 1899<211> 417<212> DNA<213> Homo sapien

ctgtccac tgtctttttt tggttttttg ttacaaccct taaaaaacgg gcttgccatt
60ctcaccccaa gttcatggt acacaagccg cagcagccag actgtagctt gccaacactt
120gctagaccat tgctcttcat gttcaaactg ccagtcagga gcacaaggac caggaagtgg
180cctgacttgg ccaggaccac tcagcccatt acagttagga ggagcgcca gatctcagcc
240ccatccactt gggaagttag gagagcagc gaacacatca cctgaaagtc agaggtcttg
300cgaaatcacc accaaagcat gtattttgtac aggtaatagt gctgagagtt caacagagga
360cagggagaag gtgactctgtg aagactgtgc agggagggag gacagccact cagggag
417

<210> 1900<211> 401<212> DNA<213> Homo sapien

ggcctcagaa gctctgggtg tgccagagga cccccagaa taacaaggga gggcgagtgg
60gtctccattc cccgagaagc caggggcagg gtgggatggg gaagaccagg agcagagtcg
120agcctcacag aagccagcgc gggctctctg tcagacccc agccggggct ctggaccag
180ggtaacagcc ccagttcatc ccaacccctc tcagagcctc aagaggggta gtcggtgc
240cggaagagag gggagcccta tccctggcaa cccctccacg tagcgtacct cagcacctgc
300caccggcttt gccatttctt tgagcttgaa gtttaactct ttagagtcta actgtggttc
360atttctgcac aggtacaata gatgacttta tttgtttaga a
401

<210> 1901<211> 407<212> DNA<213> Homo sapien

tttcagttca ctttatttac tatgacacat actttcagag tcttagatgt gctgtcatcg
60agtcccaggt cacatcgta cactcatcag cctctgcgg ccagtgtccc cacctcctgc
120catgtttccc tagtagcttg gtctttatcc agaactgtga ggctgctgtg ggggtgcagcg

180tccttaggag ggtcctgctg gagcagtggc cctaagtgag tctggactgt gtgaggcacc
240ccagccctcc acggcaaggc cggggcctgg ggggtgctggt gcctgtgtgc agcctgaagg
300ctgccctctt gctgcccttca gcgagtggga agctggtcag aggggtgggc actcctctgg
360gctccgccac ctctggcac accccatttg gtctctgtcc actcctg
407

<210> 1902<211> 407<212> DNA<213> Homo sapien
ggcacgagca ttatatata tactatatat ttcatatatg tatttcagga atttatagac
60cagacattca tatatagatg cggagggtata tatgagcgcg tgtgtatata cacatatata
120ttttatagta tttacgtata tacatatata cacatatata cgtatatatg taaacgtata
180tatacacgta aataaatata tttatatata cgtatatatg tatacacata tacatatata
240tacgtatata tgtatatata cgtgtatatg tatgtatata tgtatgtata tatacgtaca
300cacacacaca cacacacaca cacacacaca cacacacaca cacacacaca cacacacaca
360cacacacaca gagagagata cagagagata tacagagagt ttagaaa
407

<210> 1903<211> 389<212> DNA<213> Homo sapien
cgttgctgtc gggttttgcc aatcactaaa gatgcttgtt ttgcctcagc agtagaatgt
60ctgcagcaga tcagcacaac atttacccca tcagacaaac ttaaggatcat ccagcagact
120tttgaggaga tctctcagag tgtcctggcg tcaactccacg aagacttctt gtggtccatg
180gatgacttga ttctgtttt cttatatgtg gtgctacggg ccaggattag gaatttaggc
240tctgaggtac acctcattga ggatctaag gacccctatc ttcagcatgg ggaacagggt
300ataatgttca ccacctgaa ggcattgtac taccagattc agcgtgagaa gcttaactag
360gctgcataac agcttgaaaa ctggattat
389

<210> 1904<211> 390<212> DNA<213> Homo sapien
ggcacgagcc catctctact aaaaatttat ttttagccgg gcatggcggg gcatgactgc
60aagcccagtt acacgggagg ctgatgcagg agaattgctc gaaccacga tgcggacgtt
120gcagagagtc tagatcgcca tatatatata ttctatatata tgtatatata cacacatata
180tattcgtata tgcatatata cacacatata ttcatatata ggcatatata catatattca
240tatgttctca taatatacga atacacctat atgtcctat atgtatatat aacatacata
300tattgatata tgtataaata atattcataa atgtatatat gcatatatac tcatatatgc
360acacatacat attcgtatat gcgtatgcac
390

<210> 1905<211> 390<212> DNA<213> Homo sapien
ggcacgagag aatgccgact acttctccaa ctatgtcaca gaggacttta ccacctacat
60taacaggaag cggaaaaaca attgccatgg caaccacatt gagatgcagg ccatggcaga
120gatgtacaac cgtcctgtgg aggtgtacca gtacagcaca gaacccatca acacattcca
180tgggatacat caaaacgagg acgaacccat tctgtttagc taccatcgga atatccacta
240taattcagtg gtgaatccta actagcccac cctgcactc tctctcattg ccgtgccac
300tatcacctgt ctctctgcca gctgatgtgc cctgttgccc cccaccccat cccgcacaga
360accatccctg cattccacag gggactcggg
390

<210> 1906<211> 396<212> DNA<213> Homo sapien
tgcacgagcg gcgactcacc cggattgata tgccgtgatc tggctatatg gtggggcgcg
60ggcgggtgccg ctgcgacgag ctggtgctgt tctcatatgt ttcctttcaa tgggcttttg
120gtgtatgat taggcgaacc aagaacagga ggaggtgatt acagtgcgtg ttcactaccc
180ccgagtgcat aatgagggtc cctggaactc ttatgtggat tataagatat tctccatatac
240caacagcaaaa gcctttactg ccaagacttc ctgtgtgcgg cgccgctacc gtagttcgt
300gcggctgata aagcaactac agagaaatgc tggattggtg cctgttcctg aacttgctgc
360gaagacaatc ttcttcggca cctcagatga tgtcat
396

<210> 1907<211> 407<212> DNA<213> Homo sapien
cttccatagc ttggccacct atttgtctca gaatacctca tctgtgttct tggataccat
60ctcacatgtc cacctcttgc tgttcctggt caccaatgaa gttatgcctc tgcaggacag
120catcagcttg ctgctggagg ccgtgcggac canaaatgag gagctcgccc agacatggaa
180gaggtctgag cagtgggcca ccatcgagca gctgtgcagc acagttggcg ggcagctccc
240aggtctccat gagtacgggg ccgtcggggg ctccacacac acggccactg cagccatgtg

300ggcctgtcag cactgcacgt tcatgaacca gccaggcaca ggccactgcg agatgtgcag
360cctccccagg acctagggcg cctgcccctc gctggctagg accgggc

407

<210> 1908<211> 399<212> DNA<213> Homo sapien

caagccagtc aacccgcaga agtgaatatg tactaccaga acacttacca gacaatgcct
60tacgggtcat cctatggcat tccttatagt tatacggcct atggatcatc agatgccaaa
120tctcaaaaaa cagataatac agtccctttc aaaactccca gtaatgagat gactcccggt
180actattgatt tggtaaagaa acagcttaaa gacagggttg actccatgaa agaattgcac
240aaaacaaatc gacagcagca tgagaaacat ctgcaaagcc gagtggactc taccagggct
300attgaaagat tagaagggtc ttctgggggt attggtgaac ggtataaatt tttgcaagaa
360atgcgagggt atgtccaaga cttgcttgag tgtttcagn

399

<210> 1909<211> 407<212> DNA<213> Homo sapien

gaagattcac agtggacaat gtttaaggag attttagagg gcattcagta aggggtgcac
60ctgtctaagc ttttctaagg atagcagtc aatccctaat gcttcttttg accagacaat
120tagaattcat ggtttaaaat ctggtaaaac cctgaaggaa tttcgtggcc attcctcctt
180tgataacgaa acaacattta cacaagatgg acattacatt attagtgcac cctctgatgg
240cactgtaaag atctggaata tgaagaccac agaattgtca aataccttta aatccctggg
300cagcaccgca gggacagata ttaccgtcaa cagagtgtat ctacttccta aaaaccctga
360gcactttgtg gtgtgcaaca gatcaaacac ggtggctcatc atgaaca

407

<210> 1910<211> 408<212> DNA<213> Homo sapien

ggcacgagac aggcaccaag atgtccaacc gagtggctctg ccgagaagcc agtcacgccg
60ggagctggta cacagcctca ggaccgcagc tgaatgcaca gctagaagggt tggctttcac
120aagtacagtc taaaaaaga cctgctagag ccattattgc ccccatgca ggatatacgt
180actgtgggtc ttgtgctgcc catgcttata aacaagtga tccgtctatt acccgagaa
240ttttcatcct tgggccttct catcatgtgc cctctctctg atgtgcactt tccagtgtgg
300atatatatag gacacctctg tatgacctc gtattgacca aaagatttac ggagaactgt
360gggaagacagg aatgtttgaa cgcattgtctc tgcagacaga tgaagatg

408

<210> 1911<211> 392<212> DNA<213> Homo sapien

cggccgcgaa taaggattac aaggcacgct tgacctgtcc gtgctgtaac atgcgtaaaa
60aggatgctgt tcttactaag tgttttcatt tctctgtctt tgagtgtgtg aagacacgct
120atgacacccg ccagcgcgaaa tgtcccaagt gtaatgctgc ttttgggtgcc aatgatttct
180atcgcatcta cattgggtta tctaagtcaa gagaagaaga ggagctggct agtcaggaac
240ttattcatta accaccaaac ctctacctct tctctccttg actgtcacct gtaggacagt
300ttatcagtca actacctttc ctccagactt tacttccagg ctctcctctt cagtagctgg
360atgacttttag cagaaaggac tggtaaatac aa

392

<210> 1912<211> 401<212> DNA<213> Homo sapien

ggcacgagggt ctacagcctg acccagctgc ccgctatcgc aatgtgttgg aggccctctg
60gaggattata agaacggagg gcctatggag gcccatgagg gggctgaacg tcacagcaac
120aggcgcaggg cctgcccacg ccctttattt tgctgtctac gaaaagttaa aaaagacatt
180agtgatgta atccaccctg gggcaatag ccatattgcc aatggtgcgg ccgggtgtgt
240ggcaacatta cttcatgatg cagccatgaa cctgcgga gtggtcaagc agaggatgca
300gatgtacaac tcaccatacc accgggtgac agactgtgta cgggcagtgt ggcaaaatga
360aggggcccggg gccttttacc gcagctacac caccagctg n

401

<210> 1913<211> 383<212> DNA<213> Homo sapien

cgttgctgtc gggccatttg ttttgttttg gtgtcccctt tgaagccctg ccttctggcc
60ttactcctgt acagatattt ttgacctata ggtgccttta tgagaattga gggctctgaca
120tcctgccccca aggagtagct aaagtaattg ctagtgtttt cagggatttt aacatcagac
180tggaatgaat gaatgaaact ttttgtcctt tttttttctg gttttttttt ctaatggagc
240aaggactaag gaaaaccttt ggtgaagaca atcatttctc tctgttgatg gggatacttt
300tcacaccgtt tattttaaag ctttctcaat aggtccagag ccagtgttct tgttcaacct
360gaaagtaatg gctctgggtt ggg

383

<210> 1914<211> 384<212> DNA<213> Homo sapien

cgttgctgtc gcctggnttt tttttgcctc ctccctttcc cagcaccatt tattttgggt
60tctgagaaac agcttcctcc cattacaggc accaattcaa ttaggcagga gatagtgtg
120aagggtttttg tttccatcag cttctgctgt gtaaatagta gctctgtttg aaaaactttg
180agaagtgtgt gtgatgtgcc tctttctggg ttccgatccc ttctcagcct ggtgatgcca
240tggcattcaa atcaatttgt ttctcttccc ctcccctacc ctacatccat catacaaaat
300gggggtggtt gcactaatca gagatctgct tttttccccc cacagatatt ggtaaattat
360taaaaaacca taaattttct tcta

384

<210> 1915<211> 385<212> DNA<213> Homo sapien

ggcacgaggg gaccctgctc gccagatgg ctcttgga tttgccagc gtcctactga
60gcaggaactg agggcccgtg aagcagcac gccaggggga cgtgaacggg ctgcctggc
120aactgcccag gacaaggccc gctccaacaa agggctcctg gncagnattt nttntttttt
180ttnttttttt tttttttttt tttttttttt tntttttatt aatatttttt tttatcttct
240atactctacc ctattccccc ttttttttag gcaaaaaaag tgtaaacc cctctttttg
300gttctggata aaaaagaaaa atgcccgcac atagggttct cctccctaat agaaaaaaa
360gcccttttgg ggggcaaaa aggtg

385

<210> 1916<211> 383<212> DNA<213> Homo sapien

ggcacgagga cctgcgcctg tgccttttat aggttctgc ccggcatatg atgcacatct
60cgacaaacga gatgaagcac ggtgcgtgcc gataaaatgg aacagatgtg gactgataag
120cggctgatcc tgtatgtgtg gggctccaac gactttctga ggcgaggctc tatggactag
180cgtcgccctt tgcactcttg atggctcaca acgggcttgc cttctcttac tactaaccat
240tatatgctat ttgctgtccc tgcctagact ttgctccact gagtggttca tttgaggcca
300accctccctt gtgcgaggag ctcatggatg ccatgggtct tcactttgag agactgcttg
360agagctcacc ggagccctg tct

383

<210> 1917<211> 384<212> DNA<213> Homo sapien

ggcacgagaa gagccagctg atatcctcgg cgaacatgtc tctcctgagt ccagaggacc
60aacaccctca acctggtagc ttctttctgg cttgtcagag ctctcagaag gtacctatag
120gagcccaagc ccagctaca tctccactt attctgcctg attcccccaa agacaatggc
180tggaccctgc atgcagggtt gggggtggaa tggggctaac cagctcctga tggcctgagc
240caggcatctt gactggcacc tggagagccc ttaagtctgt cctggctgtg gcccatgccg
300acagatatcg tggggctgac aggtccacgg caggcttctt ttcttttata aaatggaagc
360tctgttacct tcaatgtatg actt

384

<210> 1918<211> 385<212> DNA<213> Homo sapien

cgttgctgtc gagcttagca aatctgggtg ttggttttgc ctgtttttaa accccctttg
60gagtctagta aggttaacca ctctggttag ttcagcgttc taacagggtg ctttacattg
120gaggaagatg ttcagaaggc gtggaagaca catcttcgag cagccccagc ttctgatgat
180tttgttcatc tgggttgcag acccaatctg tgtcccaggg actgggactg gccttcatta
240ccttattgac atgcttctcc cggacacaca cacacacatc acatttgcag ccattctaat
300ttagtagagg aattacacat aaccaaaca ctccccaaat gtgtgctgga gaacagctcg
360gagggatggg acggcctgtc gtttn

385

<210> 1919<211> 378<212> DNA<213> Homo sapien

ggcacgagca ggcggcagag gttgcagtga gccaggatcg cgccactgca ctccagcctc
60agcaatagag tgagactgtc tcaaaaaaaaa aaaaaaaaaa accccgccaa tttttaaaca
120accccgaaaa aatttttttcg gggccctttt ttttaaaaaa caaggggggtt tttctttttg
180gtatcccaaa aaccacttgg gggcaagggt tggggggggg aatttttttag ggccatata
240aaattcctta gggtttttgg aaagggcaat ccgggggcaa taaccctttt ttgtaaaggg
300ctaaaccctt ttttttttta ggcccttttt tttttgaaaa aggggttatt cttggccccc
360cggtttaaaaa ccttggga

378

<210> 1920<211> 379<212> DNA<213> Homo sapien

cgctgctgtc ggctcttaca ggaaaaggca ccaggctgcg gggtcattga ggacaaagtt
60gacagtttag attagcaggc actcaccatg ggcctcccc ctccctcagc atgaaaccag
120caggagaaaa tcctcaactc ttggcttctc cttggggaga caaaagagtt ggaatgtgtg
180tccagtgttt caccttttca gtgggctgag ggactggctt ctgtcttgct tgtcttgga
240agctgacagg ggctggtgca ttccagggtc ccaggagcca ctgagaacag aagacttggt
300gctgctctag aggacctatg gtagggcaga cagaggatga tacagctcag cagcttgctc
360ctacgtgtgg catgaaagg

379

<210> 1921<211> 381<212> DNA<213> Homo sapien

ggcacgaggg ggcaatgcta aatattgcgg cagttttatg cattgctacc atttatgttc
60gttataagca agttcatgct ctgagtcctg aagagaacgt tatcatcaaa ttaaacaaagg
120ctggccttgt acttggaata ctgagttgtt taggactttc tattgtggca aacttccaga
180aaacaaccct ttttctgca catgtaagtg gagctgtgct tacctttggt atgggctcat
240tatatatgtt tgttcagacc atcctttcct accaaatgca gcccaaatc catggcaaac
300aagtcttctg gatcagactg ttgttggtta tctgggtgtg agtaagtgca cttagcatgc
360tgacttgctc atcagttttg c

381

<210> 1922<211> 373<212> DNA<213> Homo sapien

cgttgctgtc gggtaaccc tttctttatg cgagccaaag gattcttggc tccaagcctg
60gtcctggctg ttagtttga actcatgcac ccagatgcta actgcctc agaatgcaga
120ggggatgaaa cactgaccgg acaattcaat ctgtatatgg agacggggtt tcaccgtatt
180agccaagatg gtctcgatct cctgacttcg tgatccgccc gccttggcct cccaaagtgc
240tgggattaca ggcgtgagcc acctcgcccg gcccatgttc tagattttt attctgggtt
300agcaggatcc aaactgcctg tcctgaagag actctcttcc tctccatc aacggctggc
360ctctaccaag tta

373

<210> 1923<211> 370<212> DNA<213> Homo sapien

ggcacgagta cagaagaaca atgcgaggcg agctcaggcg cgctgatggt ggtttccgat
60acaactcccc actcaaagaa ccccgagag ctcttgattc catctctcag tagggctctg
120aagtccatgc tgtctgaaga cacagggtct cccctgctg ctgtgccagg acagagggac
180tgccaccagc caagctgcaa tcctttttaa cgctaaaaac ggccgggctt ggtggctcat
240gcctgtagtc ccagcagttt gggtagatga ggcgggtgga tccctgtgg tcgggagttc
300aagatcagcc tgaccaacac gaataaaccc ctctctact aaaaatacaa aattaggccg
360ggcacagtgg

370

<210> 1924<211> 374<212> DNA<213> Homo sapien

ggcacgagga gagagagaac tagtctcgag agcagatctc tctctccggc acgaggagag
60agagagaact agtctcgaga cgagtttttt tttttttttt tttcccagca ccgtgagggc
120ttactggagc acattttgcc ccacaaaaag gaaatagccc ttctaattccc cgctgcaaaa
180acacaaaaac gcaacctcc cgggaaaaac ttttgagaaa cccgcccggg gcaccaaaga
240cctaggggga agatctgggt caaagggtta aaattccgta agaaagggcc tataggagct
300gtgagaactt tttttgcca cgaataacca tttttaacaa acagccctaa cccctagggg
360agagctggac gggg

374

<210> 1925<211> 370<212> DNA<213> Homo sapien

cgttgctgtc ggtttcttga agaggtagag ggatagggtta gtaagatgta ttgttaaaca
60acagggtttta gtttttgctt tataattagc cacagggttt caaatgatca catttcagaa
120taggtttttt gcctgtaatt aggcctcacc cctttgacc taaatgtctn acatgntact
180tggttagcaca tccacctgta tctaatacc ccatctggtt ttgggggatg cgctggcacc
240atttcccca aatttacgtg taagtatcac aaagagggtc tctacaatct ttagatttcc
300tttcgacaag attgcaggcg attcctctcg gagaccttcc cccggcatt ttggacctta
360tgagagggcg

370

<210> 1926<211> 150<212> DNA<213> Homo sapien

atgtttaaan catgggtccg gagcctttta ctctcccgaa ctctggagg ccctaaccgt
60gcgctttgag gctcccgatt ctcggaatcg ctgggaccgg cttttattca ctttgggtgg

120cctataagag ccgttgcccc tggcgggtgat

150

<210> 1927<211> 354<212> DNA<213> Homo sapien

ttgcttatac tctcactgga accaatgcat ggaacagggtg gtgcagacct ccagctgata
60atgcatcga gaacaggcat catatgctaa atgagtgaag ctagagatct attcgacacc
120ataaggacct gcatgaaaca aaatagcatc accacttgca tacgtaacat gatcaaccca
180caggcctata tgttggaagt gctgtccggg gctgttactg tctcttctgg ttataaagca
240gacatgtggc catcttttcc gcagggttag agtgggctcc tttctttttg gaatcctttt
300cttctccttt ggttagcagct ccctgcctcc agggcttccg ccaccagcgt ctct

354

<210> 1928<211> 336<212> DNA<213> Homo sapien

tacgtctgtt taagacgaca gaagggtga tctttcatct atttgagaaa acgcattcta
60gcagggtgta ggtaatctca ttgtggtttt aatttgcat tccctaattg ctagtgctgc
120tgaacgttgt ttgcatgaac ctggtatgct tctttttgag aagcattttc acaagccatt
180ggtgaagtat gtggatcacc accaccata ctccaacctt gttcccagtc actggtacct
240atagggtgag agtgaggttg ctcatcaacg agctctccaa gtcataagct gctgctctcc
300cactcacgat gcttggtgat tcaggagcgt tttccc

336

<210> 1929<211> 448<212> DNA<213> Homo sapien

tttttgagg atccccacaca tatggagtct taaattagtt ttgggtgtca ttttgatgcc
60tagagtcata gaagagtgat taggagcttg tgggtataaa aaataacttg agaattggct
120gaaagcaact aggaagatg ggggtagtag tatgtgtaaa catttgaggc agtagagatg
180tgggacccaa atactgttcc cttttactc aaattctgag atgagttgac atgttctgtg
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300aacaagtaag tatgcaaaat ttgtacatac ggtttcagga ataactagaa taccataaaa
360atatccacct gccttataaa ctagaacatc attgataact tggaagccct tgcatacctc
420tccatgatct catttgctct cacagctt

448

<210> 1930<211> 463<212> DNA<213> Homo sapien

tgctcgatct gcacgatccc aacgatgcga aatcggcacg agcagaaacc cggttcccag
60cgtcggcggc ccggcttccg ctgcccgta gctaaggacg ggccgctccc tctagccagc
120tccgaatcct gatccacgcg ggggccaggg gccctcgc tccccctga ggaccgaaga
180tgagcttctt cttcagcagc cgctcttcta aaacattcaa accaaagaag aatatccctg
240aaggatctca tcagtatgaa ctcttaaaac atgcagaagc aactctagga agtgggaatc
300tgagacaagc tgttatgttg cctgagggag aggatctcaa tgaatggatt gctgtgaaca
360ctgtggattt cttaaccag atcaacatgt tatatggaac tattacagaa ttctgcactg
420aagcaagctg tccagtcatg tctgcaggtc cgagatatga aac

463

<210> 1931<211> 460<212> DNA<213> Homo sapien

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60attggagaac ggtttttatt taatacagtt gcacagggtg taaaaaaact tgctttatct
120gacgaatgga attccttggc tgtttatgtt tcaatggata acacagtggc cattgaagat
180atcaaaaaaa tgtgccgtgt ccttcccttg agagctgaca catctggtga caggcctccc
240gattctttaa ctgctttcta ccacagtaaa ggcacctctg cctactgctc agcctggaaa
300ccccctgtgc tcattgtgccc ccttcgcctg ggcataaacc aaatcaatcc tgtctatgtt
360gatgcattca aagagtgttt taagatgcca cagtctttag gggcattagg agggaaaacca
420aataacgcgt attatttcat aggattctta ggtgacgagn

460

<210> 1932<211> 436<212> DNA<213> Homo sapien

cacacttgct tgctcgtttg gccgaatcgg cctaccggtc gtcagaatac gacagaaggg
60accacagtcc acctaaaggg tgctacagc ccacttgagt ttttcaaact gagtaatcct
120aaactgttca tcccaccctg ctttgccctt tccatgaaaa tgacagtaag ggctgtggcc
180tggaactttac cctcattact gcttctgctt cctgacaaa accctatgca tctcttaagt
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300tcagtgatat tggcctttct atgttgctac ttactaataa ctccatanat taaatcttgg
360gtgcatttta gaacatgctg tacctttgat tggtttgctt taggctagtg agttgagttc

420tgtgttaca ctgaaa

436

<210> 1933<211> 440<212> DNA<213> Homo sapien

cggtgctgtc gggaatagag taattttttt tcccattcca cttggaagct gtgtacctca
60agtgtgtgca catttcaaaa tgggtgaaac ataacttatg ttagtccaag cttgatttga
120cttcagtttct gcttcaacgt tttagtagat agggcactga actggatgct gaaagcgtgg
180gatctctttc tgttgcctca cttccaacag tgtggtttca ggtaatacga catgtttgtt
240acttggtttg ctgatctatg tgttggaac aatgctcacc acaggaggat tgactacata
300gcctgctttc atagcttgtg tgtatttacc cagtgcctca atagttgata ctgccagtga
360tttactcctg tggagtaaag gtaagcatgg tttattttct tgagtattat atggtacgtt
420ggagctaggt atttaagaat

440

<210> 1934<211> 444<212> DNA<213> Homo sapien

ctcgtctctt gtgcaggatc ccatcgactc tcaacatgag aaagctttta ttttctattc
60ttttcaattt tttcacattc taaaattttg gctgggaggga tcttgatttt taaaacattt
120gtcctttgtt ttctaaagag ggtcgttggg ttgcttagtt tttaaaaaaa ttgacgaatg
180atgtttttta acgaacatgt tcatcttgct aattttttgt tgtttttttg agacggagtc
240tcgctctgtc acccaggctg gagtgcagng gcaccatctt gtctcactgc aagctccgcc
300tccccacttg aactgattct cctgcctcag ccacctgagt agctgagatt ataggtgcct
360gcccccatgc ccagctaatt tttgtatttt tagtacagac agggattcac catgttggcc
420acgctgggtc tgaactcctg agcg

444

<210> 1935<211> 426<212> DNA<213> Homo sapien

tgtgaacact cccctatgta aatatgctga caataaattg tatggagaat ggtattttaa
60aagtgttttg agacttttca cctgtcctat aaaattttga attgtgtatg tgatctacat
120agaaagaata ttaaagagta ggttgaactc tttatagcca aatacagcct taaatatgct
180tgtatagcat ccactggcag aagtaaatgt tgtgcctcag acttgggggt tgcattgtgc
240cctgggggag ttactaccct tggatgcat gagggttcc tattagcatc agtgggaact
300cagtactctg tatgtatcca caaaagggaa cttgagacc acagttattc ttaatttctg
360atattaacaa ccgtacatac tgetgaattt aactcanaat atttcaggta agtgaagtg
420gtgctt

426

<210> 1936<211> 424<212> DNA<213> Homo sapien

ggcacgagga atcaagggaa taaaagctta ttctgatatt atagagcata taacagccat
60gtagatatgc atggtataga gaaatcagtt ctatgatgga tgtaccacca aagttgccga
120gcattatata gagatgcttt tgatatgagc ctaaaataa attgggatag agagggagtt
180ggtgaatttg agataatttt tcaaagaaca taccatatgg cgacgcaaac ggtagatatc
240aatcagtgat aagctatatt ttgagtctta caattgtttt tacaattacc cctgttttga
300gtatatatct tggcaaatca ttctaataaa tatttgcgtg taactgcgcg gaatacatac
360atggtacgta gaaatttgga agaataccta catattttca ggtatcattc tctgtgcaaa
420tacc

424

<210> 1937<211> 431<212> DNA<213> Homo sapien

cggtgctgtc ggacaggagg caggtgtgta tgggtgaaat tattttgaca ccttagagtt
60aacggggcct tagagtcagt acattggttc aagtaacaaa tatcaaagca gaactcttag
120tgttggcaaac aataaataat tgtctcctag attcttatac aagtcactgt ccgtcccaaa
180ttggtagctc ttagaatggc tcgagttgca ttcatgtca cagcaagaca caatggtttt
240gatagcaaag cagtagagaa actaaatgta gagaggcaga gagaactgta ttaagtctga
300ggacctgggt gttgtcatgg gcagcaggaa gtgtgaagga gaggggtttt cctccgatga
360aaggaaggct agggcttgat tcangggagc aagtgggatg ggccctgctg gtccttggct
420gtgcctatat t

431

<210> 1938<211> 425<212> DNA<213> Homo sapien

cggtgctgtc gaaaaaaaac caggtttctt tgttgagctg tgtcttgaag gcaaaagaaa
60aaaaattttc acaggagtct ttcttgtttc tagttgagct gcgtgcgtga atgcttattt
120tcttttgttt atgataattt cacttaactt taaagacata ttgcacaaa acctttgttt

180aaagatctgc aatattatat atataaatat atataagata agagaaactg tatgtgcgag
240ggcaggagta tttttgtatt agaagaggcc tattaaaaaa aaaagttgtt ttctgaacta
300gaagaggaaa aaaatggcaa tttttgagt ccaagtcaga aagtgtgtat taccttgtaa
360agaaaaaaat tacaagcag gggtttagag ttatttatat aaatgttgag attctgcact
420atttn

425

<210> 1939<211> 426<212> DNA<213> Homo sapien

cgttgctgtc ggtttaaatt tagacctttt gagttaactc ttctaatagt ttgtgctcca
60agagagccca gcacaccctt ccatgaatgg tgtcttttca aagataactg tttttgaatg
120ttcattgaaa aaattgtaga gtatgcactc atcatttttt cagttacact caaataacaa
180ctattagtag acgtgttatt ttataaaga atgaacagat gaggccagga acagtggctc
240atgcctgtaa tcccaacact ttgggaggct gaggtgggag gatcatctga ggtcaggagt
300ttgagaccag catgaccaac atggaaaaac tccgtctcta ctaaaaatac aaaattagtt
360gggcgtgggt gtgcatgcct gtaattccag ctactcagga ggctgaggca ggagaatcgc
420ttgaac

426

<210> 1940<211> 425<212> DNA<213> Homo sapien

ggcacgagga tggatcaaaa gttatgatta cacactgtaa tctaatgaa tttaaggaat
60ggcagtagct ctagaacctg cacagattta ctcatattcc ttcaggaaag tgtttaaatc
120gtctcagaggt cctgcatcaa gcattcatct ccaattgtga ctccagtaca acgactcata
180aatgggaaat gaataacatc catagtgttt agagagaaaa aaatagacca ataacctacc
240tactgacaag taaatttata caggactgaa aaccgcctga aacctgctgc aactattgtt
300attaactctg tatagctcca aacctggaac ctctgatca gtttgaagga cattgataaa
360ctgtgatttt acaataacat tatcatctgc agttactgtt tacaagactg cttttacctt
420acacn

425

<210> 1941<211> 435<212> DNA<213> Homo sapien

cgttgctgtc gagagcttca aacaagaagg gaaatggaag aaagaacaat aactatagaa
60atccctgaag ttctgaagaa gcagctggag gatgattgtt actacattaa caggaggaaa
120cggaaagtgc cacaagcact aacaggagcc aggaggaact ctctcccagt ccgcctttgt
180tgaatccatc cacgccacag tccacagaga gtcagccgac caccggtgaa ccagccaccc
240ccaaaaggcg caaagctgag ccagaagcat tgcagtctct gaggcggtcc acgcgccaca
300gtgccaaactg tgacaggctt tctgagagca gcgcttcacc tcagcccaag cgccggcagc
360aggacacatc cgccagcatg cccaagctct tcttgacct ggaaaagaaa acacctgtgc
420ataacagatc atctt

435

<210> 1942<211> 444<212> DNA<213> Homo sapien

ccggaacccc cctccccaag actatgaaag tgatgacgac tcttatgaag tgttggattt
60aactgagtat gcaagaagac accagtgggt gaatcgagt tttggccaca gttcgggacc
120tatggtagaa aaatactcag tagctacca gattgtaatg ggtggcgta ctggctgggtg
180tgcaggattt ctgttccaga aagttggaaa acttgcagca actgcagtag gtggtggctt
240tcttcttctt cagattgcta gtcatagtgg ctatgtgcag attgactgga agagagttga
300aaaagatggt aattaagcca aaagacagat taagaaacga gcgaaccaag ccgcaccttg
360aattcaccat ttaattggag aagccacaga atttattcag ccgaacattg tgatatccag
420tggtttgtg ggagggttt tgcn

444

<210> 1943<211> 426<212> DNA<213> Homo sapien

ataacgctac ttgttctttt tgcaggtntt tgcgattcaa ttccggacca ggccatcttt
60aagtctctacc cgacagtggg ggacgtggcg ctctacatgg ctttcttccc cgtgtggaac
120catctctaca gattcctgag aaacatcttt gtctcacct gcacatcat cgtctgttcc
180ctgctcttcc ctgtcctgtg gcacctctgg atttatgcag gaagtgccaa ctctaatttc
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300tatgccttcc tgcggcgagg gtactacctc acacatggcc tctacttgac cgccaaggat
360ggcacagagg ccatgctcgt gctcaagtag gcctggctgg cacagggtg catggacctc
420atgggc

426

<210> 1944<211> 413<212> DNA<213> Homo sapien

ggcacgagcc cacacaacga gcccatcgac tccaaagggc agcacagcag atggactgct
60attatcccag tggtagacat ggggaaactg agggccggga aggcagactt gcttgccata
120tgtcacataa ggagaaagtg gctgtgctag gattggaacc caggctgtca ggttctgagc
180ccttcccttt ctgtctgtgg gcctactgtg tgctcccaaa aagctgtggc caaattaagg
240aggtggcatg tctgattcat ctgtggcggg gcctgggata tataagtaact ctcaacaatg
300gtgttcatta gtccgggcat ggaggtcac gcctgtaatt ccagcacttt gggaggccga
360ggcgagtggg tcacctgagg tcaggagttc gagaccagcc tggccaacat gga

413

<210> 1945<211> 405<212> DNA<213> Homo sapien

ggctggtagag acacgatccc ctccaaagaa aatgttggtg ctacagacagg taaccactgc
60tgctactggt tttatttgtt tgtttggtca attttattta agatttgttt ttgttgact
120aggattttta aaaatgtaat atattgcagg atttataacc aggttcactg actgcttgct
180tgctttcttt tttttttttt ttttctctct taaaaaacca aaacaaagt tttttaaaaa
240tacttttagg ccccttgga gctggatttt tgaaatgttt cagaagggga caaaaatcgg
300tgggggaaat ttttagttt cccagggtta attaaaaagg tttttaattt ggtttgggat
360tttggggggg gatttttttc cctttatcca aaggcctttt ggccg

405

<210> 1946<211> 405<212> DNA<213> Homo sapien

ttaagaagga cctgatatgt aagcgctggt catttttctt ctggggttta ctgatcaggg
60tgagatttt aacttcattt agtaattact ctaggagatt ttaccttgac ttatatTTTT
120catgacgttt catgatttgc tgctggtttc aaatgaaact acaaatctgg catgttttac
180tgtgaacact tttgttattt gttttgtacc cttttttgtc ttgtttttct gttttagctg
240ccttctgaaa aaagagtgtt tccctctgtt tctgtcctca gatgatgtcc ctccccctac
300ctgtaacctt tctttgacat aattgttcat atcaatgaag gtgctgacca gctcaatata
360cagttaagca caagatctaa agctcttgaa atgcccagaa aagaa

405

<210> 1947<211> 404<212> DNA<213> Homo sapien

ttttttcgat ggaatcttgc tctggctaata tttcgtattt ttagtagaga caaggtttca
60tcatgttggc cagggtgggc tcaactctct gacctctggt gatccacctg cctcggcttc
120ccaaagtgtt gaggcaggcg gatcacctga cgtcaggagt tcgagaccac cctggccagc
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240ttgcagttag ctgggcaaca cagcaagact tcatctctta taaaaaaaaa agacccccac
300cccccaaaaa aatgggagcc cctgttctcc actttttgaa aagcttaaaa tgtgttttta
360tcttggggca gtcttttaga caccctggc caaaaatggt taac

404

<210> 1948<211> 417<212> DNA<213> Homo sapien

gtcggcacga ggctggccgg tcgtgggtggc tcatgcctgt aatcccaaca cttaaggagg
60ctgaggtggg cagagcacct gaggttggga gttcagacc agcctgacca acatggagaa
120atgccatctc tactaaaaat acaaaaatta gccgggcatg gtggcacgtg cctgtaatcc
180cagctactca tgaggctgag gcaggagaat cgcttgatcc tgggaggtgg aagttgcagt
240gagctgagat cagccattg cactccagcc tgggcaacaa gcgaaactct gtctcanaaa
300aaaaaaaaaa aaggggccgc cgaatgagga aattaaagg gttttttcca aaggaccctt
360gccccaaaaa aaacttttag ggggaccctt aatccgggaa aacattggaa agccaaa

417

<210> 1949<211> 416<212> DNA<213> Homo sapien

ggcacgagaa gcactccgct tgctaataaa accagagttt ctggatagtc caaaacattg
60gttcttagag tataattcct aaaccagcag catctgcatc acctagaaac ttgtcagaaa
120tgcaagttat cagactccac accagacctt catgaatcag aaactctagg tgtggggccc
180aaaaatgtag cttaacatgc ctttcagggt attctgatgc aaagtaaact tacagaacct
240ctgcactaga gaaaacactt ctttttgaga tagtcaaggt tgtatactgt ttctaccaag
300cacaaatata ggagcatttg agattcttcc tgtgcaataa taagaaatca acaggaaatg
360tttcagtgac tgtgtgtgtg tgtgtgtgtg tttataaaaa tatcttgata tatatg

416

<210> 1950<211> 412<212> DNA<213> Homo sapien

tgaaacaccg tctctaccag aaaatacaaa ttattagtca ggcgcgggtg cgggtgcctg

60tagtcccagc tactcgggag gctgaggcag gagaatgacg tgaaccagg aggcgaggct
120tgcatgagc cgagatcgcg ccaactgcact ccagcctggg cgacagagcg agactccgct
180tcaaaaaaaaa aaaaagggtt tcaaagtcc tttttgttaa agaaccacg taaaaggctg
240agtctattct gcatactatg cccacagaaa aggaagaaaa ctttttaaaa gggagaatcg
300catgttttca atgaaaacat tcacttggtt tttcatttgt aaaaaaaaaa agggggcttt
360tataaagaac tttggggaaa cactttgctg aaatgttggg actctggaac ta

412

<210> 1951<211> 422<212> DNA<213> Homo sapien

ggcacgaggt gactcacgcc tataattcca gcactttggg aggccgaggc aggtggatca
60cgagggtcaag agatcgagac catcctggcc agacatggtg aaaccctgtc tctactaaaa
120atgcaaaaaa ttagctgggc gtggtggcgg gcgctttag tcccagctac tcaggaggct
180gaggcaggag aatcacttga acccgggagg cggagggtgc agtgagccga gattgtgcca
240ccgcaactcca gcctggcaac agagcgagac tctgtctcaa aaaaaaaaaa gggaaatctg
300gttttttttt aacccaaaaa tttcttaggt tggggcccaa cttctttgtt ggctgggccc
360tttgcacttt gaagggcccc caccacaagg ggttttgtt gttccaggg cttttgaac

420tn

422

<210> 1952<211> 413<212> DNA<213> Homo sapien

cctatatcaa aacttatcaa atggtgttct ttaaataatg gcattttatc atatttcaga
60tatacctcaa caaagctgtt agaaacaagg agttggaatt agaaaaatta ccaaagtagt
120attcaaatat ctaattatct gcttgaagc actgaaggcc aactatggaa ctcagtggct
180ccaccagaga gaagtctggc tagtgctca ggtggcgtg cctgaccatt cagtggctga
240gccctgtgaa aacaggcatt ctgtaggtct tcggatgagg aacttgcaag agcagccggg
300tgctgccatc ctaagctggt tttccatatg ggcttctctg tgagtgttaa gaaaagctgt
360gggttgccctg tcagagttag cgccccact cagggttaacc acagtttctc cat

413

<210> 1953<211> 409<212> DNA<213> Homo sapien

cggtgctgtc gaaaaaattt ctggattctt aaaccaggaa gtatgtctgc atgcaaacat
60tgcttctgag ccatttcttg gtatccttat tgacaggctc atcctgcttt tcttcactat
120gttaactgaa cttactatct ctgtctactt ttaggctctg actttgacct tctctgtgtg
180tgaatttaat ttctccctct tagcagtaaa gcaatgcata gattactttt aatgaccac
240ccttttcttt catttgcat agccctatga tattctatat cttcttactt tcctagggtg
300gtagaagtct tggttgtt tgccagacag agcaaaagtg gcctgggac cacctaaatc
360tcgtaaaata ttctcttaca cagaacgcaa aattgcttag tactctctn

409

<210> 1954<211> 412<212> DNA<213> Homo sapien

cggtgctgtc gggcttgggc tgcaccactc acagagctcc ctccccagg cacttagttg
60gggcccagca ctgacctttc cctgagccc aggatgtggc cagagcccc tctgggaccc
120ctctcgcccc ttctctgcct cctcagcttg agctgcctgc ccgaagtctg gctgttccgg
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240ccccaaggac ctcccccat ttctggcagc caagccatta atctggagac agaaatgggt
300ttgctatcga ttctctggcc actttttctt tcattacaat ttgtaccggg attcttctca
360cccttctctg cgtccgtgca tttaaagagt tgtctcttta aatgttgaag ct

412

<210> 1955<211> 408<212> DNA<213> Homo sapien

ggcacgagga gctcctcctt tcttctcact ccttccccct cctccctcca tgcccactcc
60ccctgctcc agcaggccag gaagaaggca cagtccaggc aagtctggga gcttccaagc
120ccttgaggtc cagctgtggg gcccacatga cagccttaca aggttctac cagagaggaa
180aattccacat cccaccagaa gacaggggtg ttggcaggca tactcctatc tctcctctt
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300ttccttccct ccttactct ccttccccct cctgccccct tgcctcact cctcttctag
360actgcattag attcattcat ctcatcttcc aggacatgtt ggccagag

408

<210> 1956<211> 408<212> DNA<213> Homo sapien

cggtgctgtc gcttttttct cctattatat ttttggttct attaggattt acttaactga
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120ttcagctcac agtttgaagt gctgagaacc taagtatttt gctgtacggt actgagctgt
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240gtgggcaaga gacatgcaaa gctgaagccc tgcttgaaaa gacccttcaa ggaagtaaaa
300tggcaggggc agagtgcagc ttaacatgtt gctatccctg ttgtttttga gttgggtttg
360gaatggattc aagttcttac acaattttatt ttgaatacaa gcataatc

408

<210> 1957<211> 422<212> DNA<213> Homo sapien

ggcacgagga agctgctgtt cggaagtttg ccatggactg gaaagaagtt cttgtcggcg
60cctagcgacg cccaacacct gtccaaacaa aaaaaaaagt gaacaagaat taaaagatga
120aaaaagggat ttatttacia aatattactc caaatggaaa ggaggtaaaa aaaacacaaa
180tgaattttat aaaaccattc cccggtttta ttataggctg cctgctgaaa atgaagtctt
240actacagaaa ttaagagagg aatcacgagc tgccttttta caaaaaaaa gcagagaact
300gttagataat gaaaaattac agaacttatg gtttttgctg gacaaacacc aaacaccacc
360tatgattgga gaggaagcga tgatcaatta cgaaaacttt ttgaagggtg gggaaaaggc
420tg

422

<210> 1958<211> 408<212> DNA<213> Homo sapien

ggcacgaggt caatgtttta tacattattg acagaactta cgatgatttt aggtggctca
60gggatgtagt aaagtacttg tgttctgctg gttaggctaa gctgaagtga caaatggccc
120tcaaatgtct ggtttcaaca aaagttcatt tgcctttggt gaatgtctgg cacatgtctg
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240catgtctgac acgtgggtgt ccactggcag agggacacac gatcggggca agttctgctg
300gcccttaag cttctacca gaagtgaacca ttaaccactt ctgcctacat tcaactgggca
360aatcaggtcc catggcaacg tgagaaggga tgtactctcc cttgaggg

408

<210> 1959<211> 404<212> DNA<213> Homo sapien

cgctgctgtc ggtcaaaatc acttatctgt agagcataaa cgatgacctt gatcatgaga
60gaaatggaaa tgagaaaaag ttgaaaaaat gggatgtttg acctaaagaa gaggagcttc
120ttttaagaag taacagccac ttttaaggat ttggagttct gtcatgcaga aggatcagat
180ttgacttgac cagaaggaac tagggctcagt ggggtggaagt ttaaaagaag cagatttcaa
240ttctctttca agataaattt cctcaaaatt gtgaaaatag aatgagttgt tttgggtggg
300aggctgttcc tgttcactga caagttgggg attctagagt agaggaatcg tactgaagga
360gaatttgagc taggtgtctt caagttacct ataaactttg aggt

404

<210> 1960<211> 405<212> DNA<213> Homo sapien

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120gtgtgtgtgt gtgtgtgtgt atgaaagaga gagagacttt gacgggtgta gatatttttt
180gcgctttgcc tactatatga gtgataatca tgtgtttact aacaagtcca tgacctggct
240gtattcataa taccatttaa tattggcgtg agtgttctcg cttgacaaaa agaggcctcc
300cctgcttctt tcaacaactg tcacagagtg ggtgggctga aagctctgcc cacggccctg
360ctattggcga gagagggtctt ttgtgggagc ggtgtctcgt gcgtc

405

<210> 1961<211> 416<212> DNA<213> Homo sapien

cgttgctgtc ggttaaaata gccccctgat gagccaggca ctctgaggga acacagatta
60tctgagtctg aacacgccag acttctccac aggtttattt tggagtggaa agtatgcaga
120acacaaatta naaaattcaa tcttttgaga gattaaaata ggaaggcta ccaactgaatt
180tctggaattg cttttcaggt ccaaacttta tcttaacctt aggaagctc tctggccagc
240cacacccatc cctggtaaat gttgtaggac agagaccccc cccagagccc tgttgcccct
300tctctgcatg tttctcacct tccatgcccc agtaaaactgt tgaaaccaga gaatgggtca
360gggaagcccc atcccactcc cctgaaaaata tctgggagac tcttggtgta gggacc

416

<210> 1962<211> 409<212> DNA<213> Homo sapien

ggcacgagca ncnncnaag taagaggagc aaacaaatg tatcaatttc agccgaggtt
60ttctagggca aacactagaa tattgtacct ttgtacct gatacttat caatcaatat
120atattactga gcacttcgat gcaaggattc catcacctcc ccaacatgtg atatagaata

180gaagcaggtta aatgtttact aaatgaaggt acacagcggg cttttggaga ggaaatagac
240tctggcctcc agccatggaa taatttatac tgtctcttgc taacatacct ggagccggtt
300cctcattttg tgatccaaag agtaaacatg taaaaccagc caatcttagg ttatattctt
360gccatcctag agagtaagtg ctccaggaca tcagagtaag aagtctgga

409

<210> 1963<211> 408<212> DNA<213> Homo sapien

cggtgctgtc ggcgtgtgtg tgtgtgtgcg cgcgcgtgcg tgtgtatgtg tgtgtggtgg
60gggagagaat gcacaaacac tcgaggtggt ttgtatattt gactggtgaa ttcatagtt
120gtttttctgg gggtacttan aatttgagag tccgtgagaa gcattaggaa gaacattact
180gagaaaaaag gaggggtggg aagcccctag acttctcccc gagggatatcc ccgctgcagt
240cttctttaga tgtttggatt cccagtcct cttgttttga ggcgtgatat aaattcagcc
300tctcatacat ttaaaaatat cggttgaaca cctgctatat tctaggcacc gaggagacgg
360cagtgcagcag acgagaatgc ctgctcttct ggagccacag aaaatata

408

<210> 1964<211> 404<212> DNA<213> Homo sapien

tgccgacaag attgaagcta ggtctcaggg gtctccagtc ctcttcate agggccaccc
60cctgcagtat tgagcaccag ctggtccctc tagggagaga ttgacaacag cccggaccct
120gggcctgcc tattccatct gaatgtcgca tcgtctgttt ctactaggg gccgcctctg
180tcactcact agacatttga ggaacctcct gctgggccc tctgcttctc acaggacagg
240gacactgaac tgcgtcagcc tcagctcacc cctccttagc ccaaggtctt cctcatgctt
300gccacctact agtcatactg gcctttttaga tccctgaagt gttgttcaaa tccccggatc
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404

<210> 1965<211> 411<212> DNA<213> Homo sapien

ggcacgagcc ccgttggcgg atgatttttc taattctgca actgcctgga gcgcgggcat
60gatgacagag gaacggatcat tgatgatgca tccctggaag acctgggagc caggtctggc
120tccttggact gtatcttccg tgctccagtg ggagtacaga ctgagagggga gaagggggcg
180gggtagagat gcaccccatg tcggtatggg aatcactcta cctctcattt ccttcaatct
240ttcactccta aaatgtctag taaacctttt agtctgttct attctgcatt cattcccttg
300actttcagcc cttgttaattc acattgtttg gctgggatca ctgcttcac aaaagggaaa
360gacttctcc tgtgaagaga tccttagtat actacttgaa gaaccgcgaa g

411

<210> 1966<211> 416<212> DNA<213> Homo sapien

ggcacgagtg acaaagactt cagttagatc ttcattgaacc tccagtttcc cagtgcgtac
60agtgggtaga tgaagctaaa ctaaaccaaaa tgaggcggga aggcattcgt tatgctagaa
120ttcagctttg cgacaatgat atctacttca tccctagaaa tgtcattcat cagttcaaaa
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240tggaagccac tcaaaacaca gaaagcaatt ctaacatgga ctgtgggtta actggaaagc
300gagaattaga agttgactcc caatgtgtga ggataaaaac tgaatctgaa gaagcatgca
360cagagattca gctgttaaca actgcttcat catctttccc acctgcatca gaactn

416

<210> 1967<211> 405<212> DNA<213> Homo sapien

cgcaagagac tattggcaat ggattcttct ctgtgtacag agccagcacc cacaagtgct
60tgtactatga tgagaagaag agggccagtt tccacaactt taagtgcggg tccagcaggg
120aagaaatgaa atttcatgag ttcgttgaga aactgcggga tataagcct cgacgagggc
180aagagaggtt gtatctgcag cagacgctca atgacactgc ggtcaggaag attgacatgg
240acttcttagg ttttaactgg aactggatta ataagcaaca gggaaagcgt ggttgggggc
300agcttacctc taccctgctg ctcatgtgaca tggcaggaaa tgtgacacct gctcactatg
360atgagcagcg gaactttttt gctcagatac taggtgacag acgag

405

<210> 1968<211> 412<212> DNA<213> Homo sapien

ggcacgagag gaagtattag ctaatcagaa ccacgggtgcc aggctgactc accaagggtt
60aagattgctt tacttagtag cctcaagccc aaggaactga ttgtgaaaac cacctgaata
120aacaggaggg aggaagaggt aatactgttc atctatacat catataagcc tctgttaggc
180gctgcgcaat ctatcaaccc cagccctgcc tccccatagg aaattccttt attttcaatt
240gccacatata tagatattcc acggcttaat atacaagcaa atgtgtatat tttttcaagg

300aacagaaaaa aacagtccat cttggctggt ccctatggac cccagcccc actccttctt
360caacaaagtc cctgattttc tcaaaagttc gaaccaaag ctggaagcgc tn

412

<210> 1969<211> 407<212> DNA<213> Homo sapien

cggtgctgtc ggtatttcac taccattttc tgacttttag cttttatttt cacctcaatg
60tgatttaagc agaccaaata ttctaattct gctaattctg aaggggaaat agacaaatct
120taaaagctgc ctgaaatcaa acttgattta actcagtaag aatgtgaatt atttgttcta
180cttgggtggt ttaatttaaat cggtctgaat atgaacaaaa gggtttggat tttctaaaga
240tgacgtgttg tttctgttca tcagggttaa tttttctaac tatattgctt gtaggtgacc
300ccattctgga tttgtttggg ttggtttggt tccagttaaa agagaggaca ggaactaaat
360ggggctaacc acttcaggtg cagcttgtgc gagggtagat gggtcct

407

<210> 1970<211> 407<212> DNA<213> Homo sapien

ctcggcacga ggcgaggcca tgtggacccc cacaccttg gggccggctg ggcaaactt
60gaaccccaa tttctgcgtg gcctttgggt gcctccttc tccaaggcgt gactcttact
120ccagagactc aggcgagcac gtgtccctta ccttattttc tctcaatcaa actgaaacct
180attgtgatcc cccatagtc agtgcggtct ctgtattat tacgggtgtc tcccttcctc
240cccgtgcccc ggacaggcca tgagccagag atacaagggg cccacgcaa gatgcagggc
300tctctgtctc tggctcttta tctgtctcgg gacaccctt gtccaaactc aaggaatccc
360gggaggtctg gctttgccgc tttggctggg actcaggtac ctggggc

407

<210> 1971<211> 417<212> DNA<213> Homo sapien

gggatttgtt ttcggcacga ggggtgatgc taggatggc ctttatatgt gtccctggcct
60ctgcaggctt agggggcagt tttgaaaatg aggggaggaa gtgcttctgt ctgcacttg
120ctgggtgctg gacactgggc cgagcaccag tccctcctct tctgctaga tgccctgagtc
180ccattttaca gatgagcaaa ccaaggctca gagatgcggg gtcactcacc caagaccaca
240gatcagaggg agccctggcc tgaagtgtt gctgggctgg ccaaggccct ctctggaccg
300ctgtacttca ccaactgtcc cccaagccca gcctgtgccc ccttggtcag acccccggtg
360gccctctgtt ttggaaccca tgggaagaca gacctcatgt gaagggggct tcccaag

417

<210> 1972<211> 417<212> DNA<213> Homo sapien

nccggcacga gcgggaaccc tgctcagtc tgccgggcac tgcattgcagg gaccgtccgc
60ctgaccaga gacctgggc tgccacacc tctctccaga cccacagcca gctttgttc
120ttgaatgtgg aagatgtttc ttattccctg aagaaaggg gcctgccaca cacagcctgg
180gagggcctc atccagaaac tgggacttgg ctagcccgcc ctggggcccta gggacttctc
240actggtcatg cttctgaagc tgctcaccg gccgagggag gtcccggcag tgtcccaggg
300tggaaggtgg gggngnnnn nnnntgnnt nnttttnnn ntgtntttt gtggtgttg
360nngnttgtt ttntgtntt ttgttaggc aggggtggt ttgcttgtt ttgggtg

417

<210> 1973<211> 409<212> DNA<213> Homo sapien

cggtgctgtc ggtttccttg gtggaatttt ttgttctctg ctgctactgt aaaaacgaaa
60tgagtggctc tgctcaggt ccaatgatgt ccccaaatgg ttctgtgcct cctatctatg
120tgccctcctg atatgcccc caggttattg aagacaatgg tgttcgaaga gttgtcgtgg
180tccctcaggc accagagttt caccctggtg gtcacacagt tctccaccgt tctccacata
240ctcctctacc tggtttcatt cctgtcccaa ctatgatgcc gcctccacca cgtcatatgt
300actcaccctg gactggagct ggagacatga caacacagta tatgccacag tatcagtctt
360cacaagtcta tggagatgta gatgctcact ctacacatgg aagggccag

409

<210> 1974<211> 412<212> DNA<213> Homo sapien

tgacaagcca ctcngattt cagcagagat cccatcgatt cgcagtaaca ctggactgga
60tcggtacact cggcttcaag tgtggctgcc gggaactgcg ttccacaaa tacatctctg
120acggtcaggg caccagcacc agccctctga aggagctggc gtgtgctgac gactgcttgc
180ccctgccagt gctccctaac tggattggag gaggtatgg aacaaagtac tggagcagga
240ggagctccca ggagtggcg tgtgtcaatg acaaaacccg gacctataga atccagctgc
300agagccaaga tggcagcaca cgcacctacg aatcacagt agtcaactgcc tgcaagtga
360agaggtacac ccggcagcac aacgagcca gtcacaactt tgagagcatg tn

412

<210> 1975<211> 408<212> DNA<213> Homo sapien

ggcacgagag agagagagag agtgtgagtt tgagagagag agagagagag agagagagag
60agagagagag agagagagag agagagagag agagagagag agagagagag agagagagcg
120ctctcacaca cgcgcggggt ttttgtgttc tgcgcctccc tctctttttt gtggggggggc
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240cccacacaca ctgtctctct ctctctctgt gtgcataat atttctctgt accgagcggg
300tgtctctttt tttttctctc cctaaaactc tctctttccc gctctgtgtt tctctctctc
360acacacacac acacagaggg ggggtgtatct ctctctctct ctctctct

408

<210> 1976<211> 423<212> DNA<213> Homo sapien

ggcacgaggg ggctatggcg gaaacaaaag gagatgaggg cagggggcact tttaggaagg
60actgaggctg ctggcagtgt cacatgactg ttgagaagaa gggaatttgt tagcaagtgg
120ttacatttag taggaaaagt gttgagggca tgggtttgga ttaaaggagg gagttagcaa
180ttgaggagga agtggaattt gggcaaaaca ttccttttgg aagtttggat ggtaaaagga
240agtgtagggt agaacaaagg taagtctgag aggttaagaga gaaggaacac actttgggct
300tggcctgaaa tgagagggaa tgaggaaaac tgggttagagg gcaaggatgc tccagcctgg
360tggctctgct ctccaaggag aaggaataga gctttagaag tgtggatggc cagagttcac
420ggg

423

<210> 1977<211> 413<212> DNA<213> Homo sapien

ggcacgaggt tattagggat aagctgttaa ttttttacag gtgtggagga tatttcaaa
60acatcgtttg cctttgcaact aacatgcttt cattcttttc agtctcttcc tccattccct
120ttaaaagtctt ccccatcata tcaactgatc caaaagctag atttgtcttc attttagccg
180tatccctaaa accatgcatt ggtctggaca ggagttgacc catattccct tgcagactgg
240tcaactccatg ttctctgtta cagtaaggac cagccaagct tcagctgtcc cattctccc
300cctacaacac acacaccttt caagcaggga ggagatgac tccagcccc aagagtggag
360gctgccacat cctaacatat tatctattga acaggaagca gtgcgtatcc atg

413

<210> 1978<211> 404<212> DNA<213> Homo sapien

ggcacgagga gactgaggca ggagaattgc ttgaacccag gaggtggagg ttgcagtga
60ccgagaccgc gccactgcac tccagcctgg gcaacaagaa cgaaactctg tctcccaaag
120aaaaaaaaaa agaacttaag gttaaccgac gccagggatg gaattgacct cttacaagtc
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240aaatgctccg acttgggact gccactggga ggaggacagg tcatgggtgtg tgaaggagca
300gggcccacct tcgttcacgg cgcgctcagg gaatgtgaaa tgtgggtgtg aaaaaatgtc
360ccttgactcc gcccttctct ccttaaaac acacgcacat gcac

404

<210> 1979<211> 405<212> DNA<213> Homo sapien

ggcacgaggg agcaccagct cttggggctg ctgtctgtct ataccgggc tagctgtgga
60cctgaggcct tgggcatct gctgagccga gcccgaagcc ctgaagagt gagtttggcc
120accagttat atgcagggt agtggtcagc ctctctggcc tctgcccct ggctttccga
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240cgcaacttgg cactgctagt acggtgggaa cagcagggtg gcgaggggcc tgcagcccta
300tgggcgcact ttggggaatc tgcctcagcc catctgtctg acctggctcc tctactgcta
360catcctgagg aggaagtaac tgaagctgct gcctctctcc tggcc

405

<210> 1980<211> 407<212> DNA<213> Homo sapien

ggnacgaaaa aataccaggc ccagggccta gcaatgtatc ttcaggaaaa cggcattgac
60tgccccaaat gcaagttctc gtacgccctg gcccgaggag gctgcatgca ctttactgt
120accagtgcc gccaccagtt ctgcagcggc tgctacaatg ctttttacgc caagaataaa
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240ctcttctacc tgcgggactg gactgctctc cggcttcaga agctgctaca ggacaataac
300gtcatgttta atacagagcc tccagctggg gcccgggcag tccctggagg cggctgccga
360gtgatagagc agaaagaggt tccaatggg ctccaggagc aagcttg

407

<210> 1981<211> 419<212> DNA<213> Homo sapien

ggcacgagga ttcctggttt cagagcgttc aaaagatgat cttcagctaa gacttacgag
60agcagaaaat agaataaaac aacttgaaac tgactcctca gaagaaatat cacgttacca
120agaaatgatt cagaaacitc aaaatgtatt ggagtctgag agagagaact gtgggcttgt
180cagtgaacaa aggctaaaac ttcagcaaga aaataaacag ttacggaaag agactgagag
240tttaaggaag attgccctgg aggctcaaaa aaaagccaaa gtaaagatca gtacaatgga
300acatgaattt tcaataaagg aacgtggatt tgaagttcaa ttgagagaga tgggaagacag
360taatagaaat tccattgttg aactgaggca tctcctagcg actcaacaga aggcagccc
419

<210> 1982<211> 415<212> DNA<213> Homo sapien

cgttgctgtc gtctgagtct ggcgcggatg ctatgggcag ccaggagggtg ctgggccacg
60cgggccgggt ggctcctcc ggtctcctcc tgcaggagtt gtttcggttg atcacctttg
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240gtctcagtgg gggcaccacg cgagactgga gccagaccct caacctgctg tggctaacag
300tccccctggg tgtgttttgg tcttattcc tgggctggat ctggttgca ctgcttgaag
360agcctgatcc taatgttgc cctcactatg caactggagt ggtgctgtt ggtct
415

<210> 1983<211> 407<212> DNA<213> Homo sapien

ggcacgaggc gtcttctcgc cgctgctctt cgtggcccaa cgcccaatc cttgcgtgtg
60cttgagtc caccacac tcagccttgt gtccctcgat ccagtctccg acttccattt
120cccaccctaa accgcctacc cgggtgtctgt tccccgccg gttgtcctcg cctgctgag
180ctgagttgcc cctgttagcc tcgaccccat ggcgctgcag acgctgcaga gctcgtgggt
240gaccttccgc aagatcctgt ctcaattccc cgaggagctg agtctggctt tctgtacag
300ctccgggggtg taccgccagg cagggccgag ttcagaccag aagaatgcta tgctggactt
360tgtgttcaca gtagatgacc ctgtcgcatg gcattcaaag aacctga
407

<210> 1984<211> 411<212> DNA<213> Homo sapien

ggcacgagcc gactgtggag aagtgtccgg ttagccccg ttacaggaat gtgtttctga
60tcatctgaat cttaatcatg tccaactgcc tgcaaaattt cctgaaaatt acaagcactc
120gtcttctatg ttcaagatta tgccaacagt taagaagtaa aaggaagttt ttcggaactg
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240ttggtgttgg aactcacctg gtttgggata gtcttaccg aggagagagt ggaattgtt
300cactgggttg tgaagagtat aagagtatcc cttgcagtgt tgctgcttat gtgccaagag
360gtagtatga aggtcagttc aatgaacaaa actttgtgtc caaatcagat n
411

<210> 1985<211> 414<212> DNA<213> Homo sapien

gtactctct ctttttgcg atcnnnnat gagattcggc acgagggggt tcagaggggt
60ttcattcaat caatcctccg aatccagaga tttagacca gtctccgta ttaggactgg
120aggggggtca ataggttcag tgtttgagat gccaaaggaa cctgtctttt gatttgggggt
180tcaacataca gaggtagcag tcaccattat gtcmaaagcg gtyatcctga ttggaggccc
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300ggcaggggtc cctatgatcc aacaccatat tgaagcctgt gccaggtcc ctggaatgca
360ggagattctg ctcatggct tctaccaacc tgatgagccc ctacccagt ttct
414

<210> 1986<211> 413<212> DNA<213> Homo sapien

ggcacgagag taaaagaagt ctttcaaagc ttagttgatg atggtatggt tgactgtgag
60aggatcgga cttctaatta ttattgggt tttccaagta aagctcttca tgcaaggaaa
120cataagttgg aggttctgga atctcagttg tctgaggga gtcaaaagca tgcaagccta
180cagaaaagca ttgagaaagc taaaattggc cgatgtgaaa cggaagagcg aaccaggcta
240gcaaaagagc tttcttact tcgagaccaa agggaacagc taaaggcaga agtagaaaaa
300tacaaagact gtgatccgca agttgtggaa gaaatacgcc aagcaataa agtagccaaa
360gaagctgcta acagatggac tgataacata ttcgcaataa aatcttgggc can
413

<210> 1987<211> 409<212> DNA<213> Homo sapien

cgttgctgtc ggcgaggtgg ggtaggcgtg caaggcgggc gccgaggttt gcaaaaggctc

60gcagcggcca aaaacccggc tccgagcggc ggcggcccg cttccgctgc ccgtgagcta
120aggacgggtcc gtcctctcta gccagctccg aatcctgatc caggcggggg ccagggggccc
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240attcaaacca aagaagaata tccctgaagg atctcatcag tatgaactct tataacatgc
300agaagcaact ctaggaagtg ggaatctgag acaagctgtt atgttgcttg agggagagga
360tctcaatgaa tggattgctg agaacactgt ggatttcttt aaccagata

409

<210> 1988<211> 418<212> DNA<213> Homo sapien

ggcacgaggg catataagat ctattatgtc tatggcttca tgatgctggt gctgggttacc
60ctgtgcattg tgaactgtctg tgtgactatt gtgtgcacat attttctact aaatgcagaa
120gattacaggt ggcaatggac aagttttctc tctgctgcat caactgcaat ctatgtttac
180atgtattcct tttactacta ttttttcaaa acaaagatgt atggcttatt tcaaactatca
240ttttactttg gatataatggc ggtattttagc acagccttgg ggataatgtg tggagcgatt
300ggttacatgg gaacaagtgc ctttgtccga aaaatctata ctaatgtgaa aattgactag
360agaccaaga aaacctggaa ctttggatca atttcttttt cataggggtg gaacttgc

418

<210> 1989<211> 420<212> DNA<213> Homo sapien

cgttgctgtc ggtcattttc tcgctctgtg gcaactgttca gaggatatca cgggcccctt
60gatttgtatc cagaatttta ccgaattgct acagacccaa ccacccacac tgtcccagaa
120ggcagacctg tgaatgtctg tgtgggaaaa gagtgggtatc gatttcccag cagcttccct
180cttctctgaca attggcagct tcagttcatt ccacagagat tcagaggtca gttacaaaaa
240ccttttgcag aaggacctct ggccaccggg attgttctta ctgacatgaa tgaccagaat
300ctagaagagc catccagata tattgatatc agtaaatgcc attatttagt ggatttggac
360accatgagag aaacaccccg ggagccaaaa tattcatcca atanagaaga atggatcagn
420

<210> 1990<211> 412<212> DNA<213> Homo sapien

cgttgctgtc gtgaatttac aggtggcgcc ccgcgcgct agcggccacc cgggcatgga
60ccaagtgcac ccccaaaaaca ttccggattc ccccatggcc aacagcggac cctctgctg
120caccatttgc cacgaacgtt tggaggatac gcatttcgtt cagtgcctt ccgtcccag
180ccacaaattt tgcttccctt gctctagaga gagtatcaag gccagggggg ccaccggcga
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300catgcagggc gaaatcgca ctatcttctc tggggatgtt aaagtgaata aggagagaga
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412

<210> 1991<211> 415<212> DNA<213> Homo sapien

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300gaggtggaca caaaggaaga ggcagccaga cagctacttc agcgtcctca acgcattcat
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415

<210> 1992<211> 383<212> DNA<213> Homo sapien

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60tcagaagggg tttcatgctt ctactgataa gccaaactta catcagatcc aatacagatt
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180gacatccctg agaccacct gtcactcttg atgttgaac caggggccag gcctgctcct
240cattgtctcc tgccctctta gtcccagga gaggaaaaga aatactgtt tagagaaata
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383

<210> 1993<211> 401<212> DNA<213> Homo sapien

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120aatgtgaata ataattggtc gtctctcctc atgggtcggg agagggaac agtctcaccc

180cctaaatgtc accttgaatt acagcatgtt atataagcac atcctggccc ttccttgaat
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300tgtcttcccc ttaggaattt tactgattcc ttaaatttaa aagggcgtgt tgtaaccttt
360atgtcccccg cccctcaca gagttggtgc gtctgtgatg g
401

<210> 1994<211> 385<212> DNA<213> Homo sapien

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180agttgttttc cttgttcctc tgacattgtc caggcaagag ggcacacctga tcagatgagt
240agatttggt gagaaaaacc ctagagtaag gcaggcactt tgtggagggtg gatgatgatg
300gctcataaaa acgtttgttc tcagtcacgt tcagggctct gccagcagtc ttccagattt
360gaactgctta nacaaacct acaga
385

<210> 1995<211> 396<212> DNA<213> Homo sapien

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300aacttaggata ggagacgaac cgcaccatgc ccaccccatc ttattatgat tgcttttatt
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396

<210> 1996<211> 383<212> DNA<213> Homo sapien

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120ttttaataaa atgttatggg ttggctgtgt cctacccaa atctcctctt gaattgtagc
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360tctctattca cttttagctg nga
383

<210> 1997<211> 388<212> DNA<213> Homo sapien

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120gcttttatta accttcttca tggactctt gagaggctgt ccttatctct tactgatgat
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240tgatgagcac actagggagt tccagatacc agtttgatgc ttattcaacc atttaggtta
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388

<210> 1998<211> 399<212> DNA<213> Homo sapien

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120tcataacttg gccgggcgcg gtggctcatg cctgtaatct cagcactttg ggaggccgag
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240gggtcacgcc tggaaatcca gcactttggg aggtcgaggt ggggtgatca cgaggttggg
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399

<210> 1999<211> 398<212> DNA<213> Homo sapien

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120aaatttttaa aataatgaac tcccacaact ttaatacataa gacatgattt aacataaatt
180tgacatcatg acatgccaga ttgaaactgt aatgggccag atggcacgtt ttacattgt
240ctcctagctt ttgccctata atcccaatag caagagtga gagagagtag aatatggatc

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360aaacacataa gtgtcgggta tggtaaatgt cagaaggt
398

<210> 2000<211> 400<212> DNA<213> Homo sapien

ggcacgagga gagaacccag ttctaggtac tgtctgggcc tgggaggcga gagcagtgcc
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120gcctctggag atgataaggg ccaaaggagc agtcagggag gggcggtag ccagagtagt
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300tattctacaa acaattttgt tttctgcatt taaacatttt tgtgttttta ggagatggtc
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400

<210> 2001<211> 402<212> DNA<213> Homo sapien

ctagtctcga ggantttttt ttatttattt ttgggtcccc caaagggaaa attttttttt
60tgccttttaa aaaaaaaaaa agcccaaaaa actttttttt tttttcccc gggaagggga
120gttttttttt gggccccggg ggggttaaaa acccggggaa aaaaaaatt cccccaccca
180accgaaaatc ccaaaaaaat tgggaacacg gggggcccc ccccccccc cccccccctt
240taaaaaattt taagaggggg gggcccaaat ttttccccg gcggaattta aaaacccggc
300cccaaaggaa cccccgggt tccaaccctt aaaagggggg gggaaaaaag gggggcccca
360aacccccccc ctttaaaagg gaaaaaattg gggaccccc ct
402

<210> 2002<211> 402<212> DNA<213> Homo sapien

ggcacgaggt gacaactgat tgggccttgt aggtatgatt ggatttagcc aggcaattaa
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120gtaagacaat tgatactgtc catggatttt agaaagtgtg aagtggagtg attgtgatga
180agcttgaaag attgcctggg gccaggctgt tgaaggcttg gtttgcttag ataagtcaaa
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300tgaatatcca tegtgtacaa aatattgttc aagcaatgta ggaatcaagg gaataaagc
360ttattctgat attatagagc atataacagc catgtaaata tg
402

<210> 2003<211> 401<212> DNA<213> Homo sapien

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60cacaccatta gggagaagca ccatgctgaa tcatttcaca gttttcaact ctgggaaata
120atggagagag ttaaaaaatg taaaacttca gctatttttg ggtgaactt gcttacttga
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240tctttactat tcagatccaa gttcatgat ctacttgatc ttcattgtct ttaaaacatt
300cgaaagatgt caactgagag aaacatttca gaggggggag gcttttgga ctggtgataa
360acatccctcc aagagaaccg cctgggggtc tcttctattt g
401

<210> 2004<211> 400<212> DNA<213> Homo sapien

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60ggatagcacc ccaccatgcc agcctgactt ggagatatct cctgctgcct gcctgcaggg
120agttacccca gtttccaaaa acagtcgccc agataaagga ggaaaaggga aaggcagacg
180aatggcatgg cttttactaa agaaaagatg ttggcctcat actctatact cagggcttaa
240tgaactggaa tctgcataac tcagcagtc aaccagaagg gaaatggta aactgagctt
300gttattgcct cggagagcct aagagcacc gcacacttaa ttctactccc tgtctagaaa
360agctgtcagg gagtctgttg gaattgcaat gtagttattn
400

<210> 2005<211> 382<212> DNA<213> Homo sapien

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60gaattgtggc aaaacttgat ggtgcagaac ctaggcaggc agccagactc ctaaacccag
120tcacgtaaat ttgctgctgt aactggatct tcccaagcca caagtctgag aaatgggtgg
180cactctgacc tgaccactag attttcagga tattctcct aagagaggta tcttgcttc
240taagtgacct ctaaaacaga acctaggaaa ctctcagcca gataaattag aaattgatcc
300taaataggct tgtgccagg aaatcaacaa tgcagtaaaa atatcaggac aaaagcaaga
360atacttccca aagtcagaac tg

382

<210> 2006<211> 382<212> DNA<213> Homo sapien

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60gcacaggtgt ctttggtgat ggggtttttt tttttataac ttagtaaaaa aaaaaaagg
120tttgggaaat tttgtttttg ggaaaagcta aaaccaggt taccctgagg gggcgaggg
180ttttctttcc tgccctttta atctctttga aaataaaaaac ctggcacttg ttgatggtgt
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382

<210> 2007<211> 386<212> DNA<213> Homo sapien

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120ggcaggatcc tttagcatgt aatactttta aatggatcca cactgaactt ctgctggatg
180tactggagta agagtggcca gatttatcct cctcctcaa acaatgcaaa aaccagacaa
240gggtatataac ataagagttt ttagacacta gacaatactg ggcagtgatc cctgagagaa
300aatgaatgag gcatccctac aatttccata gcattctgcc tagatagctt ccagtctgta
360gtctgcagga aggagatcca aaacag

386

<210> 2008<211> 397<212> DNA<213> Homo sapien

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60ctgcaatgca ttagcagga aagagtaatg tttcttaaga aaaaaatgaa acaatgaaaa
120tccactaaaa tctgtctcaa ggataatatt ccatgactct acagggctta atgctgtgta
180catatataga cttctgataa gcagtttgaa ttatatgggt cagagaaatt tccaggtcat
240aggacttctc tttaaagtaa aataaatagg ccaggcacgg tggcttattc ccgtaatctc
300agcactttgg gaggccaagg caggtggatc acttgaggtc aggagtttga gaccagcatg
360gccaacatgg tgaaccccg tctctacaaa aatactt

397

<210> 2009<211> 396<212> DNA<213> Homo sapien

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60aatgtaaaat atcacattaa taattttata ttaattacat gttcaaatga tattttggat
120atactgaatt aaaacattaa aattagttct acttgtatct ttttactttt ttaatgtggc
180tagaagaaaa taaaattata catgtggctc agattatatt tctattggac agcgtgctc
240tagaacatta tattaagtgg ttattattga agtagaccaa agtttatacc ataaggatat
300tttttcttaa ataccatgtt tgaagaacaa ttatttattg atccttgaat ctgtaagatc
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396

<210> 2010<211> 394<212> DNA<213> Homo sapien

cgttgctgtc gattttttcc tggagagcct tatcatgtat tttatatgct tatgtggtgg
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120tctcaccagg tgatctacta tgcaaatcc tacagttttc tattcttaag aaataagggc
180cgggcacggc ggatcatgag gtcaggaaat tgagaccatc ctggctaaca cggtgaaacc
240ctgtctctac taaaaatata aaaaaaatta gccgagcatg gtggcgggca cctgtagtcc
300cagccacctg ggaggctgag gcaggagaat ggtgtggacc caggaggcag agcttgcatg
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394

<210> 2011<211> 396<212> DNA<213> Homo sapien

gtccagttgc tgacggactc actttttacat ggtcagcttt cagagaataa tcacagagat
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120cttttcgatt catagaatgg tgggacctca aggatgagtg aggagagaag gattcagtg
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360aacaaggagc gatagaactg tataccccag tcaatn

396

<210> 2012<211> 385<212> DNA<213> Homo sapien

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120catgtaaaat agtctttaca tgggaataatg gaaaacaatc gatggctcctt ttcttaaaa
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385

<210> 2013<211> 402<212> DNA<213> Homo sapien
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402

<210> 2014<211> 397<212> DNA<213> Homo sapien
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360gccacccat ttgctccag ggctgggtgt ttgtctt
397

<210> 2015<211> 396<212> DNA<213> Homo sapien
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396

<210> 2016<211> 392<212> DNA<213> Homo sapien
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392

<210> 2017<211> 389<212> DNA<213> Homo sapien
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389

<210> 2018<211> 398<212> DNA<213> Homo sapien
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120agtttaggaca caaggggtgaa ctgctttggg gtttgtatcc attctgttag ccttttgtat
180ttaaggccag cactgaagca gtggaggaaa tgggcaaagt aagaagagag aattctgaaa
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398

<210> 2019<211> 400<212> DNA<213> Homo sapien

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400

<210> 2020<211> 397<212> DNA<213> Homo sapien

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120ttcattttcc cgaattttca tactgtctaa ggaacagttg ggggggaatg ggcagaaggt
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397

<210> 2021<211> 391<212> DNA<213> Homo sapien

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120ctccaatttg gttgttaacc ctttggggcc caaggtttat ccaaccccag agggattttt
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391

<210> 2022<211> 391<212> DNA<213> Homo sapien

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120tgtgtgtttt tgtttttgtt ttctggagac aaggtcttgc tttgtcacc aggtcggagt
180gcagtgtcgt gatcaaggtt cactgaagcc ttgacgctgt gggcactgcc tcagccgccc
240aagtatctgg gaccacagc gtgcaccacc atgcatagct aatttatttt ttgtagagac
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391

<210> 2023<211> 389<212> DNA<213> Homo sapien

ggcacgagct tagctgagct tgttgatatt cttatcctat gttctgtcca ctcatggctg
60ggggccctgc tcacatacca tctattctat gaagctgccc ctgagtggg cttccttact
120gcctttgtac acagtaccaa acatagtgcc tagcatggaa tagatactca atagatattt
180gttgaatgaa caatgaatga atatttgttg aatgaatgca ttatccact tgggagcaat
240ccactcttcc tctatgcttt tatatcactt tgctctacc tcgttttatg gagctctcta
300catttaacct ttatttttagc taattatgct ttagatgcaa ccccttctcc agaaggtcag
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389

<210> 2024<211> 387<212> DNA<213> Homo sapien

ggcacgagga aagttttgcc ttggaagtac aagaccatgt cttccagata ccagccccag
60attaccttca gcattggggc ccagctggag acaacgttga tcataatgaa aaggactgtg
120ttttcaagaa ccatactgag gatgaatccc tagagggaat tcagccccca gtgggggagc
180atggtttgaa tacgcccttc tctgtgagga gaagctggga ttcattgaat gaggatgtgg

240aaacagaagt tctaagcatc tgctttaatg agaaggggtcc tgttcatgcc atgcctgtgg
300ttgactcagg aaacaggcag gaggataccc atggctccga tggagatggg gatggggaga
360ttgtggacga ggatgcagcg gtggcgg

387

<210> 2025<211> 386<212> DNA<213> Homo sapien

ggcacgagggc ggcctcctcc gcgcctcgcg gcatggcgctc ggagggggccg cgggagcccc
60aaagcgaggg catcaagtta tcagcagatg tcaaaccatt tgtccccaga ttgcccgggc
120tcaatgtggc atggttagag tcctcagaag catgtgtctt cccagctct gcagccacat
180actatccgtt tgttcaggaa ccaccagtga cagagcagaa aatatatact gaagacatgg
240cctttggagc ttcaactttt ccacctcagt atttatcttc tgagataact cttcatccat
300atgcctatc tccttatacc cttgactcca cacagaatgt ttactcagt cctggctccc
360agtatcttta taaccaaccc agttgt

386

<210> 2026<211> 383<212> DNA<213> Homo sapien

cccttttggg gaggcgacag ggggaattga ttttaaata tgttttcgcc tcatcaaatg
60tcaccatcca gtttagctac tgggtattcac tgggtattct caaattggag tgtcgaatgc
120ttaggttttt gaaaaccgcg gcattggaaa gctttgatag gaagtaaag ttggagctct
180tattttctcca gttagcaaat gttcgatgcc tggatactg ttagggtcca aatgaacaga
240atagaaaacc tgctttgaag gagaaaaaca ctgaagagaa actacacgta attagtatt
300actgcgcagt atagcttagg aagtgtacc gtagtagaat aatctacagg ggagtgatta
360acagtgttg ggtaggctag acg

383

<210> 2027<211> 384<212> DNA<213> Homo sapien

cgttgctgtc gcttgcttt tacagagcca tgaagcagca gatgcaaccg aatactgtgc
60agcatgagcc acagacgttt acgggaagaa ccggcaggag gcgccgggaa actaaagggc
120tcagctctc tgagtgggtg ctttgccatt gtggctgtgc gagctcagcc tcctggaaac
180ccgccttgag cttggttaac agcattcact ccagggttag cccagctcca ggttatcgca
240ggcaggactc ccgagaacag gttcatgttt gcttttggg aggtgctgcg ctaaagtga
300aaaccacctt gggccgagtg ggaacctccc agctggcgcg ctgttaacca gccaggatgt
360ctgacctga gaagtcaccg tgcc

384

<210> 2028<211> 382<212> DNA<213> Homo sapien

cgttgctgac ggcggtgga tggctcttat attccaaaac tcacccaag cctctcctgc
60aggggtggcc agagattgat ccccagggc tgggttaggc atccctggtc atgccccaaa
120gcgcctgggt ctctgctcat cacacttagt gtaaggatcc atttactcat ctgcctctcc
180cgccctcttc ccttctctcc cctcctctcc cctccttcc ccttctctc ctctcctcc
240ctcccctccc ctctctgagg aacttggtcc agctacagtc aatatctaga gaaggattg
300gcctagagaa ccttgctcaa tcttaagccc gcacacctgc cgtactttgg gatcaccgcg
360ggaaccttaa catgctgatg cg

382

<210> 2029<211> 382<212> DNA<213> Homo sapien

cgttgctgtc ggcagaacta ctactaaga actactccct gtttgtgagg attgtacctg
60ttgagagaag ttgcaaaaag aattagtcaa aagaattagt caaaattgt cctctgacct
120aggtctgaag gacatttaac acattgattg ttctcttcat ccagccttg agccctatga
180gttagtgccc ttagcctttg agtcccacag gtatggagga gctacctgtg gggacctgag
240ccatcactat tcctgcttca agttacactg gtgcctctca ctgacctgc tctgaaaagc
300cagctggaaa aatcaatgca tttgagtaca taaattcttt ggctccaaag aatgccata
360gcaatattgc ttttaattca gn

382

<210> 2030<211> 402<212> DNA<213> Homo sapien

ggcacgagat tatgattata gtaaacagac tagtgggtag taatgctaaa ttaccatcac
60agttatgtgc catctcccca cccattttt tttttttt ggatcaccaa aaaaatccgg
120gaaaccagcc tgaggggggg ctgacctgt taggaggggg gcaccaccac agggggggga
180attaacgggg accccgggct ccaaaaagac caaaaagggt gcccttgggg cccacctaa
240cctaaaaaaa aagggggccc taactggaat tcggaaacaa gcggatttga aaacaaaaa
300aaaggatttt ttggccccc ttttaaacaa gcggccttaa aatttgaaa accccggcct

360aaaaaaccta gaaaaaaagg ggaggggaaat ggagggcaaa aa
402

<210> 2031<211> 382<212> DNA<213> Homo sapien

cgtagctgtc gggaggggtt gaaggagacc atcagctatt gtgtgatatc agacaccatg
60gtgatgtaac ggatttacag ttttttgacc aggaagaat tgcgctgct tcatcaacag
120gatgtgtaac agttttcctt caccatccaa ataaccagac tctgtcagtc aaccagcagt
180ggactacagc tcactaccac acaggccctg gcagtccttc ctatagcagt gcaccatgta
240caggtgttgt gtgcaacaac ccagaaatcg ttacagttgg agaggatggc cgaataaatc
300tcttcagagc tgatcacaag gaagctgtaa gaaccataga caatgcagat agtagtacac
360tccatgctgt aacctttctt cg
382

<210> 2032<211> 401<212> DNA<213> Homo sapien

ggcacgaggt gatcaaggag atggcagctc atatccgtga ggtggagcag agccgacagg
60aggtggttcg gtctgtctta gagcctcagg cagtgccaga cccagaagag ggctcttcag
120cacctagaag ctggaaaggg atgaacagcc aagtagcttc cagcttacag cagccctcaa
180atttgacct gccaccagct ccagagcttg actggatgga gacaggacca tctctgacat
240tcattggcca tcaggatata ccaggagttg gtaacatcca ctcagggtcc acacctccct
300ggatgatcca agatgaagaa tacattgctg ggaaccaaga aataggacca tcctatgaag
360aatttcttaa agaaaaggaa aaacagaagt tgaaaaaact c
401

<210> 2033<211> 396<212> DNA<213> Homo sapien

ggcacgagat tctccgggct tatattcatt ctctgcttct ttctcccttc acccgtagga
60ctctcacctt tcttgetcat tctccagcac ccattcctac tttagtctct ttgaaatctt
120ttttggagat tttccttcag ctacaaatgt tccagtacaa ccaatattac tctgagggg
180caaagacttt ttcataattta tgtccctagt atctggtatg gcgcctggca tatggcattt
240cagaatatgt tcatagttga aacagtagga tagatatattg tcatcttgac aagtagccct
300ttgcaattta tacttgagtt cactcctggc caatggcaca tggctggaaa atgcagaaa
360caaattcact tacagcctga ggcttataaa gcttgt
396

<210> 2034<211> 396<212> DNA<213> Homo sapien

ggcacgagaa cagaagtgtc tggagtagtt ttcaggtata ggaatgagat gcctcgtggg
60gaaaggatct caccctggga agatgtgggtg cccctccag ggctctggag gatggatgcc
120tccccaggg gctctccaag ctgggcattt gggcctgggt gatgccaacc tggataacct
180gtggcccagc attgactgtc caccagcct tgctgttagg caccatgact ccaagatgaa
240gatgtggtcc ctgcccttga gtgacagccc agggacttaa tgtggccatc gggcatcaag
300cacaaggcca tgcaggtgat gatacgtcgg aatagaggca ccagccctgg taactgcac
360ttctccctt gccaccccat ggccccggct gaaagc
396

<210> 2035<211> 392<212> DNA<213> Homo sapien

ggcacgagat catatccagg atgccccaca tacaccaagc caggcagagg gcagctcagc
60tctgtccca tctgcttttg atatctttac ccaaaggcag gtaacccgaa gagccagcct
120ccactgcccc cagagccagg cccagttgtg ttggagtata ggtcaggagc tgtggaagga
180ggcagctctgt gagggactca tgcttttaga gtcctcacc ctcagactgc tgcaggacat
240tgccaggcct ctctccactt ccttcctcag catacagact tcatgctatc ttccaattcc
300ggggagtctt agctattagg gcagtttctg cttctccatt ttggggacaa aggccttgcc
360cagtacaaat ctagcccctt gtccacaga cn
392

<210> 2036<211> 389<212> DNA<213> Homo sapien

ggcaccagat ctttctcaa agcatgggtg ctgagtaccc agagttgcga ggagtttttt
60aactgattta gccaggtggc aatcatgagt gaatggatga agaaaggccc cttagaatgg
120caagattaca ttacaaaaa ggtccgagtg acagccagtg agaagaatga gtataaagga
180tgggttttaa ctacagaccc agtctctgcc aatattgtcc ttgtgaactt ccttgaagat
240ggcagcatgt ctgtgaccgg aattatggga catgctgtgc agactgttga aactatgaat
300gaaggggacc atagagttag ggagaagctg atgcatttgt tcacgtctgg agactgcaaa
360gcatacagcc cagaggatct ggaagagag
389

<210> 2037<211> 397<212> DNA<213> Homo sapien

ggcacgaggt ggctggcacc ccacctgtc ttctctgac tggtgctggc gtagggccgt
60gggggtaagt cacgtctccc cgtgggctca gggaggcctc tgcacttagg gtctgaccag
120cctccccact aggaacaggg tgggaaagtc tgctcctgag ccaggagtca ggctgggagt
180agcaatgctg ggatgggagg tgtgtggccc tcatgggcct cctctgggaa gccccagca
240cagatgtggg cccactcaga ggctgcctcc tggacctccc cttctgctgg accccggcgt
300atgcctcagc taagcccgta ttctattctg ctccagatgct cagaactcta gacatttgcc
360tccgcaatta tatcccatc tcctggagga ccaggac
397

<210> 2038<211> 389<212> DNA<213> Homo sapien

gatactatgc ctttaacttt agaccgcagt atattataat acatttgata tctgaaatat
60ctttactttt ttaagagtaa gattccatat gtctgtctgg aaggaggcca tgggtattca
120cacgaatata cctgtcactt ctccagaggt gtgaggtaac taacacgagc attctttgaa
180gactctgggc acatgaatga tacacagaat tgaatgttta aatttccact ttgagtctc
240atgaatcatt tgagactagc accagctgat cttgtgtaca ggctcagggt cagtgcccaa
300gggctcccg cgtgtgtgtc tgatcttcag tgcgtagcac attctccatt tataaaagag
360tggtcagaat aattgtggac ggtacagt
389

<210> 2039<211> 391<212> DNA<213> Homo sapien

ggcacgaggg gacatttaat tttagttagt ttacatttaa acagccacac ttgactcgtg
60agtgccttat tcgacggtgc atctctggag gacttgctcc cttcagcctg acttacaaga
120aactgtgtct ctacctgagc tccagtgtt gagcgctaag gggcaagtgg aaaccagat
180gaccatcaca tcagccttgg gagcccaaag ctgggcagag ggcttggag ttggccatat
240tcatggctgg tatctccatc agatgctgat ttggggccat ctgtgtatgt accctgtgga
300gttaagtgt ggtgattcag agcggtatag ttgtgattta cacactcaag aaatgggagt
360gcggggccang tgtggtgtct cacgcctgta a
391

<210> 2040<211> 395<212> DNA<213> Homo sapien

ggcacgagga acggggggac ccttagccct caaggaggga ccaggaaactg ccaggaaacc
60ccctgtccgt gtcccggag gggacagcca ggcaggttg cacagcagga cctccttcca
120tctctggagag ggaggaggga ggcagctgcc acagtggag taaccttgaa cctcctgtga
180gtcatggaat ggaagacaga gcagacctca gaccttggag agtcagggcc gccactgagc
240cagcccacga ggtgttatct gaggggtgag cctggcacca gcgggtgctc cgtgactgcc
300tgtggcagcc ccgccacacc tcgtgccact cgccttctg gggcgtccgc gatcgccagt
360agtgaattcc acgcggcgtc tctgtggtaa ggagc
395

<210> 2041<211> 392<212> DNA<213> Homo sapien

ggcatgagaa gaagctctgc ttgtactac tattatgaac aacattgtta ttggaattt
60aaaaactggg caactcctga aaaagatgca cattgatgat tcttaccaag cttcagctctg
120tcacaaagcc tattctgaaa tggggcttct ctttattgtc ctgagtcac cctgtgccaa
180agagagttag tcgttgcgaa gccctgtgtt tcagctcatt gtgattaacc ctaagacgac
240tctcagcgtg ggtgtgatgc tgtactgtct tctccaggg caggctggca ggttcttggg
300aggtgacgtg aaagatcact gtgcagcagc aatcttgact tctggaacaa ttgccatttg
360ggacttactt ctcggtcagt gtactgccct cc
392

<210> 2042<211> 401<212> DNA<213> Homo sapien

cggtgctgtc ggcttttttg actgtttctt ataaaatctg ggaagatggc tccagtgatc
60attctacata tattgtacaa aactagatt ttcacctggg tcataatact atggttacca
120aaccatgtgg tgctttggaa agtcctatgg caacaataac caagataaca aggcgtcgcc
180atgaaaatcc acccatgga gtaacaagt tgaaagaatg gttcaattat gttacagcta
240caagggaatga agagctaaat ctgcttcgta atgttgatgc taacaacact gagaatagca
300ctactgtgaa gaattctagt ttgttagtg gattcagagg aggttctagc tacaaccatg
360aaacagagac tatctttgca ttaccaagga tgcagcttga c
401

<210> 2043<211> 398<212> DNA<213> Homo sapien

cggtgctgtc gcggccctc ccttctccc acagccaagg acagacaggc tgcctggacc

60tgagcccaac agccttcagc ctcagaaacg catggggggc cacacactcc ttatatcctc
120ccacactaag gttcccctgg cccacaggga gcttcaggaa agccccccaa gtagccact
180gctctaggac gagctctgtg tccccacac cacaggcctc gaagcagggg gctgggtggg
240gccctgcacc ccaatcccag gtccccttgg cccctatatt ttctcgggcc cattggggcc
300tggtttctcac ctgctggctg gacccctga agggccgttc ccagaggctc ccagagggc
360tcaaggctgg gggcttatgt tgtggtcggn ggtccccg

398

<210> 2044<211> 397<212> DNA<213> Homo sapien

cgttgctgtc ggaaagctct gtgttctttt gccttcaatc tgntggcttc aaaacaaaca
60ggcaaaaaaa gcttcttgcg cgttccttc cctgaaaaac ttcctttttc ttttgcttg
120tatgcacaag gtaggactta cttcgtaaga aacaaaatgc cagtattttc ttaagccatg
180atgtgaaacc aatgaccctg tgaccacatg gcacagaaca ctaaattttg gtcccatggc
240tgaaacttga gggtgactaa agtaatgcc tgtgaaacat gatattctatc tgggatggcc
300atttgatctc taaaaggaat tttgtacact ccacagaact cctattctata gtaaaattga
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397

<210> 2045<211> 394<212> DNA<213> Homo sapien

ggcacgagca ggcggcagag gttgcagtga gccaggatcg cgccactgca ctccagcctc
60agcaatagag tgagactgtc tcaaaaaaaa aaaaaaaaaa acccccccca ttttcaaaa
120accccggaata atttttttcg ggggcccttt taataaaaaa ccacgggggtt tttacttttg
180tattttccca aaccccttg ggcaggggtt tggggggcgg aatttttttag ggccctcaaa
240aaaatccttt ggggtttgaa aaccgggaaa accggggcat taccctttt tgggaagggg
300gcaaagcctt ttttttttg ggcctttctt tttttgagaa ggggtcttcc cttgtcccc
360ctgcttaaaa accctgggtg aaaccctgtc taag

394

<210> 2046<211> 397<212> DNA<213> Homo sapien

ccaaaccac gtcaaaaatg gcttgttttc agcgatgtta taaaacaaag gcctgttttt
60tgggaattggg ggtgactggg tggtttgat tgaaatgtg acaaagatag catgtgtatt
120ttgaataaaa taaaaatttt gtaataaaac ttttaaaaat cagtgtatga aaatcaatat
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240tggttgaataa aaattgtgct atggctgcct tttcttctgc ccacacac aaagggctat
300ttctacaagg caaagatttg gatattgtct attctttact tcagattgag agttngaaa
360aactggagta aataatgggt ttcttacttg cttanaa

397

<210> 2047<211> 400<212> DNA<213> Homo sapien

ggcacgagct ctggggctac aggtgaggac agggggggga gctcccagcc tgagagttgt
60gacgtgcagt ctaatgaaga ctaccctcgg agggccctaa ccagggccag gagcagactg
120tcccatgtac tgctggtatc tgagtcagaa gtagccaaa caaagccacg tcacgccatg
180aaacggaagc ggacagcaga taaatccact agtacaagt atcctgtgat cgaggatgac
240catgtgcagg ttcttgtatt aaaatccaag aatcttgttg gagtcactat gaccaattgt
300ggaatcacag atctagtgt aaaagactgt ccaaagatga tgttcatcca tgctaccagg
360tgcagggtac taaaacattt aaaggtagaa aatgcaccaa

400

<210> 2048<211> 401<212> DNA<213> Homo sapien

ggcacgaggc taccctcct cctgttctt cctccagagg tagtctctgt taccctttta
60tttgtttctt ttatgggttt ttttctgtta ttatacaaa tcgatgcaca aagaggggtc
120tcttctctca taaaagtgt tattagtctt cagtgcgcct tttttctcc taacaaatgt
180aaactgggag cattttccca agtacatatt tataatactt acggggccta tctagtattc
240tgtgaatata tactgttaat ttattccttc ccattgacag acttaccttg ttccatgta
300ttgccattat aatcaatttg caaagaaaat tgcgaaccc ttgttttttc actagagata
360gacattttat ataataagtt gttgggataa gcagttttga a

401

<210> 2049<211> 401<212> DNA<213> Homo sapien

gggccattac ccagccccgg gccccgggtg cctctgcgtc cgtgccaggc ctctgatgc
60caaggccaca tccccgtgt tccagtacc agaccactga ccaccctgac tgtccaaacc
120tgtgacccca ggccaggga cggggaggaa accaaagaaa accattttca gggagctcag

180acgtcacagg agggagcggg agcaggatgt ggccctggcc tcgccagagc acctgaagaa
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300tccaggcctc tgttgcttac tgcaccacac ctgggggggt gggagcgtcc tctaggtgcc
360cctagtctct tgcctgcct cccagagggg gaaaaagccc c

401

<210> 2050<211> 401<212> DNA<213> Homo sapien

cgttgctgtc ggctgtctgt cagtggagat ggtgttggt gtctgtcggg ggagatggtg
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120ctgtcagtgg agatgggtgca ctctgactgc tattattcta catttcactt tgcactggta
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300gcccgtctta ggatccccac cctgctgttg aagggggccc attcttcaac gcttcataag
360acacttgtcc ggagaaacct ccgttcgggc cgaaactgtc g

401

<210> 2051<211> 395<212> DNA<213> Homo sapien

gcaaacatc cagaatgtga tgggacaaga tgggggcagg ggcctcacct ccctgcagag
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120gcacctgtgt gcagaattcc cactgtggcc agcacaggga agtcttttct agtgaaaatg
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300aggcctccag gcttctagag cagctagctt gggctggatt ctacacacca ggctgccccct
360tggattgttc tacccaagct tttccctggg gtctg

395

<210> 2052<211> 390<212> DNA<213> Homo sapien

ggcacgaggg tgtgtctgcc acccgccctt ctcaagtga gctctgggtc gagagagggg
60gggggtgaat tttgggctaa ggagcctgct gatgtcactt ttcttgtctt ttcaattatc
120tgtattggct ttttgattgt caaagtaaaa aaatgtgaag attacaggaa tcatgtcctg
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240gcagttgtct gttactcttc acacaagctc aatgaggcgg tcctgttatt accattttta
300ttttaagaat gaggagaatg cagcttcaag aaggtaagca acttgccgac cgtcacacag
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390

<210> 2053<211> 388<212> DNA<213> Homo sapien

cgttgctgtc ggcatgcac ttgaggctcag gagttccaga ccagcctagc caacatgggtg
60aaaccttgtc tctactaaaa ctacacaaag tagccaggcg tgatgggtggg cacctgtaat
120cccagctact caggagacct gaggcaggag aattgcttga acacagaagg taggcattgc
180agtgaactga aatcacctca ttacactcca gcctgggcaa cagagcgaga ctcttcttta
240aaaaaaaaa aaaaaaaaaa tccggggggc gttttttacg aaaatccaaa ctggataaaa
300accttggggg agttgggaca acccccacct aaaaggcggg gaaaaaaagg ctttatttgg
360gaaattgggg aggccttggc tttattga

388

<210> 2054<211> 397<212> DNA<213> Homo sapien

ggcacgagca gaggtgggag gtgatgagac tcaagactac agagagaaga aagggccggc
60agcccagatc ccagccccac cctcctgcc ctgcattcag gcagagcaca gagggataaa
120gaggagggtg ggttggggga caaggcagag atgcatatac ctgggacgta cacctgcgtg
180gagcccagaa ggaggcttct gtccgccaca ctgctagtcc ccagggcccc cttgcaagtg
240gacatcatgt taccacacat gcatgtgact tggccagagg agacagagtc ttcattgtga
300ctggaaaaag atccccctct cccgggtgat acatttgaca aacaaaaagt gggctgggtt
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397

<210> 2055<211> 390<212> DNA<213> Homo sapien

cgttgctgtc ggccgcaggg gagcgccgcg gtcccggcga gcaggctggg tcagcccagg
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120tctgccagct cccctctctg gcgggtgttc tgggtccaag tctgggagcc caggtagccc
180tccgcagaca gggcttctcg gcacctcaat gaggacggac gttgatgagg ccatgaatga
240gatgtcatgt ggcctgtgtt ttggaccgtg gttcgtacct atgctcctta tgtcacattc

300cctgttgcc t cgtgggtcgg ggctgtgggt taccacctgg aatgggtcat caggggaaag
360gacccccagc cgtggagga ggaagagagc
390

<210> 2056<211> 403<212> DNA<213> Homo sapien

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120gatttcacta agatcaaggg atggagggga aaatttcata gtgcttctgc atctaggaat
180gaaggtggaa attcagaaag ttcactgaaa aatcggtctg ctttctgtag tgataagcta
240gatgaatact tggaaaatga aggcaagctg atggaaacaa gcatgggttt ttcttcta
300gctcccat ctcctgtggt gtaccagctt cccactaaga gtaccagtta tgtacgaaca
360cttgatagtg tactaaagaa gcaatctact atttccctt ctn
403

<210> 2057<211> 391<212> DNA<213> Homo sapien

ggacgagggg gatgagagct gtttcgttcg ggacaagtcg ccggcggcgc ccgacggagc
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120acacacctcc cggaggccga cctcagtggc ttggatgagg tcatcttctc ctatgtgctt
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240ttcactgaga tgatggaggc ctatgtgctt ggcttcgccc acatccccag gggcacaata
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391

<210> 2058<211> 396<212> DNA<213> Homo sapien

ggcacgaggc agggagctgc tgacacagcc ctgcaggcag aaggatcccg caaacgtgga
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120tgcccttgag gaggcctccc caaagccagt cctgtgtcac caatcaaagg aaaggaagcc
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240ccctcttgga gagaccgccc agaaactctg gaggagcctc aaaatgctcc ccgagagagg
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360ggatgtccgg agatccacgg tgatctcacg ccctgg
396

<210> 2059<211> 402<212> DNA<213> Homo sapien

ggcacgagct tcctctacag ctacagcttt cacatatgac gcagcattcg ggaatgtccc
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120gggagaataa tgagcgatta tctacatcca atggaaagat gtcaccaact cgctaccatg
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240atgataaagt ggaagaatta atgaggaggg acagcagtgt gataaaagag gaaatcaaag
300cctttcttgc caatcggagg atttcccaag cagttgttgc acaggtaca ggtatcagtc
360agagccggat ctctcattgg ctgttcagc agggatcaga cn
402

<210> 2060<211> 395<212> DNA<213> Homo sapien

ggcacgaggc ggcgggcgca tctcccacca ggtcaggac aagaagattc acgtgtacgg
60ctattccatg gtgagccgca gccccgtccc gccctgccgg agggcccagt accagcttcg
120aggcccacct gagcctgctg cctgaccgg tggccccagc tgagcacgca ggcttcctgg
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240cccatggagc acacgccaga cctgaggggt gggacggaca cccccaggca tggccggctg
300tctcctctcc ctgccttggg aggccttgct gggctctagc tgtcctccag cactttgggc
360cctgggcccc cagaggcagt cagtacctgg gtgga
395

<210> 2061<211> 387<212> DNA<213> Homo sapien

ggcacgaggc ggcgggcgca tctcccacca ggtcaggac aagaagattc acgtgtacgg
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120aggcccacct gagcctgctg cctgaccgg tggccccagc tgagcacgca ggcttcctgg
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240cccatggagc acacgccaga cctgaggggt gggacggaca cccccaggca tggccggctg
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387

<210> 2062<211> 390<212> DNA<213> Homo sapien

cgttgctgtc gatgctgtgg ccgaccatcg agccaaagac ttcattcacg attctctgcc
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120ggctggagaa cctgtaaagc tgggggcccc gttgacaaca gaaacagaag tccatattgt
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240ggaaaactcc cgtgtgtatc atctggaaga acccaagtgc ttggaaatat acccccagca
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390

<210> 2063<211> 401<212> DNA<213> Homo sapien

ggcacgagca gggcctcttc aacactggca accagagaat gttaaccagg ctttcaccag
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120atatgtgtt ttcccaaaag atcagcgtgg accctatcct cctgatgttg ctagtatggg
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240tcaagagcgc ttcttgtgc ctctcagca aatacaggga tctggagttt ctccacagct
300aagaagatca gtatctgtag atatgcctag gcctttaaat aactcacaaa tgaataatcc
360agttggactt cctcagcatt tttcaccaca gagcttgcca g

401

<210> 2064<211> 398<212> DNA<213> Homo sapien

ggcacgagca gggcctcttc aacactggct tccagagaat gttaaccagg ctttcaccag
60acccccacct ccctatcctg ggaacattag gtctcctgtt gcccctcctt taggacctag
120atatgtgtt ttcccaaaag atcagcgtgg accctatcct cctgatgttg ctagtatggg
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300aagaagatca gtatctgtag atatgcctag gcctttaaat aactcacaaa tgaataatcc
360agttggactt cctcagcatt tttcaccaca gagcttgga

398

<210> 2065<211> 388<212> DNA<213> Homo sapien

ggcgccaggc gaacctcatg atctatatga tgatatcctt ctcaaacttg ggggatgtga
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120ggcccatata gctaactacc gatctcctgg aagacggacc cagcggcact attcaacctg
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300tccagccccc ctttgccaat actgtcctgt gcctaagatg ttggaccact catgtctttt
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388

<210> 2066<211> 397<212> DNA<213> Homo sapien

cgttgctgtc ggaccgccat cctgggggtc ttcctctata acaagaccaa gtacgatgca
60aaccagcaag ccaggaagca cctctcctcc gtcaccacag cagacctgag cagcaaggag
120cgtcaccgga gccactgga gaagccccac aacggcctcc tcttccccca gcacggggac
180tatcagtacg gccgcaacaa catcttaaca gaccattcc aatacagccg gcagagctac
240ccaaactcgt acagtttgaa ccgctatgat gtgtagagtc caaaggacag gaccagactg
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397

<210> 2067<211> 395<212> DNA<213> Homo sapien

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60ccaggcaggt ggggtggacga ttggacttgg aggggaatac agaggcgatg gaagtggcga
120ggctggcctg ttggcgaggg tgtcctgggtg gtggggcggg ctgagtcaag gaaggactct
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240gggtctggatt tgctggttaa caagataacc tgagggcagg accccatagg ggaatgctac
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395

<210> 2068<211> 399<212> DNA<213> Homo sapien

cggtgctgtc ggtgggcttg ctccaggggt ttggttcaac cccagcagcg gtctctgggg
60ccaggcagggt ggggtggacga ttggacttgg aggggaatac agagggcatg gaagtggcga
120ggctggcctg ttggcgaggg tgtcctggtg gtggggcggg ctgagtcagg gaaggactct
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240ggctctggatt tgctgggttaa caagataacc tgagggcagg accccatagg ggaatgctac
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360tgtcctgggt cagggacgca aaggacgctc acagactcc
399

<210> 2069<211> 400<212> DNA<213> Homo sapien

cactacttca cgggcctgca ggtgcttcag ctgctgctgc tgtgtgcctt cggcatgagc
60tccctgccct acatgaagat gatctttccc ctcatcatga tcgccatgat ccccatccgc
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240ctggctctgg agctgtgagg ggaggtgtag gtgtgtgggt gactgctctg tgctgcgctt
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400

<210> 2070<211> 389<212> DNA<213> Homo sapien

cggtgctgtc ggcagaaaat agaataaac aacttgaac tgactcctca gaagaaatat
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120gtgggcttgc cagtgaacaa aggttaaac ttacgcaaga aaataaacag ttacggaaag
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240gtacaatgga acatgaattt tcaataaagg aactgtgatt tgaagttcaa ttgagagaga
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389

<210> 2071<211> 382<212> DNA<213> Homo sapien

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60gaaggggaag aaaaggatgg catctcagac agtgatagca gtactagcag tgaggaagaa
120gagagctggg aaccctccg tggtagaag cgaagccgtg ggcctaagtc agatgatgac
180gggtttgaga tagtgcttat tgaggacca gcgaaacatc ggatactgga ccccgaggc
240cttgctctag gtgctgttat tgcctcttcc aaaaaggcca agagagacct catagataac
300tcttcaacc ggtacacatt taatgaggat gagggggagc ttcggagtg gtttgtgcaa
360gaggaaaagc agcaccgat ac
382

<210> 2072<211> 394<212> DNA<213> Homo sapien

ggcagcagggt taacagtgat gatgacagcg ggctgctggt acactgtatc tcaggctggg
60atcggacccc cctcttcac tccctcctgc gcctttcctt gggggctgat gggctcatcc
120acacgtccct gaagcccact gagatcctct acctactga ggcctatgac tggttcctct
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240attttttgaa gcatattacc tccgaggagt tctctgctct gaagaccag aggaggaaga
300gtttgccagc ccgggatgga ggcttcaccc tggaagacat ctgcatgctg agacgaaag
360accgtggcag caccaccagc cttggcagcg actn
394

<210> 2073<211> 384<212> DNA<213> Homo sapien

cggtgctgtc ggtctgaatg ccgcctgcac ggcattggtg gatgcagggtg tgcccatgcg
60ggctctcttc tgtggggtcg cctgcgccct ggactctgat gggaccctcg tgctggatcc
120tacatccaag caagaaaagg taggtgtgaa gaccaggggtg gctgaagggc agaggccaga
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240caatccact tagcaagggc tgctctaate atcatggttc atttagcagc aagtgtgga
300aaccagctc agacttgctt aattaggaag gaaatgtggg gccgggagcg gtggctcacg
360cctgtaatcc cagcactttg ggag
384

<210> 2074<211> 393<212> DNA<213> Homo sapien

ggcagcagga aaacttcaat gaaactgaat aaacaactt cctctgtcaa aagcccttcc
60atgagtctca caggctactc aacacctcgt aacctccaca tagcaaaagc cccaggctct

120gctcctgctg ccttatgttc tgaatccag tcacctgctt ttcttggtac atcttcttcc
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240gaactgcgta ttccattgga atatggctgg cagagagaga caagaataag aaactttgga
300gggagccttc aaggagaagt agcatattat gctccatgtg gaaagaaact taggcagtac
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393

<210> 2075<211> 400<212> DNA<213> Homo sapien

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120gccttgggtgc ctctatgag gagaccacac aggagctgga tgcccagcag gccaggctct
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240tggtgtgcaa gtttgaccgg agagcatacc cagcccagat caccctaag atgtgcctac
300tanagtgggtg ccggagggag aagttggcac agcctgtgta tgaaacggtt caacgccctc
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400

<210> 2076<211> 403<212> DNA<213> Homo sapien

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240gacgcctgtt cctgctggg gctttctgtg gagtcccccc ttagcgtcag ctttgctctt
300ggctgtgtgg cgtgcctgt gttgatgaac atcaaggctg tgattgagca gcggcagtgc
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403

<210> 2077<211> 400<212> DNA<213> Homo sapien

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240attaccagc aaaccragctg tgtctgttaa aaggccggcc tatcagattc aagttgcaag
300ccttatacac agtaagtgtc tcatgcacat atccatgagg attcacataa gctgccatcg
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400

<210> 2078<211> 391<212> DNA<213> Homo sapien

ggcacgaggg agcgtgggtg ggacacggtg tctggtgtan acggggagcg tgggtgggac
60acggtgtctg gtgtagacgg ggagcgtggg tgggacacgg tgtctggtgt agacggggag
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240ggtgtctgtt gtagacggag agcgtgggtg ggacggtgtc tgggtgtatac tgggagcgtg
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391

<210> 2079<211> 398<212> DNA<213> Homo sapien

ggcacgagcg gtcgcggagc tgcggccagt tttgggaggg ccggcccccg gatgctacac
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240cccaggggac cgctttgcca agcaggccat caggcgggag gtggagctgg agtggggcac
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398

<210> 2080<211> 397<212> DNA<213> Homo sapien

ggcacgagga caggaggaag aaacaagtat aaaggttttg gttttggaaa gaagttggaa
60tctccagacc ctgggacctt aagatccaca gaattgtga aagaaaaagt actaccttat
120tgaaaggatg aagaaacacg aaaagattat gattacatgc tggatcatcc agaagagtac
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240gtgattttgg tcagcgtgtg tgctatttcg gtgtttcagt ttttcagctg gtggaatagc
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397

<210> 2081<211> 403<212> DNA<213> Homo sapien

tcaattccgt tgctgtcggc ggcggccaca gttggggccg gtggctccgg aacgagatcg
60ggaaggggaac agtccactaa cctgcccgat agctatcatc tggcccggag gagaaccctg
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300gttgagatgg gtttcaatgt ggacactctc cctgcttatg caaaacggtc tcagaggatg
360gacatcactg ctccctccgt gaccaatcag ccagtgaccc ccc

403

<210> 2082<211> 394<212> DNA<213> Homo sapien

ggcacgagcc caaagtcaaa caaactgact tacagaagct ggcacagagg gaggaagccc
60tccaaaaaat acggcagaag aatacaatga gacgagaagt aacggtggag ctaagtagcc
120aaggattctg gaaaactggc atccgttctg atgtctgtca gcatgcaatg atgtacctg
180ttctgaccca tcatatccgc taccaccaat gcctaattgca ttggacaag ttgataggat
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300atttttggat gaatcctgat catgccagga attcattatc taactgtgga attcggcagc
360ccaaatacgg agacagaaaa gttcatcaca tgcc

394

<210> 2083<211> 385<212> DNA<213> Homo sapien

cgttgctgtc ggggaattca ttcaagactt tcataaactc accgcagctg acgataaaac
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360gacaataagt gcttataaaa cccc

385

<210> 2084<211> 386<212> DNA<213> Homo sapien

cgttgctgcc tgaatgtatt cgagcactat ttgggggatg acacgactag ggagcatcca
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300catgatggca ccaggaatat cttagatgat tttagagaag cttacttttg gctaaggcaa
360aatacagatg aacatgcacg agtaatgn

388

<210> 2085<211> 403<212> DNA<213> Homo sapien

aattcggcac gaggtagcat ggagggggag aggacgtagg ctgtgctctc gggctttgtg
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300ttcacaaaaa cttgcaggag catttttcaa accaagacct tgtttttctg ctattaacac
360cgagtataat aacagaaagc tgctctactc atcgactgga aca

403

<210> 2086<211> 390<212> DNA<213> Homo sapien

cgttgctgtc gctcctttgt ggccctctg caagagaagg tggcttttg attatttttc
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240tacttgattg tcatctgtgt gctgggcatt gcagccatta tagtctccca gtgggacatg
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360ggaatcattc ctaccttgca ctatgtcatc

390

<210> 2087<211> 383<212> DNA<213> Homo sapien

cgttgctgtc ggctgggtgat agctgtgtta cctgccaaat ctccaccaac aaataaaatc
60ggaagtaaat ccagcaatgc cagttggcct ccagaattcc aaccaggagt gccatggaaa
120ggatccaaa acattgaccc tgaatctgac ccctatgtca ccccaggaag tgtgctgggg
180ggtacagcca catctcccat tgtagatact gaccaccaac tgcgcggga taacaccaca
240gggtctaatt cttccctcaa caccctcgtg ccttcacctg gtgcctggcc ctacagtgcc
300tctgacaact cctttacca cgttcatagc acttcagcaa agttccctga ttacaaatca
360acatgggtccc cagatcccat agg

383

<210> 2088<211> 402<212> DNA<213> Homo sapien

ggcacgagca gacatggcgg tgttggcggg gaacagcggg gagacgtgct acagcaagta
60cggggccatg gccctcaaga gccgggcctg ccacgagatg gccctgagaa tcgtcctgca
120cagcctggac ctccgcgcca actgctacca gcgcttcgtg gtgcctgctc tcagcatcag
180cgtgacttc tacgtgcgtg tttttgtccg tgtcttcacc ggccaggcca aggtcaaggc
240ctcagccagg gccaagttct ctgcagcctg tgggtccccct gtgacccccg agtgtgaaca
300ctgtgggcaa cgacaccagc ttggtggccc catgtgggca gagcccatcc atgacctgga
360ttttgtgggc cgtgtcctgg aggtgtgag cgctaacccc gg

402

<210> 2089<211> 381<212> DNA<213> Homo sapien

ggcacgagtg cagcctgtg atcccagcta cttgagaggc tgaggcagga gaatcacttg
60aactcgggag gtggaagtgt cagtgcgtg agatcgtgcc actgcacgat ccgctgagc
120gacagaatga gattccatct caaaaaaaaa agtacttaat acctacttta aagattgtca
180tggaatatata aagtatgttg cccttactaa tgctagataa tgctttgctt tcttttattt
240gcatcttacc ctcttcctg agtattgata ctgtcttaaa catagtaggg ttgtattaga
300tatttgctgg ttgccccctt acttgcaggg gatacatata aatgttggtt ygtattggat
360aatgaatatg atgtttctaa a

381

<210> 2090<211> 367<212> DNA<213> Homo sapien

ggcacgagga gctttgtcaa aatacctggc ctctagtctt gagattttat tattgttcat
60tagaccagtg ctagggcatt aatgttttgt gtttatcttt tttttttta acctttattt
120taagggttaag ggaaccccag aagggttggc cccataggaa acctggggcc acaggaattg
180gtggaccatt taattcctcc ccccgggggg aagccccagc cctaaaaagg aattttttgg
240gcccttttcc tttccccccc ctcccccttt aaaaaaaacc ccagggccaa tggttccctt
300tttggggcca aaaagtctta acatttcctt cccctaaaaa agggaaacca gcgcggagtg
360aattttg

367

<210> 2091<211> 363<212> DNA<213> Homo sapien

ggcacgagat agggtagtct tgactagata taaccaaggg ataaaagagg attagctgac
60tcaggataac atttcaggtt tgtgaagatg aatttgcctt ttgaaacaga tctttttaga
120aagggtgttt cataatttct gaccgaagta tttgttacac gtaaaataag taagaacgga
180ctgaggccag aaagctgtg atgacagaag ggattgggtg attctcagt aattttgata
240caaattaagt atgtgggtag tttttaata catttactat atatatatat taatgaaaaa
300ttgtttccta aactgtgaaa aggtctatta aagaaattta gaggtggat gcggtgactc
360atg

363

<210> 2092<211> 380<212> DNA<213> Homo sapien

ctttgatcct tctggaatta attttgggtgc attgactgag gtaggggctc acgtttcctt
60cccgatgtca gccactactt ttgggtcttt aatctataaa agcaggggcac tgggttagaa
120tttccctaaat ctcttatata tcaaacaaag cactcactgc aaacttgatc aatagaggaa
180agtatgcttt tttgtattt taccttttac cagtttact tactgtaaat cataagggtg
240tcttacatag tagaaaaata gcattatctt aaacctggct ttttattact aaatatatca
300ctaaaaatgc tttacaaagc agtaatgatt ttatttcttg gggaataaaa tcaagaaagc
360taaaggagct gctatgccac

380

<210> 2093<211> 375<212> DNA<213> Homo sapien

ggcagcagac gaaaggaaac cttacagaaa catgaagccc tcaaccatct gctactcagt
60tattcggggc tgacggcggc ttctagaaca tccaggtgtt ctgcagatgc gagaactcat
120cctgtagtca ccagatggag tcccaaacag ccaagcagat gtaaggcctg tgctgtggct
180ctgaggccct gaatacagaa gggtcacttt cttagtggcc aaagagcagt tgttgacatt
240gatgtctaatt tattgaacac gaccagtcatt tttactgagc tgcggtgagg aacactgac
300catagaagat caagccaaat gagggattgc aaatttctg attcttttga attaggattc
360cagatggggg cctca

375

<210> 2094<211> 369<212> DNA<213> Homo sapien

ccgttgctgt cggttgtagg acttatctgg ggttctgaga ctccctgtcc cggaccgcag
60cggttaaaagg atctgaacaa agtctgtctca aatctcctgc tgtgaaccag cagaattttt
120gaacagggtt cttcacatat aaaaatctat tgtaaaaata cggacagaa tggcagcggg
180aacgcagaca ctgaactttg ggcctgaatg gctccgagct ctgtccagtg gtgggagtat
240tacatccct cctctttctc cagcattgcc gaagtataaa ttagcagatt atcgttacgg
300cagagaagaa atgttagcac ttttccttaa agacaacaag ataccttcag accttctgga
360taaagaatt

369

<210> 2095<211> 377<212> DNA<213> Homo sapien

cggttgctgtc ggccacgaac acagccttgg gcccaagggtg atgcgcgcgc ctcttgagtc
60cctcagatgc caaacgcaaa aaaaagcctt ctctctctaaa gacacggaaa tgcaccgagt
120ccggctctgc ctacccccca aatccttcgc gtccccaac tcggcagcca aaatcgaaaa
180ctactctcgt ctacgcgcgc ccgctgttga ttacctgcca ttccgcacgg gcgcctgcgc
240cccgcccgct gtgcgcgact taggacggca tcccagagact accttctca aggcgctatg
300accagtcga gctgccatga tagactctcc gaagccggtc gtcacctgcc ggaccagccc
360tgcagcaccg tctctcn

377

<210> 2096<211> 372<212> DNA<213> Homo sapien

cggttgctgtc ggccacgaac acagccttgg gcccaagggtg atgcgcgcgc ctcttgagtc
60cctcagatgc caaacgcaaa aaaaagcctt ctctctctaaa gacacggaaa tgcaccgagt
120ccggctctgc ctacccccca aatccttcgc gtccccaac tcggcagcca aaatcgaaaa
180ctactctcgt ctacgcgcgc ccgctgttga ttacctgcca ttccgcacgg gcgcctgcgc
240cccgcccgct gtgcgcgact tcggacggca tcccagagact accttctca aggcgctatg
300accagtcga gctgccatga tagactctcc gaagccggtc gtcacctccc ggaccagccc
360tgcagcaccg cc

372

<210> 2097<211> 148<212> DNA<213> Homo sapien

ctangaaaga ccccttctctc ttgcagtgtg tctccagcgc cctctactga caaagtatgc
60catcatgcaa gctgcaaagg aaacatttca agagtctata tctattttca cggagcgggc
120accaacagtg aatgtggagc tgagagag

148

<210> 2098<211> 379<212> DNA<213> Homo sapien

ggcagcagag aatgcctcca ggctggatcat tccatgtgac tagtgcaggg ttgcatggga
60gaggatagct gatgaacca gattgtgaaa ggctttgtgg ctctgtgctga ggattgtggg
120cttaactctg ggtattgtgg agctgttaaa acacatatta aggagtgcag tgatcagatt
180ttccttttta aagtgcattc tgtggagcag taattcttag ctatggagtc caccacaaac
240tttgtcatga taggttgtga ggtatattaa gtatatgta ccaataataa aatatcaggg
300cttacacatt aattgatttt ttaataagtt aaagcaagtt gaggttatca ctgtgatttt
360cttcattcac ttacatct

379

<210> 2099<211> 375<212> DNA<213> Homo sapien

ggcagcagat acattttata ttggaagggt tgtccaaggg caggtgggag cagtatagta
60tatgcagct caggcagggc tagagtttga cctcaccacc tcaccagtca tattagagta
120gctgtccaga caagggtgtgg gacacaattt cttatcagac caacaacctg caaagcagtc
180ctcagtcctc atttccctcc tgcttgtgac cagctatcaa aacctcaact ctggctaatt
240ccagcaatcc gcctaggttg ctgagcactg ctagagacaa atcatacaac tatgcaaat

300agtgttacta tatgatcact aacctcgtat gaaccttcac tgtgcttgca acatcagctc
360ccattcctac_cactt

375

<210> 2100<211> 371<212> DNA<213> Homo sapien

cgattcgaat tccgctgctg ccgaaaactt ctggattttt acccacgaag aacttcacgg
60gtccagtgga ttgcccctta tggccgagtg tccatacaca ctccaaaatt catttatcag
120ccacaagatt agttcgtggt tcaacatctg tagcttcagc acatactgat ggaaaaataa
180agatttctgtg tcataaatac cttattggag tgtagcata ttgacagaa ctggcaattt
240ttcaaattga gtgaagcctt atgtggacta taagttatag attatatact cttattgata
300acttgcctaa ttgctatgct gaaagagact gcaggagaaa taggcatacta tctctgcac
360tgttttcccc a

371

<210> 2101<211> 373<212> DNA<213> Homo sapien

tccgttgctg tccgtttcct tgttggtttt tcttgttctc tgctgctact gtaaaaacga
60aatgagtggc cctgctcagg ttccaatgat gtcccaaat ggttctgtgc ctctatcta
120tgtgcctcct ggatatgccc cacaggttat tgaagacaat ggtgttcgaa gagttgtcgt
180gggtccctcag gcaccagagt ttaccctgg tagtcacaca gttctccacc gttctccaca
240tctctctcta cctgggtttca ttctgtccc aactatgatg ccgcctccac cacgtcatat
300gtactacccc gtgactggag ctggagacat gacaacacag tatatgccac agtatcagtc
360ttcacaagtc tat

373

<210> 2102<211> 381<212> DNA<213> Homo sapien

cgttgctgtc gaactgcccc acatcatctg cagtaggacg ggggagttgg agccctggtc
60aggccactct gctactgacc acagttttct catctctaaa aaggcgcagt aacaatataa
120ttaccgtatg cagtccccca ggatacaggg tcaaaggaga ccacaacat cgcagatgga
180agcccattggg gcagggccca ggacacagtg agcatacaat agacattagc tgctgtgggtg
240tcttgatttc aagcccagtg cagatgcac tgacttacga aacttcagtg acacctgctc
300tgtgccagac actgaagatg gagcagtga cagcactgac ccagccatgc ctctgttgc
360ctgcaggcca gaagcaaggt c

381

<210> 2103<211> 362<212> DNA<213> Homo sapien

ggaccaagac aaagttaagt aaactctgga gcagtgtatg tgatgagtgt gtggcagggg
60gttttttatt ctgcgaaatt ttgtgtacgt ttgaagctac cacagaatag cagatattag
120aatgattcct gctgactcac cagtatttc aactgttcac aggggtcagg caggaagcag
180atctcttggc ctccctctga tccaggtcac ttagtccagc ccctgaaagc agtggatgga
240caaccatgcc accctctttc ttccaatata cttattttg tatectgccc tttttgtgta
300gcattagatc atgagcattt tctctgtcta taaatgtccc ctcaaatatg ttgattcttg
360tg

362

<210> 2104<211> 375<212> DNA<213> Homo sapien

cgttgctgtc ggtcttgagg gaaggaagcc ttctctttt ggcagaagtt tcaaatgggt
60cttatttctt gtctcactaa ggcagtaata gcatagtgat ggacctgggt gggtagtggg
120ggacagctga aaaggcagga gttttacttt tgtttgaaaa gagaccacat cacatatagc
180atctcaccat tcacaaagtg tacatccacc gatactactc cactgttaga gccttcgtcc
240tcttatggca gtagtataag aaaccttcca ccaagtcaga gtgctctaac tgatgcaaaa
300cctaaacctg gaaataaaga ttttcttgga gcagtaagac ttcagactgt tgggtgagct
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375

<210> 2105<211> 367<212> DNA<213> Homo sapien

ggcacgaggc cgatggagga ggggaggtct gagcagagtt cgggtgtgag gcgtaatggc
60cctcgtgccc tatgaggaga ccacggaatt tgggttgag aaattccaca agcctcttgc
120aactttttcc ttgcaaaacc acacgatcca gatccggcag gactggagac acctgggagt
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240ggagctcagg ggccgctctg ccgtggagct ggggtgctgg acggggctgg agggcataat
300ggctgccctg ctgggtgctc atgtgactat cacggatcga acagtagcat tagaatttct
360taaatcn

367

<210> 2106<211> 375<212> DNA<213> Homo sapien

acgggacgag ggctcttgct ggtcccatgt tgctgccc cagaggagcc tcgccaggca
60gcagctgccg cctcatcagg cgagaccccc caccagggtg ggcaaaccga gggccccata
120ttcggagaca cctccaaatt ggccatgtcc acagacccca gccaaagccca ggtgccagta
180gggctggacc agtctgaagg ggctccctt cctgctgctg ccagccctga aaggccccc
240atctgcagcc atggcatgga cccaaccga ctgggctgcc ccgattgtgc ctgcaagacc
300cagggcccca gcacggggct ggactgacca cagcagggga cctgagccgt gttccccagt
360ctccatattgc agctn

375

<210> 2107<211> 370<212> DNA<213> Homo sapien

cagggtgtgc ggaacactgg agttttgctt agctacctac tcacgcca acatgaactg
60ccctctggca tagagtgggtg taatgcgaaa ggaagagaca ttgtcagcct ggctcgagga
120tgggccgcgtt ctgggggaga gagttacctt tggcctaaat ctccctctgt gtctcttgaa
180gaacttacgg tatcttgctt atactagtgg atgttccttg agctgtgtgg tatgtttcct
240aattgtgggt atttacaaga aatttcaaat tccctgcatt gttccagagc taaattcaac
300aataagtgt aattcaacaa atgctgacac gtgtacgcca aaatatgta cttcaattc
360aaagaccgtg

370

<210> 2108<211> 381<212> DNA<213> Homo sapien

cggtgtgtgc ggcaggatga tgggcaggac agggagaggc tgacctactt ccagaacctg
60cctgagtctc tgacttccct cctggggctg atgaccacgg ccaacaacc cgatgtgatg
120attcctgctt attccaagaa cggggcctat gccatcttct tcatagcctt cactgtgata
180ggaagcctgt ttctgatgaa cctgctgaca gccatcatct acagtcagtt ccggggctac
240ctgatgcacc cgccgaggcc cgagtaccag actccgtttc tgcagagcgc ccagttcctc
300ttcggccact actactttga ctacctgggg aaccttatcg acctggcaaa cctgggtgcc
360atttgctga tctctccacc g

381

<210> 2109<211> 377<212> DNA<213> Homo sapien

ggcacgagct gaagcgttct ctgcttacca agttgcctcc atatctaatt tttgtatca
60agagattcac taagaacaac ttctttgttg agaagaatcc aactattgtc aatttcctta
120ttacaaatgc ggatctgaga gaatacttgt ctgaagaagt acaagcagta cacaagaata
180ccacctatga cctcattgcc aacatcgtgc atgacggcga gccctccgag ggctcctacc
240ggatccacgt gcttcatcat gggacaggca aatggatga attacaagac ctccagggtga
300ctgacatcct tccccagatg atcacactgt cagaggctta cattcagatt tggaagaggc
360gagataatga tgaaacc

377

<210> 2110<211> 143<212> DNA<213> Homo sapien

tcaagttaca aaagctctgg aaccctgtgg cttcaaattc tttgggaagg gtgactgttg
60tttcccctac acacagtga agccggaatg ggaatcgtg aggctctgat ccacttctaa
120gaacagaagg aaagtgaagg cag

143

<210> 2111<211> 354<212> DNA<213> Homo sapien

tttcttgtgc tagaagacaa ccgaattgtt ttggctaaga aacactaatc tagctgaatt
60cccacacact caaaaatatt ttctacaaa ccccaaatca attgatgtct ccattctaca
120tggtgtgtct caatgtcagg aaactcacta tattccaaaa ttccatttgt tgtcgaagag
180aatcattata gagagacccc ttcatgtgac ctgcgacctg cgatatttaa tttcatttaa
240aagacagaca cacagggaaa tatatagctg agagatgctt tcattaatag agaatcctgg
300gaacccttga gtaatcacat ttgaccaac tctagtgaat agaccatttc cctt

354

<210> 2112<211> 332<212> DNA<213> Homo sapien

tacggctgctg agaaacgaca gaaggggaga ggagggtgct agatgatgac ttggttttgc
60ctggattgag tctgggatgg ggatgagaca tcatgtttta atggtcttat agggagtagg
120aaagaggcta aaacctcaag agatagagga aattcaagta caggattaag ttgaacaaaa
180gtgataacca accccacaag gtgattttta tttcgttaacc tcagtgggga aatcttcggt
240gcagggcagt ggtctcatt tggggtgatt tttgtctccc aaggacatt tggcaaagtc

300tagaaatatt tttggttgtc acaactcggn gg

332

<210> 2113<211> 337<212> DNA<213> Homo sapien

ttttcggtcg ccagattacg acagaaggga aacctttaaa gtctttgagt ttcgaaggac
60aaactttggg atttccctgg ttaaactcaa agtgactgtg tgacagaagg ggtggattag
120ctatattctt tgctgtattt ttataactaa agctacaatg attagggag ttgcaatgct
180aaatcaatat tctctcattt gtctaccaga aagcagtctt actagaaatg cacatacata
240agatttttga tttggttcca gttgacactt gatgtgtcaa gtaccaggca gtaaaatgca
300gatccagtaa catttctttt tcttttggtg ctgctg

337

<210> 2114<211> 337<212> DNA<213> Homo sapien

tacggtgcga gaagacgaca gaaggataa acaaattttt ttaaataaat gagagatagc
60taagggtttt taaaaattat tatactaca ttatgagaag aaggccttta ttgtccttgg
120aggtatgcat ttccagaccc ctacttaag agtccttga atgtggttct gcttgacaga
180gttctgtatt agcacttga taccagaggc agcaccacaa tcaagctgcc aggccagaga
240atgtttcctt tccaaactca gctgcctct tgcacttaat ctaattgggt agttagataga
300aagtacagtt gttactaaaa cactcttttg cctggag

337

<210> 2115<211> 222<212> DNA<213> Homo sapien

ctgaaagttt tgaatttgat taaagttatt catgtcttgt taatctctgc aacatttgta
60gttgctgttt tctccttttg tctttgaaga attttgccg attttttcc tagtagtttt
120caaagaacca gcttgtagct tgagtgtatc tgggtgtttc tagctcatca tcggattttc
180tgcctctccc cgtccagctg cttaaagtaa tttttaagct ca

222

<210> 2116<211> 462<212> DNA<213> Homo sapien

cgttgcgtgc gaggatatgc tgttgggtga ggtggattt aatgttgata caagtatttt
60gggtctgagcg tttggaagaa agttggcact gaggtggga gtcgagtta gttttgtag
120tttttgatgt gtttaagttg agatgctgat tcttcagaga agtctaagct ggagaactat
180atagagagtg gaaagataac aatagacatt gaaagccatg atacaggata aggtcatttg
240gagagaggat agactgcatt ccaacatgag attggttgac aaagagaaac caaccaaggt
300aattaagagg tgctcccact gcacttgatc tcagaaggct gaggttaagt tgttagaggc
360cagcctgggc accacaggga gacccatct ctaaaattta gccaggaacc atggctcatg
420cctgtagccc caggaatttg ggaggctgag tggggaggat cg

462

<210> 2117<211> 454<212> DNA<213> Homo sapien

cattacgtca gcaacgncnn cnnngnnng atcccatcga ctggaattcc gttgctgtcg
60aaataaatga ctggatggtc gcttctttt aagtttcaa ttgacattcc agacaagcgg
120tgctgagcc cgtgcctgtc ttcagatctt cacagcacag ttcctggga ggtggagcca
180ccagcctctc cctgccctag cagatgctaa tccaccgtgc gtcctggcag aggttgaagg
240gggctcctca agtcccaggt ccagcttgg gtggttcagc tactcgagag acatctgctg
300ctaattgatg agcagtcaac ctggacgcag gaaatcattt tttatttggg gcaaagaggc
360agaggaatgg agctcagagc ttttagagaa tatgggccag aaacaggaag ggtcacgac
420ctgataacgg gaaccagcgg acagtgaacg cagt

454

<210> 2118<211> 442<212> DNA<213> Homo sapien

cggtgctgtc ggatttaca aagaatctac ttgactctgt ccctggagtg aaatccttag
60ggttggaact tgtgggaaca ttccaacttg ctaagcaggg tccactggga gggaagctct
120atctgggaac tcacccccag cgcacacaca tctccccag ggtcccaagg ccccgagct
180tctctccccg accaaacccc aagacctgga tcccaggaga caacagtctc cacagtgaga
240gcaacattaa gggcaaagcc atggagaaat gtgggagagg ccggcctcaa atctttccat
300ttaacaaacc ccagtgatgg gtatggacag catgcagggc ttttggggnc gcttcccccg
360ctcctccatc accctcagcc ttcacacttc aaagttcaag ttcaaagctg ttcaagtttc
420ctaccagcaa agagccctaa ct

442

<210> 2119<211> 436<212> DNA<213> Homo sapien

cggtgctgtc ggatttaca aagaatctac ttgactctgt ccctggagtg aaatccttag

60ggttggaact tgtgggaaca ttccaacttg ctaagcaggg tccactggga ggggaagctct
120atctgggaac tcacccccag cgcacacaca tctccccag ggtcccaagg ccccgagct
180tcctcccccg accaaacccc aagacctgga tcccaggaga caacagtctc cacagtgaga
240gcaacattaa gggcaaaagg atggagaaat gtgggagagg ccggcctcaa atctttccat
300ttaacaaacc ccagtgatgg gtatggacag catgcagggc ttttggggcg cttcccccg
360ctcctccatc accctcagcc tccacacttc aaagttcaag ttcaaagctg ttcaagtttc
420ctaccagcaa agagcc

436

<210> 2120<211> 434<212> DNA<213> Homo sapien

cggttgctgtc gaaagttatc aagtaaataat gtctctgtg ttctgtttca tgtgatggag
60ggggtttcag tctgtgttct tggagccaaa gggttcctca agggtgccctc aagagtaatg
120gtttaagaaa agaggggcaa tgagagggag cgagggggaa ggcctagtgtg gtatttgagc
180aggggcctta agctccatat cccaccccc tttacccaaa acagcccatt tttcttatgt
240atattggaat ttcaagtaag ctttcatggg gtgcagtggg gcggggagga atggatggga
300taaaaaaagt ggagattttg ctgctttaaa aaagttgaga actacttgtg taggttttaa
360ggatttttaatt gtatttcatt ttggcaaatt caactgccac aaagcagcta tgcataagtg
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434

<210> 2121<211> 434<212> DNA<213> Homo sapien

tcgttnaatt cggcacgagg atgccaggc caccatggag ctatataagt tggttgaagt
60cgagtgggaa gagcacctag cccggaatcc ccctacagac tagtggcagt ggggacgctg
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180tccaccagct ccacatcttt ggaagctaga tttggggaga gagaagctct accccagact
240taatacccat tgaaatttca cctcaggtgt tgtgtcctgt gtctgggttaa gtgtcccatg
300gaaggggaaa gccttcacgt cagaacccaa ccctatacct tttacttctt anatgggtgt
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420gcatactggg aaat

434

<210> 2122<211> 431<212> DNA<213> Homo sapien

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120actgccaacg ggcattgggt gaaaggggaa gacgagagcg ctggccttga caggaggggc
180ttcagcagct ccagcccaga gcaactcggc agcatcgact ccaccaaggc ccccagacc
240cccagagtg gagcgcccaa tctctgcgat tctcaggaaa cgaactgttc caccgctggc
300cactccaaaa cgccgccaag tggagcagat tctaagacgg tgaagctgaa gtcccctgtc
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420gcccttttctg g

431

<210> 2123<211> 423<212> DNA<213> Homo sapien

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120ttgttatttt caggtcccc accccccaaa aaaggggggg gtttgtctcc tttaaagggg
180tgggaagccc taattttttt taaaaaaaca gtgccacac tttcccaaac caaaagggg
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300aaaaaaattt aaaatgtatt aaaaagtga ccccgcccc tttgaaacct aaaaaaagt
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420agn

423

<210> 2124<211> 170<212> DNA<213> Homo sapien

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120gcaaagaag ccccatatc cccggtgaaa aagatggagt cttgctctgt
170

<210> 2125<211> 424<212> DNA<213> Homo sapien

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300ctcacaagca tggcccccca ctgctggctt tccttcccca ccttccaccc tctccttggc
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424

<210> 2126<211> 424<212> DNA<213> Homo sapien

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120tgagaaactt acaagtattt tcgttgagtt ctgcttcac tattatttac ttacaatgg
180atatgaagtt cagatttcat cttatttact gaaggtagg aaaggatgtg gaagtagggg
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420cagg

424

<210> 2127<211> 423<212> DNA<213> Homo sapien

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420ggc

423

<210> 2128<211> 426<212> DNA<213> Homo sapien

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420ttaggc

426

<210> 2129<211> 424<212> DNA<213> Homo sapien

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120ctctccatc cccacttca cccatccca taccagttcc atccagggtc tgcttaactg
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420gccn

424

<210> 2130<211> 428<212> DNA<213> Homo sapien

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360ggggctggcc acatttaagg cttaaaaatt ttttaatttt gtggctgatg atagcaaaca
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428

<210> 2131<211> 424<212> DNA<213> Homo sapien

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420tttt

424

<210> 2132<211> 427<212> DNA<213> Homo sapien

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300ctgcctgctc tggcgaccct ggggtgaggga gtgggtgcgg gctgccttct gcttcgccc
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427

<210> 2133<211> 427<212> DNA<213> Homo sapien

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300attagaaaaa tagctgccct tgaaaatgag ctgacttttc ttcgctctca gattgcagca
360attgtggaaa tgcaggaact gaaaaatagt acaaattcta gttcctttgg cttgagtgc
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427

<210> 2134<211> 427<212> DNA<213> Homo sapien

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60cagacggacg tgagagaaaa acgcaagagt ctcttcatta accatcatcc tccaggacaa
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300aaatccgaag tgccaccaga ttatgacaaa cacaacccag agcagaagca gatttaccgg
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427

<210> 2135<211> 429<212> DNA<213> Homo sapien

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429

<210> 2136<211> 417<212> DNA<213> Homo sapien

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120ggaaaatgga aaagccattg tataaatttt tttttgaggg ggagtcttgc tctattggcc
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240gattctgctg cctcagcctc ccgagtagct gggattgcag gtacccatca gcccattgccc
300agctaatttt gtatttttag tagagatggg gtttcacat gttggccagg ctgggcttga
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417

<210> 2137<211> 417<212> DNA<213> Homo sapien

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417

<210> 2138<211> 419<212> DNA<213> Homo sapien

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360ttttttttaa aaaaaaaaaa ttgtggggcg cccccctt ttttttttaa aggggggggt
419

<210> 2139<211> 417<212> DNA<213> Homo sapien

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417

<210> 2140<211> 418<212> DNA<213> Homo sapien

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240tagaggaggt gtcaatgtca gatccactgg caagccacca aagaccgtca ctcccaggat
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360aacctgtgca tgcactgcct tcctctgcca gccagaaacg tgtggaccag aaacgttg
418

<210> 2141<211> 421<212> DNA<213> Homo sapien

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240aattgaccag gaaaaaccgg ataaccacaa ccagtttttt taaaccgggt tttggaacct
300aaaatttggg aaagggaacc ccaggcccat aaacaaaaac cggggccttt aaaaaggaca
360aaattttccac cccagaaaaa gtccaaccca attccaggct ttctgaaaaa aaaaatttca
420t
421

<210> 2142<211> 422<212> DNA<213> Homo sapien

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300acaatgctca gatccctttg gctaattggac ttgactctca cagtatcaca agtagtagaa
360gaacgaacgc aaatgaaggg aaaaaagaaa catgggatac agcagaagaa gactctggaa
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422

<210> 2143<211> 417<212> DNA<213> Homo sapien

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417

<210> 2144<211> 417<212> DNA<213> Homo sapien

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417

<210> 2145<211> 419<212> DNA<213> Homo sapien

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419

<210> 2146<211> 418<212> DNA<213> Homo sapien

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360gagaagcaga aatctacatg gcaaaaagaga gtaacaacc ttcctaact tctcaccg

418

<210> 2147<211> 422<212> DNA<213> Homo sapien

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360gcattntatg acagtcaaac atgggaaaac attcttaagg ataggatggg atctgcactg
420at

422

<210> 2148<211> 413<212> DNA<213> Homo sapien

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413

<210> 2149<211> 415<212> DNA<213> Homo sapien

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300tgagtcgggtg gcaaaccgtt tattttttta aagccccac ctttttttta aaaaattctt
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415

<210> 2150<211> 411<212> DNA<213> Homo sapien

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411

<210> 2151<211> 416<212> DNA<213> Homo sapien

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300actcaaacca agtgaagcaa gaggggacaa ttctagaatt ggctgtgcca tgtaggtttt
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416

<210> 2152<211> 411<212> DNA<213> Homo sapien

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240aggcgtgagc cactgcgccc agccttactt atttttaaat cagatttttt aatcaactaa
300aacagctatg agttaagtac ctgccctgca aaaattttta gaagaagttc taggattatg
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411

<210> 2153<211> 411<212> DNA<213> Homo sapien

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120aaccattgc agcaaatgtg ggcaacaaaa aaatcagct ttcaactggg gagagccacc
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300tatagcctta gataatgggt tctttgggaa agaccttaaa ataggagtta ctggggaatg
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411

<210> 2154<211> 415<212> DNA<213> Homo sapien

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180tcgattttga agagactagc atttcttggg aatgaagtgg agtatatatc catatatttc
240tgttttcttg atgagaagac taacctaaat aagtaggaac cttgaagaat catgttcttc
300ctaggaatta caaatcccc gaatccatgt ctaacataat ttctactggc ctctttgctt
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415

<210> 2155<211> 413<212> DNA<213> Homo sapien

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120aggggtgagaa gaagctgcag gaaggtgggt ggtatattgg aagaaatatt tttgcagtca
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240ttgcatatac aggggtgatta taatcctgca aaataaaaaa tttattggga taataaaga
300ctgacaggaa aattttttaa gtgttaacat tgggttatgt tgggttgggt aggctgggtg
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413

<210> 2156<211> 414<212> DNA<213> Homo sapien

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120ggcagcctgt ttttaaagaa atgggactaa tgggagaagc tgtttgtcac tctaagagca
180tccaagccct ggcccgctc tgcactctg gtcctgggg agatatactt gccttctaag
240aaggcaggcc aggtcttggg cacagacctg catttgttga ccttgcactc caactatagt
300gccttgcaag tgcacaacag tacatattgg aatgaagtcc ctatgagagc catttctggc
360catgttctat acctcaaagt gaggtggca ggtacagaga tgaactgtac acag

414

<210> 2157<211> 415<212> DNA<213> Homo sapien

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120tgggacactc tcttgttttg cattcaggaa ggagtgaata tgtttttaa gcaagaaaaa
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300gcatgtaata atattttaga ttcctatgag atgtttaatt tgcagtcaaa agctgtgaaa
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415

<210> 2158<211> 413<212> DNA<213> Homo sapien

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120tgatgggact cctctcacia atgtattctt ctttctctc tttcccgacc atctttgct
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300ccctgtgggt tgatcatgtg accgccttct tgacaaaatg tctgccgcca tctttatttg
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413

<210> 2159<211> 416<212> DNA<213> Homo sapien

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120gacccctgga actgcaattg tcctgtgagt tcctgagtga ccagagcctg gagaactctac
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240ccccgaaaag ccccttctct ctggccaaca ccttaagcct gtgtccacgg gttaaaaagg
300tggaactcag gtccctgcac catgcaactt tgcacttcag atccaacgag gaggaggaag
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416

<210> 2160<211> 412<212> DNA<213> Homo sapien

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240tatcagtcac ggaacgggtt aacttgtttg gtttctggag ccgattcaac ggaactaaca
300gtaatgggga aagaaaaagac ttacagctct ctggtttgaa cagcccagga tctgtcttag
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412

<210> 2161<211> 412<212> DNA<213> Homo sapien

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120tccaagtcac atagccacta aaactcgact atcagaagaa agtgctcgtt tgggtggcagc
180cacagttacc atactctctg atttaccatc cctttgttca cccgctggat gtatgacaat
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300agataatcag gtctctccac cagtcagtgc agctcttcaa gggattaaaa gtattgtgac
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412

<210> 2162<211> 411<212> DNA<213> Homo sapien

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411

<210> 2163<211> 415<212> DNA<213> Homo sapien

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120ttgcacccag aagccctgaa tcagattctc agagccctga gtttgaatcc cagagcccta
180ggtatgaacc ccaaagccct ggctatgaac ctccggagccc cgggtatgaa ccccgagcc
240ctggctatga atctgagagc tctagatatg aatcccagaa cactgagctc aaaacccaaa
300gccagaatt tgaagctcaa agttccaaat tccaggaagg tgcggagatg cttctgaacc
360ccgaggaaaa gagtccctttg aatatctccg taggagttca cccctggac tcctt

415

<210> 2164<211> 412<212> DNA<213> Homo sapien

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60caggaagtgg atgcttttga agaattaagc aggcagcttt ttctggaaac agctgatcta
120tatgtacca aggagagaat agaatactcc aaaaccttca aggggaaata ttttaatttt
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240gtttttgatc gagtgggaa aacggatcct gtcacaagag gcattgagat cactgtgaat
300tatctgggaa tccaatttga tgtgaagttt tgggtcccaac acatttctt cattcttgtt
360ggaataatca tcgtcacatc catcagagga ttgtgatca ctcttaccac gt

412

<210> 2165<211> 407<212> DNA<213> Homo sapien

ggcacgagga gatgtgatgt atgctttata aggtcatca gccatgcgag agcagcgatg
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120gtgagaggaa cggatgcgga gaggttctga acttgtaggt caaaatgtga aattcgaaa
180aatacccaaa aaacctaaga aaattttgta aaggaaaata gatttattat taagcagatg
240aaaagatgcc caacatcagt agccatcagg gagatgccaa tcaaaaccac aatgagatac
300cacctcacac ctggggctgt cagaaaaaag gcagtaacaa gtattcgcaa ggatgtggag
360acactggaac tcttccacac tgttgatggg aatgtaaaat ggngcag

407

<210> 2166<211> 405<212> DNA<213> Homo sapien

ggcaccagat cacatgtatg atttattttt aatatttgat aggaactagg ttctagtga
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120aactgaaatt tgtcactttt ctgttacgca gagaatcaga ccttttgata atatttggga
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240tgcggggggc gggggggaca gagtctcact gtgtcactca gactggagta cagtgatgcg
300atctcggctc actgcaacct ccgcctctg ggttcaagcg atttctctgc ttcagcctcc
360tgagttagctg ggattacagg tgcacaccac cagcccgc taatn

405

<210> 2167<211> 408<212> DNA<213> Homo sapien

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60agagagagag agagagagag agagagagag agagagagag agtgcgagag ttagaccag

120agagagaggg ggtgtttgct cttgattgcc cccgcccctc cctctctttg ggattttttt
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240tctctttttt tactctttac cttttttttt tttctgccc gcacactttt tttttatccc
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408

<210> 2168<211> 408<212> DNA<213> Homo sapien

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120gaaggtgcag aaaagggcat caaaaagagg ctggattttt taaaaggcag ctttccaact
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240gcagaaacaa aacctgtaaa aatgactaat cagctgcaca tattgatgct ctctgcaagt
300tacctttaag tgtttttttt cttatacttg aagttgcttt tacgatatta ttttgggtggc
360tttcttttct ctctttgatg ggcaatagag gaagtagata atgggatt
408

<210> 2169<211> 405<212> DNA<213> Homo sapien

ggcagcagct cagnannctt ctttcaactc tagtttttga ggtggggaca caggaggtcc
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120aaagtgtcga aacacaccag agggggcagg caccagccag ggtatgatgg ctactaccct
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240gaaggaagcc aagaggatca ctgctgctcc tttttctag aggaaatgtt tgtctacgtg
300gtaagatatg acctagccct tttaggtaag cgaactggta tgtagtaac gtgtacaaag
360ttaaggttct tgtgggtttac ccatctgaaa tatgtttcca tcaca
405

<210> 2170<211> 408<212> DNA<213> Homo sapien

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60gaaaaaatat agagaggggt ctagactgct taatagagga aagaagtatc ctggaaagct
120tggttaagaac gttctagagc cacaacatga ttgtaggcca agggcttggt tttgtgacct
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240gtaataataa ggtagtttgc cttttctgca gacattttta ggagtctttt tgtgtgagtg
300gtggtggagt gtatagtttt gttgaaccta gctaaattct gaatatcttt ccactaaaag
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408

<210> 2171<211> 406<212> DNA<213> Homo sapien

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60caaaagtgtg ggatttttct cctcttaact ttcttaatat ttggacatgc cgctgtcgcc
120aaacttgggt attcatggaa tttctagtaa atgaaatacc tatactttga tactgaagac
180tgccaaatac ataggaattt tctttcttaa aaaacagtaa tgaagactat atctcctttc
240ccagcactga atgttttact agcactgggt gctcaccatg caactgaaga aaatgtggaa
300actcaaaagg tcaggacaga cttccaagca cttgcaactg atgttactgt cttcaatttt
360aataattaca catatttgta tatttcacag aagcttttaa tatttc
406

<210> 2172<211> 405<212> DNA<213> Homo sapien

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60gtcaacaggg caggttggac agcgtgccag cgccgcgcag ggccacctcc ctgggtggat
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180gtcaggggtca atgggaatct gtcgggacac tcaacatggg ggtgggtgca ctccctggag
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300ttcccgccag gaggtggaca ccagccaga ggcctggctc aaggtgacct caccttcacc
360atgggcttcc tgggtgcccg ggcctgagcg caggttgttt tgtac
405

<210> 2173<211> 409<212> DNA<213> Homo sapien

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120gtgttggggc aacccccgcg tgaagggcgg ggaaaaaaag gctttttttg gaaaattggg
180ggggctgtgg ctttttttga acccattgta aggggcataa agcaggttac caccaccatg

240ggcattcttt tttggttaca ggttcggggg gggggggggg aagggttcaa nattgcctac
300gggagaaaaa aagaaaaacc tcagcttgca aatttttgtt cagagatggg atcgttcttt
360gtcggttgag ggatttacat taaaaaatt cacgagatat tgctcatgg
409

<210> 2174<211> 410<212> DNA<213> Homo sapien

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60gtacctcacc acagaccaca gatgacctcg tgtcatactg tgggctgatg agaggtagag
120catcatgcat cgaggcctga ggggtcaggg cgccctctct tggcctggag gaattgctcc
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240ccacagtcct tgccctgtca tggacctcct tcagagcacc tttctacaga ctggactgcc
300cagctccgtg ggggtggcatc tggtttctgg tgctattctg ccaagttatc gagtcctcc
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410

<210> 2175<211> 408<212> DNA<213> Homo sapien

cgttgctgtc gggggctgcc cagcacctgt catcctgctg ggatcagggt ttcttagtgc
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300acagctgtct tttccccacc tcagaatagc attcctttcg aacaccacgg caagtagctg
360ctcgtctccc atcggaaggc agcactggat tcctggctcg gtggcttn
408

<210> 2176<211> 406<212> DNA<213> Homo sapien

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300aagtgtaggg tgggacacag gtgcactctg tgtttcgtaa gtatgagctt agatatggag
360tgtggtagaa aaagaatgaa gagaggataa tggagggaagg gaaaaa
406

<210> 2177<211> 406<212> DNA<213> Homo sapien

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60tgaaagcggt tgagaatctt ttaggacaag cactgacgaa ggcactcgaa gactccagct
120tcctgaaaag aagtggcagg gacagtggct acggtgacat ctggtgtcct gaacgtggag
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240tgggctcgag gtcatgaca agctgtcct ctgatatcac gttgagaggg gggcgtgaag
300gttttgaaag tgacacagat tcggaattta cattcaagat gcaggattat aataaagatg
360atatgtcgta tcgaaggatt tcggctgttg agccaaagac tgcgtt
406

<210> 2178<211> 407<212> DNA<213> Homo sapien

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240ggggcgccca tgctgggcag cccacacaag cactgtcac ctgctgtcgc cacctggccg
300accctgggtg attggggaat gctgtcagcc ccgcagcccc tgtggccata tctggggccc
360gagcttgtgc tgggtcctgc tggagactgg ctgggttaag gctgcn
407

<210> 2179<211> 405<212> DNA<213> Homo sapien

cgttgctgtc ggttgcagg ccctggagg caaggccacc ctgtgtggg tcctgttgg
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120tgcagcctaa tttgggtgt aggggaagct ctgctggccc ttgctccttt gtatgttggg
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360taagatatag tgggggtttt tttgggtgga ggggggtttg tttng
405

<210> 2180<211> 409<212> DNA<213> Homo sapien

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60ggaaccaagg gtgaccaagg ctggcgccac catggctctg ctgccgtcac ctccctccctt
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409

<210> 2181<211> 408<212> DNA<213> Homo sapien

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60gagagagaga gagagagaga gagagagaga gagagagaga gagagagaga gagagagaga
120gagagaggtt tttttcccc cttgtgagag agcctctgtc tctctcccc cccccctct
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360tcacaccccc accccccccc ccacatagt ttttctcccc tccccgcg
408

<210> 2182<211> 406<212> DNA<213> Homo sapien

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60ctgtcgccgt ggattgttat tttgtgtcac taagtaatcc ataaagcgcc aacatgggaa
120agaaacggac aaagggaaaa actgttccaa tcgatgattc ctctgaaact ttagaacctg
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360gcagaaattc tcaggagcag catgccttga agcactatct gacgcn
406

<210> 2183<211> 409<212> DNA<213> Homo sapien

gtggggactg gaccgcccga cctgccatac ccgtttctta cggggctcgt cgccgccagt
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120ctcaggggtg gaccgagatt cccgacgaga gatactgagg ggaagagagg aaagaggggc
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240caaccgggga gctgctgctg cccaactggc aaggtattgg ctccacggg ctgatcatcg
300cccagagggga cgacggcgctc tttgtgcacg aggtgacgca gaactccct gcggcccgca
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409

<210> 2184<211> 407<212> DNA<213> Homo sapien

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120tgtgtgccgc gactggcctc ggtgctgcta tactccgatt atgggatagg agaagtggcc
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240tctccaaagc agccgggtgc tggctactac cgtggcgctg tcggtggcac gtttgaccgc
300ctgcacaacg ccacaagggt gatgatcagt gtcgcgtgca tctggccca ggagcagctt
360gtgggtgggag tagcagacaa agatctgtt aagagcaaga tgctccc
407

<210> 2185<211> 408<212> DNA<213> Homo sapien

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180actttaaaac aacttaaaga caggtatcct cggaaacgggt ttgtggctgg agtaggagca
240aacagcaaaa ttagtgcact gaaaggctcc aaaggaaaag actgggaaat ccctgtgcct
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408

<210> 2186<211> 406<212> DNA<213> Homo sapien

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120ttacttccca tcttgattcc ctgccgtcta agtaccatgt gacgtttttt ggagaaacag
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406

<210> 2187<211> 410<212> DNA<213> Homo sapien

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120tcttccagac agacaccgc atctacctcc tagcctattg gtctctgctg gccaccttgg
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300gtatcatctt tgaccggcca ctgctctatg tagccgccac tgtatgcctg gcggtcttca
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410

<210> 2188<211> 405<212> DNA<213> Homo sapien

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120ctaggggctg agaagagaaa gaggacaacg gtagccaaat atggtgatgt agatgatgcg
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405

<210> 2189<211> 406<212> DNA<213> Homo sapien

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120tctctactat cttcaaaata acctggactc tatgcaatga aaagaaacag tatgataaag
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406

<210> 2190<211> 399<212> DNA<213> Homo sapien

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120cagatgcgcc tccactaagg ggcataatgcc acgctcgtct gacctggaa tgaggatga
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240ggcacaaggg ctgtgtggaa gtagggttg tctccatgga tgacgtccag aaggatgtca
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399

<210> 2191<211> 404<212> DNA<213> Homo sapien

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300agccagtaag gaaatgaatt tctggactaa ttcataataa acaaaggggc aagtttagtg
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404

<210> 2192<211> 403<212> DNA<213> Homo sapien

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120gagagtttct ctctctctgt ggtatatata tacaccact ctctcttctt tctctctaga
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403

<210> 2193<211> 404<212> DNA<213> Homo sapien

ctgcaagaga ggatttcagg aaaccttgta tgtgtggaat gaacctaaat ggtgcattaa
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120ggtgggagcc ggtgtgggag cttttactgc cgttttgctg gtggctctga cctgctactt
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404

<210> 2194<211> 401<212> DNA<213> Homo sapien

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300caggttaatgg agtctgttcc tttgcatctc aggaaggaat tgactttgct ttatgtatca
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401

<210> 2195<211> 398<212> DNA<213> Homo sapien

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60gagcctcccg aatagctggg actacaggca cagccacta cgcccagcta gttttttgta
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398

<210> 2196<211> 404<212> DNA<213> Homo sapien

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404

<210> 2197<211> 399<212> DNA<213> Homo sapien

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360tactttaaat ggaataactt tttggttgca aaacagaga
399

<210> 2198<211> 399<212> DNA<213> Homo sapien

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60ttgttttttt tttttttttt tttttttttt tttattaggg ggggcccagc gcgtcctaaa
120aggggaccca ccccccccc aaaaatcccc cccgcgaaaa aaaaaccccc cccctacgc

180ccccccgtaa aaggacgcat acctcacgaa ccgggggggg gggggggccc ttttctcttt
240tttataaaagg ggggaaaaaa accccccccc ccggggaaa gaaccccccc cccaaaacct
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399

<210> 2199<211> 402<212> DNA<213> Homo sapien

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300ttaagacaac agaaatttag aacattttac atgcttcttt gttaaattgg gaagcaaggg
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402

<210> 2200<211> 398<212> DNA<213> Homo sapien

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60cacaaatcaa gaaaacttta caaggattga agggactggc acaggatctc tttctgggaa
120agccttgggg tcaagtggat atgtcaaaga aagtgatgga ctagaaatga cagatgtgga
180atgaagcaat ttgtacgtat taccaaagaa accaaaaact gcctttgact aaggggggtg
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398

<210> 2201<211> 401<212> DNA<213> Homo sapien

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240atttgctctt ccttgcccca tctctggcca gtttcacaat ctagctcgac agagcatgag
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401

<210> 2202<211> 404<212> DNA<213> Homo sapien

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60acatatagat accaagcaaa attataagaa acctataagg tgttcaatac gcttggtgtt
120ccaaaatttca ctgtacatga tcagtttggg gttcttgtag cacagttttt aactgaagga
180accagttgta acagtctcaa ttttaactaa aacttgaaga actaaaacaa caatgcaaac
240ctttcagcat tgtttggcca aacttgtaa aactgtaatg caagaaccaa atgcactgtg
300atgtggcacc aactaattag caagcatgaa tttttcacc aagagtgaag aaaggaaaat
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404

<210> 2203<211> 404<212> DNA<213> Homo sapien

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120tggtccaga tgaaaaggc accatctcca gctcttgga gcagagaggg tggctctttg
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240aatggataaa ggaattactc agcttgaagg gatctggttc ctttactctg gcctgatgtg
300tggggagaaa ggggccaaaa agtttacgat ttggagttaa catcgaaatt tctgctttgt
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404

<210> 2204<211> 401<212> DNA<213> Homo sapien

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60gtttctgctc accctgaaga ctgctggatc agttagttag acaaattcca agaagctggc
120ttggatgtca aattggctctt gggctcatag agaggaatgg attgttgcc ctgaaaagga
180gcgataactc tagtttttaa acatttgttt tagttcagat aattactgcc cttattcatt
240gtgtccacct gattcagaaa gcattgctgc tgttgcttgg tctaaggag gaggaccag

300gcatgtaacg gactgcatgc tggccagttg tgggtggtcag agcaagctgg aggccagcga
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401

<210> 2205<211> 402<212> DNA<213> Homo sapien

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240ttacatttag agtttgctgc tctttctctg gaattattgt tgcagcgctt cccggataga
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402

<210> 2206<211> 402<212> DNA<213> Homo sapien

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402

<210> 2207<211> 400<212> DNA<213> Homo sapien

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240gagaagggca gaccattctt caaagaccac catgtccaag gtctgacagc tccccactgg
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400

<210> 2208<211> 400<212> DNA<213> Homo sapien

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240tgagattctc catcttaatc tacttggagg caagagcaga tgggttggtt cattatggat
300ggaggggatg atggtaacct tattatcaaa aagaggtttg tgtctgagga aaaactagat
360gaacggccca aaaggaggca agaagaatgg gagaaagttn

400

<210> 2209<211> 398<212> DNA<213> Homo sapien

cggtgtgtgc gcatatgtgt ccataatag agaacttgct aaatgattta tactaccttt
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120gaacaatccc catggtgggg ggaaaagtaa ggtgcagaac tgtatcatag atgttctctc
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240atggcaaaca agatatcttt gcaatagttt ttttctggga ggggactcat ttaaaaaaat
300tctcccatat tgcttggttt gttttgttaa agacatccat gtattcctac ttgggttaag
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398

<210> 2210<211> 400<212> DNA<213> Homo sapien

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240agtcaggatc tccatggcta tccaacagat caagaattgg atgaaatacc tggcacaaag
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400

<210> 2211<211> 398<212> DNA<213> Homo sapien

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398

<210> 2212<211> 399<212> DNA<213> Homo sapien

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399

<210> 2213<211> 398<212> DNA<213> Homo sapien

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120tctttcctac tattgtaca atagtggta aattgatgtt cagtagtgtt aactctaatt
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240acttcaaaca gcagcaatat ttacgacagg cacaccgcaa aattctgaat tatccagaac
300aagaagaagc ataaaactga cttctggtt ttctgcagtt ctctcactct tatgaatctg
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398

<210> 2214<211> 404<212> DNA<213> Homo sapien

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240gtccctccct ttgcaacctc ctccgggtcc atgttcccc tcggaccaag gtccaagtcc
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360gacctcagac ctggagcagc ccacagaact ggattctctt ttcn

404

<210> 2215<211> 404<212> DNA<213> Homo sapien

gacggtgggg aagatggcgt accagagctt gcggtggag tacctgcaga tcccaccggt
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120tgccacctt tcattatctg ggctggatat gactgggtct tcaggaaact ggggtttggg
180cctccgggag gccagaggg gctgggtccc gggatgggtg gaggcgtaca gggattactc
240tggggttcga gttggcgcca agaattgctt tccagtgcg cgagaaggga gtgctgcttc
300atggggggtc agcagttgga attgatcaca ctttttcagg tgtacttcaa tcctgaatta
360atctttaaac actctcacat atggagatta atcaccaact tctc

404

<210> 2216<211> 401<212> DNA<213> Homo sapien

cgttgctgtc gggaggccaa gagcaccatt tggctgcacc ccgtcaccgg cgaggcgggtg
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120tttgaagggt caagatacta tataaacat aatgaaagga aagtgcctg caaacatcca
180gtcacaggac aaccatcaca ggacaattgt attttttag tgaatgaaca gactgttgca
240accatgacat ctgaagaaaa gaaggaacgg ccaataagta tgataaatga agcttctaac
300tataacgtga cttcagatta tgcagtgcac ccaatgagcc ctgtaggcag aacttcacga
360gcttcaaaaa agttcataa ttttggaag aggtcaaatt c

401

<210> 2217<211> 401<212> DNA<213> Homo sapien

gcctgatggg atatattcag tcatggcgtc cgaactttcc agaaaacctt gctcagaagc
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120ttgggtctct tgtaaaactc caatgtctgg atcttagtga caatgcctta gaaattgttt
180gcccagaaat tggctcgtctg agagctttac gtcattctcg attagctaata aaccaactgc
240aatttcctacc tccagtacct cactgtggac cgaaatcgtc tatggtatgt gccgcgccat
300ctctgccagc tgcccagcct caatgagctc tccatggctg gaaaccgtct tgcatttttg
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401

<210> 2218<211> 399<212> DNA<213> Homo sapien

ggcacgaggg cactgtgctc ctgttctggc ttgtgctttt tcccatgatg ggcagatgct
60agtctcaggg tcaagtggata agtctgtcat agtatatgat actaatactg agaataact
120tcacacattg actcagcaca ccaggtatgt cacaacttgt gcttttgcac ctaataacct
180tttacttgtc actggttcaa tggacaaaac agtgaacatc tggcaatttg acctggaaac
240actttgccaa gcaaggagca cagaacatca gctgaagcaa tttaccgaag attggtcaga
300ggaggatgtc tcaacatggc tttgtgcaca agatttaaaa gatcttggtg gtattttcaa
360gatgaataac attgatggaa aagaactgtt gaatcttac

399

<210> 2219<211> 401<212> DNA<213> Homo sapien

ggcacgagat gcattgttgg tgttttggga tgcaaggatg aattctcaga atttatctac
60aactaaagac tcaattgggt catattcaga gacacatagt gatgatgtca ctcaagtacg
120tttccatccc agcaatccca acatggtagt ctcaagttca tctgatggcc tggtaaatgt
180atttgatatt aatattgata atgaggagga tgcactgggt acaacctgta actcaatttc
240atcagtaagc tgtattgggt ggtctgggaa aggttataaa cagatttact gcatgacaca
300tgatgaagga ttttattggt gggatcttaa tcatctggac actgatgaac cagttacacg
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401

<210> 2220<211> 404<212> DNA<213> Homo sapien

ggcacgagag aacagagagc agtgtacgat gagcatggaa cagtggacga ggactctcct
60gtgtcacccc aagaccgaga ctgggagggc tattggcggc tactctttta aaagatatct
120ttagaggaca ttcaagcttt tgaaaagaca taaaaagggt cggaagaaga gctggctgat
180attaagcagg cctatctgga cttcaagggt gacatggatc agatcatgga gtctgtgctt
240tgctgtcagt acacagagga acccaggata aggaatatca ttcagcaagc tattgacgcc
300ggagaggtcc catcctataa tgcctttgtc aaagaatcga aacaaaagat gaatgcaagg
360aaaaggaggg ctcaggaaga ggccaaagaa gcagaaatga gcag

404

<210> 2221<211> 404<212> DNA<213> Homo sapien

ggcacgagga tgaccccaac gatccatact aggagcatgg attgatactg ccaaattggaa
60acattaactg gaactgccca tgccttgggg gaatggccag cggctccctgt ggagaacagt
120ttaagtcagc cttttcctgc ttccactata gcacggagga gatcaagggg tcagactgtg
180tagaccagtt cggggccatg caggaatgca tgcagaaata cccagacctc tatcccgaag
240aggatgagga tgaggaagag gaaagagaga agaagccagc aaaacaagca gaagaaacag
300ctcccattga ggccactgca accaaagaag aggagggatc aagttaatga aggccacaag
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404

<210> 2222<211> 397<212> DNA<213> Homo sapien

ggcacgagac tggatgtata gcagtttttc caagaagctt ggctcagaag ggtagcagac
60aggatgacaa atggaaagag aaatgaggtc actggaggat tgttaaagag tacagcatgt
120ttgagtgtca cttgaaaggt tccagtggag aagctgaaga agtaggtaaa ggtaagaata
180accaagggac agaagtcctg gagcagggag gagggaaatgg gattctttta aacctcttca
240tcaagaaact agggaaaaaa accaaagctg taccatctca gatttcagag aaagggaatt
300tagaaggaag taatataagc aaagaacaac aatattctgt gactgttttt aataataact
360agggaaaattc ctagtgcagt taactctgaa caaaatt

397

<210> 2223<211> 396<212> DNA<213> Homo sapien

cgttgtgtc gggggagggg gaggagcatt tggtatgtgg ggcagtcaga aggaacatgt
60aaagactcaa aagtgtgtaa tgtttcatgg aagccatcaa caaagcgat gactttcttt

120atttttttga gacagagtca aactctgttg ctcaggctgg agtgaaaaac atatacctca
180tctcactgct gactcagaca tttgtgtcaa agagaatatc ctgcctaatag cctccgagcg
240agtcttatta cagatgcgca ccacccctac ccagttgtgg tcattataga catcacttac
300gcccataatac ccctttccag tattgtttgg aaaaaattgt tcttattctg tgaccaccct
360cttggaattt atagtgtcgg gagacatccg cctgcg
396

<210> 2224<211> 395<212> DNA<213> Homo sapien

gatcacttga gcctgggagg tcaaggctgc agtgagctgt gattgcatca ctgtactcca
60gccttgggtga cagagcaaga ccctgtctca aaaaaaaaaa aaaaaaaaaa ttttttggg
120cccttttttt cttaaaaacc aaaattaaaa aaacccttgg gaagtttggc ccaccccccc
180ccaaaaggcc gggaaaaaaa ggcttttttt ggaaaatttg ggaggctttt ttttttttt
240aaccccttaa aaccgggaaa aaaaaagtta acaacaaaaa ttggtttttt ttttttttc
300cggttccggg gggggggggg aagttttccc nccctcctgc tgcgtagncg aacactctac
360ttcctttgca cccttaaacc acaacttgag cgtcg
395

<210> 2225<211> 392<212> DNA<213> Homo sapien

acctcctggt aaggagctac taccaaatac taaagctact ttttcttact cgttcgtagt
60actgtcgaga atcagcttat cttcaccctc ttagactata tgtgaaaagg cacaatagga
120agtttgggca cattagagac aaatgtgcta tactttacgg cttagcctgc gcccggttct
180tattttatcgt caactgtgga caaatgatt ttgtttcatg agacaaaggg ggaccaccaa
240cttctacggg aatgtctgcc ttttgctaga tagactgtct attacataac catatgtagt
300ttatttttaa ggagaattac atatttttct tcacatgtca ctgttagaag taaatcccaa
360tagtaagatt tccctaaaca aagtatttct tg
392

<210> 2226<211> 397<212> DNA<213> Homo sapien

ggcanaagct cagtatgtct ctttcaactc tagtttttga ggcggggaca caggaggctc
60agtgggacac agccactccc caaagagtaa ggagcttcca tgcttcattc cctggcataa
120aaagtgtcga aacacaccag agggggcagg caccagccag ggtatgatgg ctactaccct
180tttctggaga accatagact tcccttacta cagggacttg catgtcctaa agcactggct
240gaaggaagcc aagaggatca ctgctgctcc tttttctag aggaaatgtt tgtctacgtg
300gtaagatatg acctatccct tttaggtaag cgaactggta tgtagtaac gggtaaaaag
360ttaagggctc tgtggtttac ccacttgaaa tatgtta
397

<210> 2227<211> 392<212> DNA<213> Homo sapien

cgttgctgtc ggtgaaattc tgtattgatt tttctctaag gagaatatga catgcttgtg
60cttaccaaga tcaagtgcac tgaggggagc tttgtttgc ctgaataaac gtaaaggaca
120agtaaacatc ttgatgataa gctacagttt ttcttcaaaa gttaaatttt ttttatgag
180ctgatagttg gcttttgaat ccattatttc atgctttttt ttaaaaaaaaa aaatatcat
240aataactttt tgaagaggca tttgggtccc atataaattc ttttactttt attcactggg
300tgactaaat aatgagaacc ttgggtggat tttgttttac ttcaaaaaaa caaggtagg
360gatgttttta ttcccctacc ttgaagaaag tg
392

<210> 2228<211> 395<212> DNA<213> Homo sapien

ggcacgagaa tggatctgaa tttgacaaat agcatgccac actaatacta cagtcaacaa
60cagcccagag aacaattact atgtcagctg gaggctatat tatgattcta aattcttaaa
120ggtttttttc cctccataaa tcaaaaatta ctttatgtaa accaaaaatt agttggtatt
180tatggctcatg atcttaattc tcaagtttag cttaatcttg tatttcattg tttgtcttct
240aatatgacag cttaaattca gatttttaag tgactcagca aaataggagg agtgtcccaa
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360agttaacca tttatttctt ggtattctgc tgctg
395

<210> 2229<211> 393<212> DNA<213> Homo sapien

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60ttcttttact tgacatgcac aagaataagc tggaggcgat tatttccttt catcacagat
120tcatgaattg ttttaaatgc ttcttaaagt ctggctttat aaccgtttta aatcaactat
180gatgatttta gataaccaag taggtattat aatacaaaac aattttaagt gtaagaaact

240atagtataat caaagtaaat tcagttattg tatttgtggt gttgccttgc cttgcatgat
300gctgggggaa aaagagaaaa gaaatggttt tctttttgta ctttcattca gtgcacaggg
360aaaaaagcat gtattgtgcc accggaagac aag

393

<210> 2230<211> 159<212> DNA<213> Homo sapien

acaaacgatt tctgttcatt ctttaagcat ctatatttca tttgttgtgc acatatgcat
60atgagcccat ttaagatatt tgcataact tgatagaaac cataaagggtg tagcagttaa
120gtccagccac atttggttaa tcagtgtttg atataattg

159

<210> 2231<211> 394<212> DNA<213> Homo sapien

cgttgctgtc ggccatggtt gtgacaaact ctgaatacca gaggacacaa agggagagga
60aaaactgttc tattttttt cccaggtac atgtggaaaa attttgtgc actgaaaata
120acccttgctt ttctcttgc cagggtgcc ctttcttgg gcctgggggt gttgttctcc
180tttggtcagca ttcccttgg catctatgac tgggctgct catcgagtag tgacgaaggc
240cactgaaacc cgccgagaaa aagaaacatc cctgttgtct gtcagacaa gtccccacac
300atcagcaatc tctcaccact tcttttgcaa gtttacagaa gcaaacagaa atgtacagga
360tacttaaaat ggaataactt ttggatgca aaac

394

<210> 2232<211> 395<212> DNA<213> Homo sapien

ggcacgagag actctgtctc aaaattaagt atctctaaat acaggattat aatttctgct
60tgagtatgga gttaactacc ttgtatttag aaagatttca gattcattcc atctccttag
120ttttctttta aggggaccca tctgtgataa aaatatagct tagtgctaaa atcagtgtaa
180cttatacatg gcctaaaatg tttctacaaa ttagagtttg tcaattattc catttgtagc
240taagagaaaa ataggctcag ttagaaaagg actccctggc caggcgagc gacttacgcc
300tgtaatatca gcactttggg aggccaaagg aggcagatca cgaggtcagg agttcgagac
360catcctggcc aacatggtga aaccccgctt ctact

395

<210> 2233<211> 393<212> DNA<213> Homo sapien

cgctgctgtc ggggtcaccc tgcataaaaa cacatggagc agactgctga gccagctcag
60gggaagcggg gagacccag gagtgacggt gagaatgcaa ctcaattgtc attacacagg
120aatatggcaga tcggatttga ccaacaaaat ggggaggaac tgatccagat gtggaatgtg
180acagagaatc ccttccact gccatggaac atttataaaa ataatacat gttaatcaat
240gaagaaagg agccacacat ttaaaaaagc agaaatcgta caggccactt cctcagataa
300ccatttctaac taggggtcaaa ttatacatca ggactgaaac caciaacata taggaaataa
360gataaagtct tttggttttt ttgagacgga gtt

393

<210> 2234<211> 391<212> DNA<213> Homo sapien

gaaatctgtt ctttcacatt gcaaaacaga gtctgagagc aagaattcac attcgaaaac
60ttcagggtgaa aagaaccacg tggaaaaaga taaaatgaat acattggaca ttttgagaat
120ggagactaca gagagagaga atccagaagc tgaaactgta tctgtactcc tcaacacatg
180gaagatcaat cgcgtaaaga ttttgaaagag gaagatggca tattacagcc tgagaaaaat
240gattcttttc aaaatatgca gccagatgag cccaagggtc ttagtgaatg tgtaagcggt
300caagagaata ataaggcgga tgaacttaac caagtcccaa ttctaaggac tcgatttcag
360aaaccaaagc caaatatagg aagaggaact g

391

<210> 2235<211> 396<212> DNA<213> Homo sapien

ggcacgagag agagagagag agagagagag agagagagag agagagagag agagagagag
60agagagagag agagagagag agagagagac tctctcactc ttgcgcgtgt atttatacac
120acacacacgc gtgaagacac ctctctgtgt gcgcgcactc cccctctt tgtttcgtga
180gaactgtgtt ctttttgca tatgtgtggc gctctatctc tttgtttacc ccctatatcc
240cccgcctctac acgttttctg gcgcgcgtgt gcattttttt tgtgacgcag gcacgggggg
300gtgtgtgaca tttttaacct cncacgccc cccctcgcta cgatgttctt tctttctttt
360tcgtccttgg ctttttgcct atagtgtttt cccact

396

<210> 2236<211> 392<212> DNA<213> Homo sapien

ggcacgaggg ctgacgtgga ctgtccacag tgttcatgtg ctggagtcag ggacggccgc

60acctgcctcc gccggctcca gtgtgcgggg agcctctgcc tgagtgtgca ccaggcccat
120gtttattgac cacagtctga gcggggggga aggggactgc ggtggacacc agaggaagct
180gtttcctgtt gtgatgttgg acctgtagta ggacatggtg atttgttaat tcccatggga
240agccatgatg gcctagcatg gagggaaatct gtccccaggc cctgcctgga agttgaggga
300aagtttagac atctgcagag aggcaggcag cccagcccag gggacccgtt cctcttgaac
360cagtcattgc ctgtggcaaa tgtgtgtatg aa

392

<210> 2237<211> 395<212> DNA<213> Homo sapien

ttgataaaaa gtcaaagatt agcaaagata tatgtctatg caataacaca tatatgaagc
60acagaagcaa aagctggact cagaacaaaa atagcaagtt gagccttaaa cacactgagt
120ttgccttggg agtagaatgt ccaggcagag aagtccatca ggcaattgaa aatgtgaatc
180tgcaacttgt aaaaaatgta ttattcagcc tgggctgtca tacaatagac cacagactgg
240ttggccttaaa caacaaaaat gtatttctaa ccattctgaa ggctagaagt ccaagatcag
300gatgtcagca tgggttgggt ctattgaggg ctctcttctt ggcttataga tggccacctt
360cttgcctgtg cctcacatgg ctaaaagaat aagag

395

<210> 2238<211> 394<212> DNA<213> Homo sapien

cgttgctgtc ggcaggctgt gatcggtatc ctacagcctt accctcgtgt cctggatctt
60ttccttccat ttctgtgta cagccttttt ggggacactg ccgttaccctt actctagcta
120gcatagctct gtctgtagggt gctccataaa ggtgatagga ctgaccacac cgtcaccttt
180cccggaaacc caagagggag cgttccacag agggagcgtg tagtgggggg aactgtttta
240taaattaatc cgtttattga aaggttcaca aggacaaaga ggcaacagca agagtcaggc
300acagaaataa aggacgcaga agtagaagtg cgccttgagc ctggaggact cttccagagt
360gtttatcact tggtgacctg gtaggagggc tgcg

394

<210> 2239<211> 396<212> DNA<213> Homo sapien

ggcacgagga ttgtcccagg acctgaaggg agcatggatg gcctcagggc ctggtgaagt
60ctgctactct gtccttactg ctgaacatcc tgctgtatc aggaaactca gaagcagttt
120gccttgtcaa attcaatctc aatggccatt gtccacataa ctgacacccc atggctgctt
180ctcctattat ctattatcac tgaaacttag tagcctgctt tttttttttt ttttttaaaa
240cctatgggaa atttcccttg ttgggaacct tggccccggg ttgggttttc ccttccttgg
300gaaaattaaa acccaaaagc cctttttttt tgggtgaatt accggagggc cttgccttaa
360ggggctgccc tgcccccttg ggggaatata aaaaaa

396

<210> 2240<211> 391<212> DNA<213> Homo sapien

ggcacgagct ttcttaaaac catctaaaat aaaaccttct tatttttagta gtgtcagtga
60aaataagcag tgacatttct tagaattctc agctttcaaa tctacatgct gtgatcctgt
120ctgcctacca tctggacagt ttttgtttac tcttgggttc ccccatggag taaaagtctc
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240ggctgagatt acaagtgtga gccactgctc ccagcctaca gaggactatt gagcatccaa
300tgactatgct aggtatgcag gtatagtact aagtaacagg agttccta cctaagagggt
360tctccatcta gcagaagaaa accaaacact t

391

<210> 2241<211> 392<212> DNA<213> Homo sapien

ggcacgaggt tgctcacagt ggttcacgag ttatcgaaca tgatacagtt aatgatttcc
60gagagaagat gatgtataaa gctatacatt gtgttcaaaa tatgaaacca gaggagtatg
120ctcataagat tttggaatta cagatgcaca gtataatgga aaagaaaatg aagaccaaga
180gaaatattgc caagcattac aagaataacc catcactaat aactttcctt tgcaaaaact
240gcagtgtgct agcctgttct ggggaagata tccatgtaat tgagaaaatg catcacgtct
300atatgacccc agaattcaag gaactttaca ttgtaagaga aaacaaagca ctggcacaaga
360agtgtgccga ctatcacata aatggtgaaa tg

392

<210> 2242<211> 391<212> DNA<213> Homo sapien

cgttgctgtc gagaggttta accttgaat aaaagaaaga atcagcaa atcattatctg
60agcctacata cactttgtaa aaagtatact tccactgttc agaattagat gatggcacia
120aacctgttga ggtcttcatt catccttaca aatgtttatt atgctgagtg tcccagggtga

180ctggatacag tggagtgaat tagaaatttg aaattattgc cctgagggga cctacattct
240tcttggttga gtgctgtgt gtgggataag gtagacaaat aatataggaa attcaaaaaa
300ttgtttcaga ccatagtaag ttctatgcc aaaaatgaata gtccatatga taagaggaac
360agacattgtg agatgttgga tctataggaa a

391

<210> 2243<211> 396<212> DNA<213> Homo sapien

ggcacgagat aaaaccagc tgtgtaagaa ttattctaaa tttaaagttt attcttatta
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120ctcttgccag cttatgggtc ccgtttcctt tggataacag gatacagctg gtggcaaaat
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300acatgtccat gagttcctct ttctagaggt accaaccatc atgtgggatc ctaagtatag
360tggttaagtag ctctttgtcc tccccttcac ttgtgag

396

<210> 2244<211> 392<212> DNA<213> Homo sapien

ggcacgagggc aggggtggagc cctctgagct gcccgtgat ctgcagcact ggatctccta
60caacgagggc agcagccagc tgcctccgat ggagagtagg ctgagtgatg tcaccaagga
120ccagtgaacc ccaccttcac accgtctgcc ctggccacca tccctgggctt gggggctgcc
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240gcccaccctg ctccaccac tgggcccccc cagttattga taccctctg tgctgggctc
300cacgctaggc agaaggagga gtggcattgg catcctgacc cagctctgcc ctcaaggtgg
360ggatggatgg gcaaaggaga gtcctgcctg gn

392

<210> 2245<211> 397<212> DNA<213> Homo sapien

cggtgctgtc ggttttcac caattcctac tcgtagcagt acattagaaa ctacaaagag
60tctcttacc attgataaaa atgagcattt tacagtttac agagatcctg cacttattgg
120gtcagaaaca ggagctaata atatttcacc ttcttaagc cagcatcctt ttctcttca
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240accccattta ctagccggat catctagtca aactccatta cctaccatta acactcatcc
300tctgactagt ggtccacacc atgctgttca taccctcat ttacttccca ctgtgttacc
360tgagtgctt actgcctcct tacttggtgg ccacca

397

<210> 2246<211> 396<212> DNA<213> Homo sapien

ggnacgagnc cgcctctccc tggcctgagg ttcaaaggcc tcatcgatg gtcagtacag
60tggtgtcacc tgtgtttct atacaacagc aggggaaggg ccatggagct ttccctgct
120gggtgctcct gctttggccc agccacctt tctggtgct ccaagctagg aggtgtggc
180cccagcctga ggagggtgtc ctggcctcca ggtgtgcagc aggggctgtg tgctggggga
240ggttccagtt aggcgatgg atcctgcagt ggtctggtgg catttcttgg aaccagattt
300acctgaggag ctctgtcctg ctccctgtgg agggctccag atagctcaga aatgaccagc
360caatggcctt ttgtttggg gcctgaggtc aagaga

396

<210> 2247<211> 395<212> DNA<213> Homo sapien

cggtgctgtc ggggcgtaag cacatctctt ttctggactg gccgactcct ttctggctcc
60atcctctctt gaggcttctc tgtccagctt aaagaaatcc ttgcagaaaa ctggctcagga
120tcttggtatg ggtgggaagg agcaaggaga ttgctctggg attggcagtc ctgttctcta
180tgaatcgggtg tctttgggg aggcctggac tgaaatacta accagataac tcccctccca
240cctccatgag gagctgcatg tggattgaga gctgtttang gtaggcaaaa atgctgtcaa
300gattctctta ccttgtgct cttactctgg acagccctga ggttggtgct ctgccttctt
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395

<210> 2248<211> 391<212> DNA<213> Homo sapien

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120attcactact gcagagccac cgtgtgctgg gaactaaagg gaaacatggt ggtccttgtg
180cacgacagtg gagatgcgga ggatgaggag aatgacatcc tgcgtaatgg cctcagtcac
240cagagccatc tgatactgcg ggctgagggc ctggccactg gcttctgcag ggatgtgcac

300gggcagctga ggatcctgtg gaggagacca tcgcagcccc cagtccaccg ggatcagagc
360ttcacttacc agtataagat acaggacaaa a

391

<210> 2249<211> 395<212> DNA<213> Homo sapien

ggcacgaggc catctggccc tcacctcccg ccgtagctgg ctgtgacgcc cgccatgggc
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120aggcagaact tgatgaccgc ggagcccccg agcctgagct tgttcacaaa gaagccgccc
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240ctcacatcac cccacactgc aggagggcgg ctctttcctc tcggccacac cttaggcctg
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360gccaaatgta aatggattct gaagaatcag gaaca

395

<210> 2250<211> 397<212> DNA<213> Homo sapien

ggcacgagct ggcgccatta tctgcgggct tatgctgaca ctaagctggc taatgtactg
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120ccagggcctg tgaactcgga gctgttctcg cgccatgttc ctggatggct gcgcccactt
180ttgcgcccct tggcttggct ggtgctccgg gcaccaagag ggggtgccc aacacccctg
240tattgtgctc tacaagaggg catcgagccc ctacgtgtga gatattttgc caactggcat
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360agcaagaggc tggcagagct taggcctggg gaggatg

397

<210> 2251<211> 392<212> DNA<213> Homo sapien

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60gatgcgaata aactgctttg agaagtatgc acacggagac agtgtaatgg accaaaggca
120tatataaaag gtgaaaggaa gcatgtttac accaatgcca aaaagcacat gctaatttct
180cttgctactc ctgatcttac tcttcattta aagagatttc agcaggctgg ttttaacct
240cgcatagtta acaaacacat aaagtttccg gaaatcttag atttggtcc ttttgcacc
300cttaaagtga agaattgtgc agaagaaaat acaagggtac tctattcctt atatggagtt
360gttgaacaca gtggtactat gaggtcgggg cn

392

<210> 2252<211> 396<212> DNA<213> Homo sapien

tcttagacga ccaattatag gttatggagt ataattttac aagagtttcc ggggagaaac
60tttaggatat actcggttcc aagggtttta tctgcctttg ttgtgggaac agagtttttg
120ttggaaaagt ccgattgctc tgggttatac gaggggccac ttctctgctt tggttgccat
180ggaaaatgat ggctatggca accgaggtgc tgggtgcta ctcaataccg atgatgatgt
240caccatcaca tttttgcctc tgggtgacag tgaaaggaag ctactccatg tgcacttct
300ttctgctcac gagctaggta atgaggaaca gcaagaaaaa ctgctcatgg agtggttgga
360ctgctgtgtg acggaggggg gagttctggt tgccan

396

<210> 2253<211> 393<212> DNA<213> Homo sapien

cgttgctgtc gattgccgtg gcgagcgaca agtcctcttt tgccactcct ggggtgaacg
60tcgggctctt ctgttctacc cctgggggtg ccttggcaag agcagtgcc agaaagggtg
120ccttgagat gctctttact ggtgagccca tttctgccc ggaggccctg ctccacgggc
180tgcttatcaa ggtggtgcca gaggcggagc tgcaggagga gaccatgcgg atcgctagga
240agatcgctc actgagccgt ccggtggtgt ccttgggcaa agccaccttc tacaagcagc
300tgccccagga cctggggacg gcttactacc tcacctcca ggccatggtg gacaacctg
360ccctgcggga cgggcaggag ggcatacgg cct

393

<210> 2254<211> 388<212> DNA<213> Homo sapien

ggcacgagga tctttatgca ttcccacta ctcccttact gtcttttagc attcacagaa
60aaagccaact tgcttaaaga ggaatcactt aaaaggtagg catatctaag atgctcatag
120aagaggaaga atgggacatg gccccatgct tatttttgtt tacaacgtaa catggcatga
180gagagggcag agaaactaag ttgctgggga aagttagagg aactgaaagt ttgggaatag
240gctgaccaca tattatgcca gtgaccagta tgacaggaga tggggccctg ctgccagta
300tctccactga ataaagaata atgctctct ttcagggtaa taaagtggg aaaaggaacg
360tcttctcaat gcaagaacat aagctttt

388

<210> 2255<211> 387<212> DNA<213> Homo sapien

cgttgctgtc gatttttgaa ctcaacccta tgaacaatgg gccattcaaa tggaaaaaaa
60agctgcaaaa gaaggaaatc gcagagaacg tgtttgtgca gaacatttga ggaagtacaa
120tgaggcccta caaattaatg acacaattcg aatgatagat gcgtatactc atcttgaaac
180tttctataat gaagagaaaag ataagaagtt tgcagtcata gaagatgata gtgatgaggg
240tggtgatgat gagtattgtg atggtgatga agaagtagat gatttactca accctttgaa
300actggatgaa acagatagat ttctcatgac tttatttttt gaaaacaata aaacggtgaa
360aaggggtggct gaaaaccag aatatgg

387

<210> 2256<211> 385<212> DNA<213> Homo sapien

cgttgctgtc gcttattttt gtcttttact atcgaggcc ttagaagagg tctacctgcc
60tccagtctta ctagtccag tctacccctt ggagttagaa tggccatcct gaagtgaana
120gaaatgtcac attactccct tcagagattt cttgtagaag agccaatccc tgaatgccac
180caagatctta atcttcacat ctttaattct atctctttga ctctcttta caccggagaa
240cggctccagc tgttctagct ctctttcagt tctttgaacc tcccacctt aggggtctata
300aggggtccctc tgcccaaaat ggtctactct cccttcttct tcaacacatc cttcagttta
360agcacttgct tctctcagtt taaac

385

<210> 2257<211> 388<212> DNA<213> Homo sapien

ggcacgaggt ccagccctgg taatcctgat gcagagggtc cacaaccaca tttgggaaat
60gttgacctaa tgcacagcag gaaagcatt tcatttgcta agaagtttcc atatgaaggg
120ccacgcagac ctgagcatgt agaaaggcaa ggggccaggg aagttactag aacctgact
180ctgggggttat attgcctggg tttgaatcta atcttggtcg cttactggtg atgctacca
240aggtgtctgt accttcattt cccacctgt agaaataggg ataggatagt ggaaggtatt
300gagatgagct gagaccatct gcatagaggg ctaacatag tgactgggac ttancaaag
360ctccatgagt tatgattgct ggcactgg

388

<210> 2258<211> 389<212> DNA<213> Homo sapien

cgttgctgtc ggctgaagct gtcaccttgt ggaatatcag atattaagga tggccagaag
60ggcagtgagg agagccagag agtgtttctt gaagcctgtg acagatttga agggcctggt
120tcataatatct ataaactgaa gagctacatt gtttaaagaa tttaatttgg aaataaattt
180acctgagat gtgtgtgtgt gtgtgtgtgt gtgtgtgtgt gtgtgtgtgt gtgtgtgtgt
240atgcatatat aaataccacg gccaagagga ccatcccttc ctttatctga gaaaggaagt
300atacaaaatc cgcataaatt taccggcagc agtccccctg cttgcattgt aggtgtcaaa
360gcccgggtgc ctgacttga cataggaag

389

<210> 2259<211> 385<212> DNA<213> Homo sapien

tacggttgct agattacgac agaaggggag tcagatggga gtgctgttta accttttcag
60gaactgtcag actgttctga agaggggtaca ttattttaca ttccaaccag cagtgtatga
120gaattccagt ttatccacat cctcatcaac agttgttttg tctgtctttt ttattatatt
180catctcgcat gtgaagcgcg tatctcattg tggctttgat tcacctctcc ctgacgggtg
240acgacccac ttctcattgc gtagcctcat tacctcccg cggcctttct tcatacactg
300gttgctccag gaattacctc attcatctcg cccccgattt ccctgttgcg cccgcttctt
360attccccctc ctccgcttc gtccc

385

<210> 2260<211> 390<212> DNA<213> Homo sapien

cgttgctgtc gctctgaagg aggtcttcaa ggagtatttg attgaactgt ttttcttgca
60acactttcaa gggaacatga tggatttctt agctttcaag aagaaacatt atgccccatt
120acaagcatat cttaggcaga atgatttga cattgaagaa gaggaggagg aggaggaaga
180ggaggaagaa aaatctgagg ttatcaatga cgagcaagcc ctgcagaggc gcctggtagc
240aggggcccga agcacagtag agacggacct gttaagagg cagcaggcga tgcctccac
300aggaggaatg cccccacgc cgcaagccgc gcagctcgct ggacagaggc agagtacga
360gcagtatgac ccctccacgc ggctcccg

390

<210> 2261<211> 386<212> DNA<213> Homo sapien

ttttacgatt ctaaaatcct aacagatttt aactgttgc taaatattat ttcttggcat
60atatagcttt ttaagtctgt ggggtcaaga tagatgtact catttgagac ttagtgattt
120gtttttataag tatgttgaat aagttgagcc agtttgaatt gtgtccttct cttttaaaga
180aaagatttcc caaatTTaaa cctggattta gatgtttttt gggTTaacc tactgaactt
240tccaaaattt tcaggcttct gggcctaact caaactgtaa ttcatgagg ccggccaagt
300gatttttaat ctcatTTaaa agttaccata agctctactt gaaccatttg ggttttagta
360taataaaaagg gcacatgtat tgggtt

386

<210> 2262<211> 389<212> DNA<213> Homo sapien

cgttgctgtc gatcattttg atatttcatt ctgatttctg attctctgat ttctgattcc
60taatgaggac agtaggtctg gatccaaatt ctacagtaa aatcaagcag taattttctc
120tcatatctat tagggaaaga aaaatgatca cagtctgcta agagtcttga tttctttgt
180aatgcctcac atagtatgat aatcagctct caaagcatca catgataatt acaatgatac
240cattaacatg tcaaggaaat tatattattt atggttgta aaaattatga agtagtgat
300gattataagc agatatggca aatttgttca gtaaaccat agatgactac attttgagaa
360ataactaagat aatactaaaa attatgcn

389

<210> 2263<211> 388<212> DNA<213> Homo sapien

ggcacgagcc ccagttttgg ggctcacttg tctgtatcc taacaactat ttacatagta
60tttacattat attagccatt gtaagtaatc tagagatgat ttaaagtata tggaaggatg
120tgtgtaaatt gtatgtgaat acaaacattt tatataaggg acttgagat ctgtggatct
180tgatggggtg ggggggtgtcc tgaaaccaat ccccttgga tactgaggga tgactataca
240cttaagccac cagacatctt gcatatcata gacaattgtt tgggggtccat gagctttaat
300tacaaaatgt aatgctggga gaacatagag aagagtgatt ttgtttttta aatgtacact
360tgaatctgta gaaatatact acatttgn

388

<210> 2264<211> 386<212> DNA<213> Homo sapien

ggcacgagac taaacctcc cctagctttg gttccccg cagtctgaag actctaatac
60ttgacactcg ttcagagaga tgtttgggga atttatagac acttaacatt tatgcatcct
120tatataatcg gggcgggagg aattacagac acttaacca ttactgcctt ctctcTaaa
180agaataacag ctttggtaac tgggttagca gaggtgttag tggacttagg gttgtaaaaca
240gatactcatg gcactgacat cgatgagtct atgagggaaa ttagaaagat aaatacatct
300gggatgtaaa ctcggaagg cgaggctgtt caaatgttg gtgctattga attgtgattc
360tcggtgttg tacattgcta ataatg

386

<210> 2265<211> 389<212> DNA<213> Homo sapien

ggcacgaggc tggcccatct ggactcatgg tagtggttaa gaactggatt actgcaatag
60ccagggttg ggcctatgtg ttcattggtg gaaggcaaaa tgtgtcagg tctggtacc
120agttaattac ttaaagctga taaactaggc tgggtgcagt ggctcatgtc tgtaatgcca
180gcagtttggg aggccaagac aggtggatca cgaggtcagg agttcgatac ctcttgacc
240aacatggtga aaccccgttt ctactaaaaa tacaaacatt agctgggcat ggtggcacgc
300acctgtaatc ccagctactt gggaggctga ggcaggagaa ttgcttgaac ctgggaggca
360gaagtgcag tgagctgaga tcatgccat

389

<210> 2266<211> 389<212> DNA<213> Homo sapien

ggcacgaggg aacatgaggg aatgggcaag cctagagatg gtttcatgcc atctctagct
60ttgggagcca aattctgaaa cagaaacttt ctgtttccca taattctccc tcaacctcac
120atttttatat ccatttggat gcagaggcaa tatccccatt ttacagcaga gggagatacg
180atttagttgc aactacatac agttagcaag aggtagagcc aagactggaa tcttcagttg
240ctagcttcag aatctgtgct ctttgtgtgc aaaatcattt ctaagcaaga acaaggattc
300tagattgtcc tcatccttac tacagagtca tatcagactc ggggcaagac ccaaaggctg
360caggcaccct gggcagggtt ataatttg

389

<210> 2267<211> 390<212> DNA<213> Homo sapien

ggcacgaggt ggTTaagaat ttataccctc caaattatgc gtctggtgcc ttggttgaaa
60gtattctcac ttcattggtg ctgtattaca ggtacggtat tctcacaaa atcattttctc

120tttgttaatta tgatactgat tttaatgccg cacatttgca tactatatgc ttgttacagt
180gatccccaca gtaactcatg aagcagccac tcattgtaca aatgaacgtc tccatataat
240agtttagcta ttatacagta catggcagaa acacaattca aactcaagtt tatacgaata
300ctttcaagtc tccttacctg agagcagaaa gtgacattta aatttaaagg agttcccagc
360ctttgttttc agtgcagttt gtttcatggn

390

<210> 2268<211> 390<212> DNA<213> Homo sapien

ggcacgaggt gtgggattac agttgtgagt cactgtgccc agcatggagt ttcttatatc
60aggtgtttta gggagctcgc ttgcttattc cattctttaa tccttacagt gtgccacacg
120tataaagttt ataacgtatt aatgatctca ttacccaaaa ccagaacata atttcacaag
180ggttcctact tctgtattgt tttattatct caaaaattta aataacatgt tctgctgggt
240attggtcttg ttatccactg tattagcacc ttccctgatg tgctttggag gttgatcaat
300gaatttctga gactttctgc tgggaattact ttaaggggtg cttattagat gatgaaaagt
360tggtgagac acccttcaag tgaccatgtn

390

<210> 2269<211> 387<212> DNA<213> Homo sapien

ggcacgagcc taaaccatga gtccttatt tgtaaagggg acattagcca ctctccagca
60acagccctgg tacttcttca gtcttgggat gggacgtatg attagcctaa gcgaaccaga
120aaatccaggc cgtgaccag tgacttgatc agggctggcg atatcttag gtaggccaac
180caggtggact cagtattttt gtgggtgcta ctggaaaatt tatttaattc taactgaatg
240tagaaacagc aacagacatg aaatggcagt tgtattgctg tcttatcatg aggtgagggc
300ctgaagctat ggtagccacc ctgtgaacct tggaaggagg gttctacagg aactggcaga
360gtgagactg ggacgcaacc catgtn

387

<210> 2270<211> 385<212> DNA<213> Homo sapien

ggcacgaggc tgcatacagc tggggtcttg agtccaggct tttggactga aacaaggacc
60tgaaacatct aaaactacct cttgattcta taggaaggag ataggtgctg aacttgctca
120agagcccaga gagctgggtg tagctcacac ccgttccctg ggcattgttg ttctgtctc
180ggctgctcc caggagtcc caacctgggg tagtgtaaat tctgtctctg cttattatca
240gacgtgtgct cggaggtggc cgtgtttcac agtggggatg ggggtaggga ggtccccaat
300gtgctaagct acaatcattc tccctgagat ttccatttag caccagttt cttaaacagt
360gtttcagggc cctgtctgga acttg

385

<210> 2271<211> 386<212> DNA<213> Homo sapien

ggcacgagga aggcagttat atggnTTTTT actttttcat caattccata ccacggggag
60taactaaatg aaacatactt caaagaaaga agtcaaatta aatgactgtc attgccatt
120aataaaaaaca acaatctgag cttacaaaaa aatttaacaa acagggaga cagaagatg
180gtatatttat tgcctgacta cactggcata actcacttta acaaaaatta tcacatttaa
240taatataacc tggtatagct aaatattaaa cacatattaa ttagggccaa ctttgaagga
300tttctaattc atccatttcc ttattcacta ttatatatga agcactacac taggtgcagg
360gtcattataa acaagttttt tctttg

386

<210> 2272<211> 388<212> DNA<213> Homo sapien

ggcacgagct tagccatcca ttgtgtctca aaactgtttt ggaggtgaat aactgtgagg
60caggatggag aaccttttgc tctcccatcc agaagggcac ctaaccaggc ccctggagca
120gacaaaagga gcaggaagtc aatcacttcg atcccagttc tctgaagccc aagaagaaaa
180cggattttcc ttcgttttgg ttcggaggcc tagtagagaa tttgattcc accaagttct
240cttttttcaa aaaaagttaa cgttccagag cagacaaaaa ctgtggaaac ttgaggcctg
300ggtagtagtg gttttgtttg attttgaggc tttaaagaga taaggagacg gtggtggagc
360tccgccacgc cgcgtggctc tcacttcc

388

<210> 2273<211> 390<212> DNA<213> Homo sapien

cgttctgtc gcttatgtcg tattgttta cagccactac acttggttc ctgttgatta
60acttctccat tctcttaagc accttagaa gatttagaag tttcctagtt ttaagtgtt
120caccagcaag tattccatac ctacttgatg ttgctggctt ggtgtcttat ttcctaaagt
180gaagcatctt tttttaaaaa agaatttgat tgacaatata tccagtccaa tataagtatg

240aaggattctc tctcctgaga ttgtagcagg cagccaaaca ttttcaaag atgcccgaagg
300tttttagctgt cttgtgtgca tccacagtct gcgaagaaga catgataagg acatcaggga
360gccacaaga ctcctaatag cctcactacn

390

<210> 2274<211> 389<212> DNA<213> Homo sapien

ggcacgagcc ggggcggggc ggggcgaggt cctaactagc tgggttagta agcggcgcg
60gcgtgcgagt ttctgtcgcg cccgcgtcgt cccagctccc tggactacca gtattgtcgc
120ccacgtgggc ttctctttcg tccgctcagg cctcactttt ctccgtaaac accccggcac
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240gcctcgaaag ccgcaggggc ggcagctcgc ctcggaatga cctctgacgg aagaaataaa
300acggggcctg ggacgcttgc acgaaagac ccgacaaaaa ccagagccc cactcactct
360cgtactgggg aggtggactt cagggaggg

389

<210> 2275<211> 389<212> DNA<213> Homo sapien

ggcacgagac actgtcttga ctaanaaaaa taaaagggg aaaaaaaaa angggcggtt
60ggtttttggg gcccaaaaag ggggtgggga aaccccggtt ttttgcctt atgcccccc
120ctggacttcc ttgggaaaaa aagcctattg gcctttccca aaaaactttt ttttcaaag
180gaccggcttg tgggaaaaaa gccccctgg gggctttttg gggggggtta aacccaggg
240agaccggga acctcatttc ttggccccg tttttatttt ttgttaagct ttgaaaaac
300atttttttgg ccttttttgg gggaggcccc cctttttata accccagggga aacaaggtg
360caaactgctt aagacttccc cggggtggc

389

<210> 2276<211> 390<212> DNA<213> Homo sapien

ggcacgagcc cgagcggggc tgggactctt ttaagatgcc cacgttcgca cagagacccc
60ggatcgcgga agctcgcgtc tcgaaaggcg gtctcacgcc ctgcccgtcc tgggttcacg
120gttttttcac acctgcygt gtctcgcgt cgaccacagc tgtgcaggag gggcaggagg
180tatctgttgc tgcagttacc ggaacctttg ccaggactag tacaggacca cgggctggt
240gctcagggat gtctcgactg tgagttacag ctgcacgctc tccaggaaag aaggaatttc
300ctcttctctg gaaacccac cacacagctg gtttctcatt ggtgctgctt gccattccc
360tgagctgtga ctgccagagg agtgggaggt

390

<210> 2277<211> 386<212> DNA<213> Homo sapien

cgttgctgtc ggcagaggcc atagccatag ctggggtcga aacgagctgt cccggggggc
60cagaggccgg acaatgccaa gcccaaccg gacctgaaac tgcaggctgg ctccgacctc
120cggaggcgac ggcgggacct tggccctcat gcagagggtc agctggcccc gagggatggg
180gtcattggcc ttaacccctt gcctgatgtc caggggaacg acctccgtgg cgccctggat
240gcccagctcc gccaggctgc ggggggagct ctgcagggtg tccacagccg gcagcttaga
300caggcgctg ggcctccaga ggagtcctag cactgctgg ccatgagggc cagccagcc
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386

<210> 2278<211> 385<212> DNA<213> Homo sapien

ggcacgaggc aaagcctcgc ggcgaggata gcacgagtat tcaagcgcg ctgaggccct
60ccttggttag tgctgggaca tggagccccg gcagccaagg ccaaccttgt gcattccgcc
120cacgtaggcg cctggggccc tggcttctct cgactgcctc tccactgcct ggaggctc
180aaatgcccc ggaccacctc ctacgtgcca cagctgtgt tggccatcca aggttccata
240ttgagcataa aacagccctc tgccctaaag gagttaacct gttggaatca catacaaagg
300attctgacta ccaagcgct tgaagttaag ttgaactctg aagacagatt gcctggctac
360aaagctcagt tccactacat atggt

385

<210> 2279<211> 390<212> DNA<213> Homo sapien

ggcacgagggt gtcttctctg accttccact tccaccatgt gccgacactt ccctgacccc
60agtaacctct tctcttgggt ggggtgaatgc cacctgctga tgtctgattt attcatcggt
120tttcttctgt gtagtctgtc ccccttgggg acagggactc gttgctcatg ttcacccggc
180aggctggaca cttcgtggag ggctccaaag ccggcagatc ccggggccgc ctctgtctct
240cccaggccct gcgtgttgcg gtgagaggag catttctgtc tctgtggtt gctgctggag
300ctggtgaccg ggagagaaac aaggagaca agggtgcca gacaggtgcg gtgctcatcc

360aggagggcaga agacgtggac gtgtcccggg

390

<210> 2280<211> 386<212> DNA<213> Homo sapien

gttgctgtcg ctacgcccc acaaaacccc acagccccc cccccgtccc ccccaatgaa
60gtctggagttg aagatcgcca tctcagaggc cgagcagtct ggggctgctg agggcactgc
120gtctgtcagc ccccggtccc caatccgcca gtggcgaact caggaccaca ataccccagc
180acttctccct aagccctctc tgggcccgaag ctactcctgc cctgatctgg ggccccctgg
240cccaggtacc tgcacctggc cacctgctcc accccaacca agccgaccac ggccgcggcg
300gcacactgtg ggtggtgggg aaatggccc agccccgcca cccctcggc cctgtctccg
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386

<210> 2281<211> 390<212> DNA<213> Homo sapien

ggcaccaggc gctttgtgac tggaggtctt cgtgggcagt tctatcagtg tgacttagat
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120ggaaagactg ttctggcatc agatacacac cagcgaattc ggggctataa cttcaggagc
180cttacagata ggaacatagt acaagaagat cactctatta tgtcttttac tatttcaaaa
240aatggccgat tagctttggt aaatgtagca actcagggag ttcatttatg ggacttgcaa
300gacagagttt tagtaagaaa gtatcaaggt gttacacaag ggttttatac aattcattca
360atgtttggag gccattatga aaacttcatg

390

<210> 2282<211> 390<212> DNA<213> Homo sapien

gcggagcgag caacacagtc ctttttcttt cgtgcgctcc gggccaaggc ggaaaaagac
60gaggacagtg ttcttcacag tactggacag ctacagctcc gggctaagca ggggctacct
120tcacggacca taaaactcca agaggctcaa gaagggacag atcagccatc acttcatggt
180caactttgtc agggagcgct aggagccagg aattttacctg tgcggccaga tggcaccttg
240aactcatttg ttaagggctg tctcactctg ccagaccaac aaaaactgag actgaaagtgc
300ccagtcctga ggaagcacgc ttgccccag tggaaacact catttgctt cagtggccga
360accccagtc agctgaggca gtcaagcttg

390

<210> 2283<211> 385<212> DNA<213> Homo sapien

ggcacgagga cttctcagcc tgccgagcgt actggaagac aacgctctct gctgagcaga
60acgcacacat ggaggctgtc ctgcagagaa gtgccgcgca catgaggcac cttttgatgt
120cccagcagac cctgaggaat gtgccaccga tagtgtttgt tcaagacaag ggaaatgcag
180ctctagctga gcttgatcag ttactggcag tcgcagactt tggaccccg gatgaaagag
240acaactttgt acaaaatgat ttcagggacc ctgatgcccc acaaccctgc ggcaccacag
300agccgaccac aagctccagt ctgtgtggga tcgatcatga ggcgctcaac aagcagatta
360tggagtacaa aaggaggaaa gataa

385

<210> 2284<211> 386<212> DNA<213> Homo sapien

ggcacgagag tcaagattgg ctgcctcatg ttgaggttca gagttacgac tcggactgga
60cagaggcgcc ggcagctgtg gtgattggcg gggagacctc cggcgtgagc ctggagtccc
120tgcagctggc cgagagcact ggtggcaaga ggctgctgat ccccgttgtg cctggtgtgg
180acagcctcaa ctgcggcatg gcggcaagca tctgtcttt cgaagggaaa agacagctgc
240gggggagggc ggaggacttg agcagggaca ggagttacca ctgaggacgc agaagtgact
300tctgcttgag gacgtctgca gctcctcta caccagcaca ctggtgggag gctggcggag
360tcagtgacta tggccccac gttcag

386

<210> 2285<211> 385<212> DNA<213> Homo sapien

ggtgatggag ctgaaattgc agaaaaattt gttttcttca ttggcagtaa aaatggggga
60aagactacta ttattctaag gtgtcttgac agagatgaac caccaaaacc aaccttagct
120tttgaatata catatggaag aagagcaaaa gggcacaaca caccaaaaga tatcgctcac
180ttttgggaac tcggtggagg aacctcttta ttggacttaa tcagcatacc catcacaggt
240gacaccttac ggacgttttc tcttgttctc gttctggatc tttcaaaacc taatgatctc
300tggccacca tggaaaatct cttgcaagcc acaaaaagcc atgtagacaa agtgataatg
360aaactgggaa agacaaatgc taaag

385

<210> 2286<211> 389<212> DNA<213> Homo sapien

ggaagcaaaa aagattatat tcaggaaaaa cagatgagac aagaagagca gaggaaaaga
60catttagagg ctgccgctct gctgagtga aagaacgcag atggtttaatt ttagctagt
120cgtttccacc cactccctct gctgctgtct ttgctggact ttgtggcccc ttaaggccg
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240aggggagggg tcatcaacct caggctgtct gaaacctggc tcagaaatta tcaggttttg
300ccagatcgaa gtcatcctaa actgctgatg agtggagggtg ggggttatct tctctccggc
360ttcaccgttg ccatggacaa ccttaaagn

389

<210> 2287<211> 388<212> DNA<213> Homo sapien

ggcacgagtg aaaatcaaag gagaagaatt tcctctgact ctgggtcggg atgtctctgg
60cgtggtgatg gaatgtgggc ttgatgtgaa atacttcaag cctggagatg aggtctgggc
120tgcagttcct ccttgaaac aaggcactct ttcagagttt gttgtagtca gtgggaatga
180ggtctctcac aaacccaaat cactcactca tactcaagct gcctctttgc catatgtggc
240tctcacagcc tggctctgcta taaacaaagt tgggtggcctg aatgacatga attgcacagg
300aaaacgtgtt ctaatcttag gcgcttcaag cggagttggg acttttgcta tacaggtaat
360gaaagcatgg gatgctcatg tgacagct

388

<210> 2288<211> 386<212> DNA<213> Homo sapien

cggtgctgtc gtggcactat tacagcgttt gctttgggtc tggaaacctc aggggcccgt
60tgggggactg gaggatatga ctatgatgtt aagctttggg attttgctgg aatggatgct
120tcttttaagg cattttgatc ccttcagccc tgtgagtgcc atctgatcat gttattacag
180tttagtaaca caggagacat gattcttgtt gtatctggaa gctctcatgc caaggtgatt
240gtcagagatc gcgttttgat gtattggaat gcttaaaagg agaccagtat attgcggaca
300tggccatcac caagggatcat actgcattgc tttatactgg ctcatggcat ccctaaatat
360agggagaatt tatgacttgc tcaccg

386

<210> 2289<211> 385<212> DNA<213> Homo sapien

ggcacgaggg acaagagaaa tacttgttgt tgcattgatat ctcaaatcg gaatttctaa
60ctgaagctga aatcatttgt gatgttgtat gcctgggtata tgatgtcagc aatcccaaat
120cctttgaata ctgtgccagg atttttaagc aacactttat ggacagcaga atacctgtct
180taatcgtagc tgcaaagtca gacctgcatg aagttaaaca agaatacagt atttcaccta
240ctgatttctg caggaaacac aaaatgcctc caccacaagc cttcacttgc aatactgctg
300atgccccag taaggatata tttgttaaat tgacaacaat ggccatgtat ccagaggatc
360attacagaga cagactctcc cgagn

385

<210> 2290<211> 387<212> DNA<213> Homo sapien

attcaattct gcacgaagaa aagctgagaa aatgaccact ttggtgctat ggggaggcct
60tgccatcatg ggcacaccgt ttggcatttt gggccggctt acctgggtgg aatattctg
120ggacatcatg gagccagtaa catacttcat cacttatgga agtgccatgg caatgtatgc
180atattttgta atgacacgcc tgggaatatgt ttatccacaa gccagagaca gacaatactt
240actatttttc cataaaggag ccaaaaagtc acgttttgac ctagagaaat acaatcaact
300caaggatgca attgctcagg cagaaatgga ccttaagaga ctgagagacc cattacaagt
360acatctgcct ctccgacaaa ttggaga

387

<210> 2291<211> 384<212> DNA<213> Homo sapien

cggtgctgtc ggtttttgta caagagcgca tactcatttc tttctctctt tttcaaatgt
60gactaaatca cacttcccag ggacaccaag ctgtttctga ttgcaactgt aacagcctgt
120gtaccagctg ggatttttgt attaagcagc tctatggggc tactatacca gcagaaaatt
180agaagtcttg ctctaaaaag cattttcagc aaatacttgc tttgttctta aagtttttac
240tgctcaatt tgtcagctaa tggatcacaa gtgattggga ctgcctggag cttttttcag
300ttatggtctt agatgtgagt cagagaatat tatctattga gtttcacca cttctctgcc
360cctgtgcttt tacagactgg cctn

384

<210> 2292<211> 381<212> DNA<213> Homo sapien

ttttggttgt cacaactggg gggatgttgt ttctatctag aggatagagg ccagggtgct

60actcaacatc ctacaatgca tgggacaact cccacaacaa agaattatcc agcccaaat
120gtcattagt ctgaggttga gaaatactcc tctaaagtag ataaactcct tgagtaaaga
180gaagtttacc atagcaactt tcagtagtac ttcaaagaag atagctgtat aaatgtcatc
240aaactatact atgtagagaa tcttaagtga taaccaggtt caccgattcc aaacatgtca
300ttataaattg ttttatatgg tgctcactgg tgcatttttc cttttggata agggaaaaca
360ttattccact tactgttttt g

381

<210> 2293<211> 383<212> DNA<213> Homo sapien

cggttgctgtc gctgggtgcg gtggtgctg cctataattc cagctactcc agatgttgag
60gcaggagagt tgcttgacc cgggaggtgg aggggtgctg gagccgagat cgcgctactg
120tactccagcc tgggcaacag agtgagactc cgtctccaaa aaaaaaagg ggggtaaaaa
180ccttttga aaa tggaccccg tttttaactt tttattggaa atcctaaagg gggcttcggg
240ttttcaaaag aattttccaa accaaccccc ggcgggggga aatttgacct tttttggcaa
300acgggggaata ttttttttcc tggagcccct gggggggggg ggggaatttt gccttaagac
360ccttggggggt ttttggggca aag

383

<210> 2294<211> 384<212> DNA<213> Homo sapien

ctgacctcag gtgaccacc tgcctcggcc tcccaaagt ctgggattac ggggttgagc
60cactgcgcct ggcgggggat tatgttttaa atgttatctt tcacagcgtc tgaagttctg
120tgcttgaaac ctaagtcatt tggaaatgtac ttgttttgtg ggtgtgctga gaggatcggc
180aacatggcaa ggtagttatt ataataaag gtgagatggg gcggtatgtt gtanaacctt
240ctaanaactac cactctacac tcactcttca agattctttt ctgagctga tcaaccatga
300ttttgatgac gtccttaccg agccctgaga aactaaaact tcctagaggc caccctttgt
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384

<210> 2295<211> 384<212> DNA<213> Homo sapien

cggttgctgtc gcgttttcaa attcacagg gagggggaat gtctcact ccagccctcc
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120cctcggatta gagatgtca acctgcatca acaaatctaa agcctgcac tggctaccct
180ggggcgagtc ctgtttacag tgcctattcc tggagctcgc ctctttttgc cttttgttg
240attatgtgat gtattacttt tcccagcagg ccagtgctag catactggaa gagggattta
300ataagctggc acccttgatg ctatgtcct aatccaacct tatttgctc attggccatt
360tccattatgg tggcagccct ccat

384

<210> 2296<211> 384<212> DNA<213> Homo sapien

gccgcactcc actgcacagg acacttatgc caccctcttg ccagatgcct ttgaagaaag
60agtcagactg gtccaccctc cccagcccc tggggctcct tgagcctctc tccagccttg
120gcaggaggag gaaaagcagc acctccctca gacagctgga aaggccctct tcttcccag
180ctcagtgggt cgggccaagg gtcaccagac gggatattgt cccacctcc ctaccaaccc
240caagaacaca ctccacaccc ctcttcgctg ctgcgggtgtg aagcttcagc ctaaccaat
300cccacagagt ccatctcgac agcctgggat gacacgggtt cccagaggg ggacagagt
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384

<210> 2297<211> 379<212> DNA<213> Homo sapien

ggcagcaggc tatacacagc tctgttttgt caatgacctt tgttgtaagt ctcccaacgt
60cctattagga gccacagcag gtgaggcatt tgggtgcagca ggaaacatgg ggactgccta
120ggctcgaatc tgtggcaccc tgagcaatta cttaaattgt ggagcctagt tctcatctg
180taagatggac ttgagattcc tacctctcat gattactatg gagattgaat aattggtaaa
240attctcctag ctcaagtact gccacaggat gggctcttca gattttggct ctcttttagt
300tctgtgttctt gaaagaaatt aatctgtata taacataaga aactttgaaa gtcaaaaaaa
360caaaaaattt taattcctc

379

<210> 2298<211> 384<212> DNA<213> Homo sapien

ggcagcagggt tttctcctgt taagctccat tgcctctctc cacattttgc tattattata
60ataaacatta taaatgttaa aaactcaaca atatgttgnt aaacttattg ttttatgtac
120tctatgcttt tttttttttt ttgaaaagga atttttcttt ttttccccca gctggaaggg

180aatggcctta atttttttta acaaaaaactt cgccttgggg ggtaaagaa ttttcaaatt
240taacccttct gaagaactgg gaataaaggc ttggcgaccc ccccttcagt tattttgttt
300ttttaagaaa accccgggtg tttcaaagta aaaagggggg gcttggaaact ccgagcccaa
360gggggtgccc cccaccttga aacc

384

<210> 2299<211> 384<212> DNA<213> Homo sapien

ggcacgagca aagaatttta ttcaattaaa cttgaaatgc atctggattc ttaaagggtc
60agtagtgatc actgggacag ggcgatcata aaactgaatg ggctgtcgga aggtgtcgag
120gcagcagcaa ggggtgacatt gccactgacg ggggcttccg aactggggac gtttgtcatt
180gggatgtgtt acaagttcgg gctgtggaaa ttactcgatg aaaaacgcac attaacgata
240gccatgaaat attagtttaag ggaaactagg ttgagaaatg agacagcagg atctatcaga
300gcctggcatt gttcgccaca gccaggttag tgattaaaac gactgtcaag cggcagtggg
360tgggagctga ggagcacggn gctg

384

<210> 2300<211> 384<212> DNA<213> Homo sapien

cgttgtgtgc ggtgtagtcc gagtttccac agccaggtac tactccgcca gtgacctgg
60acagtaacaa aacatataaa gcccgagccc aaacccgcc accatcatag gtctgtagtt
120actgtggaat caataagcca tggcatctaa gaaatttgct gttaaaagac ggggtttggc
180tatgtaactc aggctagtct cgaactcctg agttcaagtg atacaccac tttggcctcc
240caaagtgtct ggattacagg tgtgagctac cattcctgac ctaggggctt ttctaaggaa
300ggcagaaaat gtttgcctaa cacagtgtgg gaattttgct gtccctgtgg atcttcatat
360cttgccacaa ggttcaaaca aagg

384

<210> 2301<211> 384<212> DNA<213> Homo sapien

cgactctcct gctttggtat ttgagtttga tttaaacaaa gcgtcgtgga tgggaggtgt
60atcatatgat cattttaacc attgtgcctt ttaatgtgga aaatctgccc aaaataggac
120ctgctgcagt ggttttcaca tatacaaga agtggctaga atgttctctc agaacagcac
180acgggattag aaaggacatt tggccgctgg aattcttcag tgagaattca gtgattaagc
240ctgccttctg ttttccttgt gggccgcaag gttcctgtgg atgtcccccac cctcagattg
300ctggagtaga aaacttaact ttccaaaaca ctgagttgtt ttcagcccag cattagaggt
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384

<210> 2302<211> 380<212> DNA<213> Homo sapien

caagtttgat graacataaa ctgataaagt ttgaaataaa aagagacagg ttggtaggaa
60agaccattca tatectatcc ccaaactggc ttaagtccac tcccactgcc ccagctacc
120accttttttac tttattctac ctgctatttc tttggccacc ggaataataa gcctgatgta
180aattctgttt cactatccca cagggtcaact ttttttgag tttgacaata attattccaa
240gtcaagtaat tcattgattt tagtggaaga ttgttttcca ggtgttattc ttccatgcgc
300ctcaccceca tctcataaag tagaaaagag atgatttaat ttatgggtct agaaaataaa
360aatgtaaata cttgcttgtt

380

<210> 2303<211> 380<212> DNA<213> Homo sapien

ggcacgagat tttggagacg acatggtgag aggttagctc tagggatggt ttagaaaata
60aagtcacctg gggactggtc caccctcttc cggctccctt gcctgttggg gtcagggtg
120ccctgggaag ggcagcgacg ctgggttggt aggagcatag actgcagggc atctgcctga
180gtgtagagtc cctgggcctc taattctgta aaatcgcggt aatagcatcc gcttctctga
240gctgttagag gtgtaacagg taaacccatg taagggtgctt aggacagggc tgggtgctggc
300taagtgccgt taatatcgtc agcatcatta cctgcgttat ttagcactg atcgccatgt
360cagctgcctt caaggtcttg

380

<210> 2304<211> 383<212> DNA<213> Homo sapien

ggcacgaggt gtgttcctgt tgtggctatt tttagaatc ggtgtttctc agaattgata
60agaccatggc acaaaaactgt gacgattggc tttggagtaa ccctgtgtgc ggttcctatt
120gcacagaaat cagagcctca ttcctttatt agtgaagcat tgatgaggag agcagcgtct
180ttggtaacag atagcacctc tacctttctc tctcagacca catatgcgtt gattgaagct
240attactgaat atactaaggc tgtttatacc ttaacttctc tttaccgaca atatacaagt

300ttactttggga aaatgaattc agaggaggaa gatgaagtgt ggcaggtgat cataggagcc
360agagctgaga tgacttctaa aca

383

<210> 2305<211> 379<212> DNA<213> Homo sapien

gggaagagca cctagcccg aatcccccta cagactagt gtagtgggga cgctggtgat
60atgaggaggc agaggcagca cccaggagaa acagggcagt ggaccaatgg acagctccac
120cagctccaca tctttggaag ctagatttgg ggagagagaa gctctacccc agacttaata
180cccattgaaa tttcacctca ggtgtgtgt cctgtgtctg gttaagtgtc ccatggaagg
240ggaaagcctt cagctcagaa cccaacccta taccttttac ttcttaaatg gtgctaacca
300caggtgtccc aggtgtctct gtgccagtta agatttttaa ctttcaaggg gcagggcata
360ctgggaaatg tagtttccc

379

<210> 2306<211> 154<212> DNA<213> Homo sapien

aagtttctcn nnacacgatc tgatgggggtc ttgggctaaa ggaggtccct gctgtcctgg
60agaaagtcct agaggttata tcaggaatga ctggtggccc tgccccaacg tggaaagggt
120gcaaggaagc ctctcccat tatcccaat gaaa

154

<210> 2307<211> 384<212> DNA<213> Homo sapien

cggtgtgtc ggggtggcttt tgcctttgat cccagctatg ccgaaggctg aggcaggaga
60attgcttgag cccaagaggc ggaggttgcg gtgagccggg atcgctcat tgcactccag
120cctgagcaac aagagcgaaa caaaaacaaa caaacaacaa aaaaaaaccc acccaaattc
180tttttttaaat gtagtagggt ttatatagat atactaatat aattgcattt ggagaattag
240agtatgtatg gagcccacac atactgtgat ataaagtgtata tacaagata tttggatatt
300ttctagtttg catgatgatt aagagaacca gatgggaaaa tacaatctcc aaagtgatgt
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384

<210> 2308<211> 384<212> DNA<213> Homo sapien

cggtgtgtc ggggtggcgtt tgcctgtgat cccagctatg cgggaggctg aggcaggaga
60attgcttgag cccaagaggc ggaggttgcg gtgagccggg atcgctcat tgcactccag
120cctgagcaac aagagcgaaa caaaaacaaa caaacaacaa aaaaaaaccc acccaaattc
180tttttttaaat gtagtagggt ttatatagat atactaatat aattgcattt ggagaattag
240agtatgtatg gagcccacac atactgtgat ataaagtgtata tacaagata tttggatatt
300ttctagtttg catgatgatt aagagaacca gatgggaaaa tacaatctcc aaagtgatgt
360ttatcctgga attacccaat ttag

384

<210> 2309<211> 379<212> DNA<213> Homo sapien

ggcacgagcc cgagctgcc cctggctctc agggaccctg gccagcagc ccgggaagt
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120caaccggggt gtgggggctc ccaggctggc ccccgccaca cggactcgtc ctgcttgctc
180acgcctccca gactccact tggcctgag cctggggacc ccgactggc agagtccggc
240ggccccctgtg gaaaagcgt cccagagagg cagaggaatg gaccagcgg cctccggggt
300gcagctccgg aaggagactc tgcagccctt gcggaggagt cccctccagc cccgtccagc
360cgcagctcca gcaccgagg

379

<210> 2310<211> 380<212> DNA<213> Homo sapien

ggcaccaggc gctttgtgac tggaggtcat cgtgggcagt tctatcagt tgacttagat
60ggtaattctc ttgactcctg ggaaggggta agagtgaat gcctttggtg cttgagtgt
120ggaaagactg ttctggcatc agatacacac cagcgaattc ggggctataa cttcgaggac
180cttacagata ggaacatagt acaagaagat catcctatta tgtcttttac tatttcaaaa
240aatggccgat tagctttgtt aaatgtagca actcaggag ttcatttatg ggacttgcaa
300gacagagttt tagtaagaaa gtatcaagggt gttacacaag ggttttatac aattcattca
360tggttttgag gccataatga

380

<210> 2311<211> 380<212> DNA<213> Homo sapien

cggtgtgtc ggcacttctc cctaagccct ctctgggccc aagctactcc tgcctgatc
60tggggccccc tggccagggt gcctgcacct ggccacctgc tccaccccaa ccaagccgac

120cacggccgcg gcggcacact gtgggtggtg gggaaatggc ccgagccccg ccaccccctc
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240ccacatcttg ctctgccacg gcattccatt ctttctccga accagcagaa cccagggttg
300gttcaaccaa agggaaggag ccaagagcct caaaggacca ggtgctttca gaacctgaga
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380

<210> 2312<211> 378<212> DNA<213> Homo sapien

cggtgctgtc ggccagagtg ttagaggtat ggggcagctt gagaagaaag ggaatggctt
60aaaaaagcca ctatgcagat caaaaaaggg aacagggttaa aggtgagtag aatactgacc
120agccccatag ataacaataa acaatgttaa atatgcgaat gacagaattg aaagtcattc
180aatgcaactt catcaaagggt gattcaggct tggattgac aaaagaaaga ggaaaactca
240cagtgagtta gtggagtcca ttatgtagt tatgtgttct acctttttaa attgtagtaa
300actgagtttg gatatagattg attctttcat acattctact ccagttagta gatattaaat
360atatacatat attttatg
378

<210> 2313<211> 152<212> DNA<213> Homo sapien

catgatatcc tgaacccac ggcaggaact gaacctggta aagagaataa ggagtttggc
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120agcataagag gggaatgtgc tctcagcatt tg
152

<210> 2314<211> 377<212> DNA<213> Homo sapien

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60agctgggact acagggtgtg gccaccactc ccagctaatt tttgtatttt tagtagagac
120aggggttttg catgttggtc aggtgtgtct cggaaactct gacctcaggt gatccaccg
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240acgcttttga ggttgagtgc aggccttgtg ataactaagt gctacttttg acgagcctc
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360ggtcttctct tttattt
377

<210> 2315<211> 377<212> DNA<213> Homo sapien

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120tgagggcacc tctcaagata caaaagcatc tgagagctcg aagccatggc cagatgccac
180ctacggcact ggttctgcat caccggcctc agcagtttct gagctgagtc ctccgggagc
240aagcccagct ctcaaaagcc cctccagtc tgtgggtggtg aggcggcggt caccctgctc
300tagccccgtg ccaaaacta gtctccact ttccagcaca tcccagatgg gctcaactct
360gccgagtggg gccgggt
377

<210> 2316<211> 153<212> DNA<213> Homo sapien

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60tttttttcta atactgtgat ctatctgac tgcagacaag aaccttgtct ctgttgaaga
120gcatcaaggg gagattatgt acacattgaa atg
153

<210> 2317<211> 376<212> DNA<213> Homo sapien

ggcacgaggt gtgttctgt tgtggctaac tttaagaagc gnggtttctc agaattgata
60agaccatggc aaaaaactgt gacgattggc tttggagtaa ccctgtgtgc ggttcttatt
120gcacagaaat cagagcctca ttcccttagt agtgaagcat tgatgaggag agcagtgtct
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240attactgaat atactaagc tgtttatacc ttaacttctc ttaccgaca atatacaagt
300ttacttggga aaatgaattc agaggaggaa gatgaagtgt ggcaggtgat cataggagcc
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376

<210> 2318<211> 378<212> DNA<213> Homo sapien

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120ggtgtgagcc accgcgctg gccagttggt acctactct taacacctt ccttgcctg

180acgtccaagc ccccccttc ccacaacccc tgttcctctg gggaatacac tgtttttgca
240ctttacctcc ctaccagcag ctctttccag attgcagggg cgagctggtg ggaagcttgc
300agattgtttc gcactgccgt gtaatctgtg tgcttgacac tggggtctgt tcttccttga
360gttggtacag tgaaatat

378

<210> 2319<211> 373<212> DNA<213> Homo sapien

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60aggcggagcc cctatttttt actggcgggg ggggcctttt aggggttttt aacccccctt
120gccccctttt taaaaaaaaa ccgttttttt ggggcttgga aaacttcgaa aaaatttttt
180tttaaaaaaaa ggggcctggt ttggaaccgt ttttttccca aaggaccggg gcggaaaaaa
240aacttttacc ttggtccaaa aaaaaaagg gaaaccctgg cccttcttag ggggaaaaaa
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360ggggggagac ccc

373

<210> 2320<211> 377<212> DNA<213> Homo sapien

ggcacgagat ttgaagtttg ttaatggagt gacttggggc caggaccag gaagttaagc
60agctcctcca cttcacccag ataacattga aaactccggg tgctgaccag ttttctgccc
120ccactccttt cccagctgtc accttcttga gactagaggt ctgagatgtc cagggtgtag
180atgggagaaa gcctggagag gagaagcaag agtcttctat aatctctaga taatcagtag
240cttagctaata tgaataaaga actgaataaa tgattttaat tgaaatattg ccatggtaat
300gctagtgttg taataaagat gtggcatgtc aggaggaaag tgcaaccgat atttgggtct
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377

<210> 2321<211> 377<212> DNA<213> Homo sapien

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120tccgtcttga agagaaaaaa aaagggtggg gggctggttt ggaatcataa acataaaat
180tgaaagtgtt ggtgaccttt aatactacaa ttgtgtggtc tgcagtcggg gagcatagag
240atgggacctg gtatttaata ggttgtggtt gcaatcagca tggcctgagg gccaggaag
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377

<210> 2322<211> 373<212> DNA<213> Homo sapien

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120tccagaagag gagtgggcac cactctcatc cagaggcccc tctgagagg caagtgaggc
180tgtgtctgtt gcctgggctc ccccaggtgg cacctgtcgg tctgtggacc tgggtgaggc
240aaggatgccc atctggacat ggagccgaca caggtagtca gggggccagc gggacgctta
300ccaacagctg tcttttcccc acctcagaat agcattcctt tcgaacacca cggcaagtag
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373

<210> 2323<211> 375<212> DNA<213> Homo sapien

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120gtaacaccac tgtgccaat gccccccagg ccaacagcga ctccatggtg ggctatgtgt
180tggggccctt cttctcatc accttgagc ggggtggtgt ggctgtggta atgtatgtac
240agaagaaaaa gcgggtggac cggctgcgcc atcacctgct ccccatgtac agctatgacc
300cagctgagga actgcatgag gctgagcagg agctgtcttc tgacatggga gacccaag
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375

<210> 2324<211> 377<212> DNA<213> Homo sapien

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120tgtgggcctc cctgagtgc ctgagttagg tggcagaagg ggtgagaggc catggcgtct
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377

<210> 2325<211> 377<212> DNA<213> Homo sapien

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120actggagatc tcctggatgg agttggatta agacagaaga tggctggaag agatgtgaat
180cttgtagtca gaaacttgaa agagagaata accgttgtaa catcagtcac agcattatct
240taaatagtga agatggagaa atattcaata atgaagagca tgaatatgca tcgaaaaaaaa
300ccatttttaga aatgacacaa atactcaaaa ggcatggcta ttgcaccttg 360ggagaagcct
ttaatcg 377

<210> 2326<211> 368<212> DNA<213> Homo sapien

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60tgggtattca gggaagagaa ctagaagcca accatgtaga atctatgcag gtgctcttaa
120gacattgggt tgactggaat tatcttcttg ttaggtctta ggaatctcct tccaggtaac
180tttttctatg attagacaat tgatttgttc agggtcacag agcaaagtcc acatttaatt
240ccacatggcc aataaaaagt aggggctaca aggtgagatc cagggggccag agttatcaaa
300gtgatacagc acttttagga ataggacagg gaatggagga attggaattc cagtattact
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368

<210> 2327<211> 372<212> DNA<213> Homo sapien

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120gacattgggt tgactggaat tatcttcttg ttaggtctta ggaatctcct tccaggtaac
180tttttctatg attagacaat tgatttgttc agggtcacag agcaaagtcc acatttaatt
240ccacatggcc aataaaaagt aggggctaca aggtgagatc cagggggccag agttatcaaa
300gtgatacagc acttttagga ataggacagg gaatggagga attggaattc cagtattact
360ttcaaaagca gt

372

<210> 2328<211> 150<212> DNA<213> Homo sapien

gaatttaaca cangnggata ccgaacttcc attcttttagt cattccaggc ggatctgagt
60tttatattcg aacttttaat acagcttttg agttttgagt gacttgaatt tttatcttt
120nttttaatac gtagcttaaa tgaacatatg

150

<210> 2329<211> 368<212> DNA<213> Homo sapien

ggcacgaggt ccagggtaca gttccttttag aggttcctca ggtgaaacca aagagaactg
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120ccatctttga gctgaaatct gtggctgctg gctgcccctgt gttgctgggc aaagacaacc
180caagcccggg tctttcaagg gattctcaga aacccacttc cccactgcag tcagcaggag
240accatttggg agaagaacta gatctgttgc ttaattttaga tgcacctata aaagagggag
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360tccaagag

368

<210> 2330<211> 372<212> DNA<213> Homo sapien

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60tactgttgat agcaatgtca atgtcaaata taatacttgā aagtttttat ctcaacacat
120ttcttttctg aacctcagag ctgtatgtcc aactgcctgc ttacttcagt atctccactt
180gaagatctta aattcatatc cgtttgctta aacctgaact catcgtcttc ctccaactgc
240tctaccacac gctttcccca tctcagttga aggcagcgcc atctccact cctatcgctc
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372

<210> 2331<211> 367<212> DNA<213> Homo sapien

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60ttggcagcca ggtccctaca caaacaagta atcctgtttg gcctcctagg ttttgcatat
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180tgggtgactt taatggctgg ccacataccc ctttctccca gctactcatt cactgacttg
240ggtaagtctt aagacagttc gcacttagaa aagaatgtga cacatcaaca ttaacttttc
300ctgaaaagaa gagtttgcct aacatgggtcc taaagaagct tggaatttat aagactttcc
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367

<210> 2332<211> 367<212> DNA<213> Homo sapien

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60ggccacctcc gtgtctgggt tcatcggcag tccccaaagac ggtgctccag gccctagac
120agggagtgcg atcccacggc agtgggcagt cctgtcccgc gagcccggcc ctgagtctga
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240cggggggggc ggccatgctg ggcagccac acaagccact gtcacctgct gtcgccacct
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367.

<210> 2333<211> 364<212> DNA<213> Homo sapien

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60atgactttcc acttgcctgt agttttttgt ttgctttgggt ttggtttgat tttatatttt
120tttctcctaa tctatgactt tattgttttt tcttaggtta gtaatagcat ctttgatcct
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240gaattaacta ttttaattaca gtgagctcat ctcttaaaaa ttgttcaggt gtaaatctta
300tgagaaacat gaaaaagcac actgatttat ggagagttga gctaaaaaca tttataaata
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364

<210> 2334<211> 366<212> DNA<213> Homo sapien

aattccggtg ctgtcggcat cttttatgta cacttgctta ttcagacaag atcctcatga
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120aagcttggtta agaacgttct agagccacaa catgattgta ggccaagggc ttgtttttgt
180gaccttgatc taagataatg ccatggttga ttgtatgttg gaagaatctt tgattggaat
240ttggagtaat attaaggtag tttgtcttct ctgcagacat ttttaggagt ctttttgtgt
300gagtgggtgg ggagtgtata gttttgttga acctagttaa attctgaata tcttccact
360aaaagc

366

<210> 2335<211> 364<212> DNA<213> Homo sapien

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120aaaaaattcc ggggggcttt tcaaaaaaga tctttagggg gaaaaaatt tttttaacca
180agacccaaac ctaaaacccc caaaagggaa aaccggacaa acttggcccc tgggtttttg
240gggaaaaaca accttccggt taaaaacca aatgggggccc gggggttttt ctgcccggaa
300ccccccacct ttgggggggc aggggcaacc ccccttttgg gcctaggagt gggaaacccc
360ccgg

364

<210> 2336<211> 147<212> DNA<213> Homo sapien

cgcgtgctac gttcccatat ccaaatattgg aagaaaccac aaggctgcct ctgactgagg
60ccacaaatgg gcacatagtt taccttccact ttttgaaaac catattaaga ttgagtcagc
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147

<210> 2337<211> 359<212> DNA<213> Homo sapien

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120tagaaaaaag agaaattctt tttatacaat ataagttcct gcagaatgca gacactttct
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300cttctctcct gcctagaaaag gatcgtccct ccactttcac caactaatcc cttctcacg

359

<210> 2338<211> 144<212> DNA<213> Homo sapien

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60ttaacaaatt gctgcatgta ttccatttaa aaatatgctt aaaatgtcct aaaacaaata
120attatctccc taagaggatg catt
144

<210> 2339<211> 342<212> DNA<213> Homo sapien

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60ttcttttagcc agagactcct tctaccagc tgcagacca cctttgtgca gtggaggttg
120agaatgcccc aaggatgcac gtaatggacc agcctttcca gcatttggct ttggctccca
180gaaattttga gctttggcaa atcttacaag ctctgtgagc ctctgtttcc ccatgttctc
240atattcagag gtgctgggct ggactccac tgccagttcc ctgagctgtg cagggactcc
300tgctctgcat ggtttgtttt ggtgctcatg ggaccataag tg
342

<210> 2340<211> 188<212> DNA<213> Homo sapien

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60cgcccttcac accaccaccg aggacagtgc aggggtgcac actgagttct aggccagtgg
120gtccctgact gctgcacatg gcacaggccg ttcccttccg gaccaggca ggctcagctc
180tggggagg
188

<210> 2341<211> 460<212> DNA<213> Homo sapien

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60ttgctgtcga aatgacttat tttatatggg atgatacaca taggttattt gcaaatacta
120cactatttta tatgagagac ttgagcattc gcagatttcg gtatccacgg gaggtcctgg
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240ttacttcagt ggtccttcta ttttcattaa cactgatatc tagtttaata tgaaaaggaa
300cttgaaatct tgaaaattag aacatcgtaa ttttttcta cttgcaatgg aaaatctatt
360ttgtttttt gcttctagga aaatattctg attatgatat gtgatattt ggctactcaa
420agtcaagaact tttcaaagta atcagtaa at tgaatcaaca
460

<210> 2342<211> 465<212> DNA<213> Homo sapien

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300gcctttgggt caacacagga gaggtgattc caacyttaac aagttggta aggaaactgt
360cagctgttta tttttatttc aatcttctct gttaaaactat aacacactga ttgagcaact
420aaacactaat atgcagagag gaaaaaaca caaaaaatat attgg
465

<210> 2343<211> 466<212> DNA<213> Homo sapien

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120ccgggactat tatgcactct tccccaggc cgaagacatc agcttgctgc agcaggcctc
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360ggagaactcg gaggaagagg agtgcattgg agcagccgcg gctgtgggccc ctgccatgtg
420tggngtggaa ctggactctc tcatctccca agtgaaggac ctgctg
466

<210> 2344<211> 453<212> DNA<213> Homo sapien

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180atgagtggat aaaccattc ctcaaaagaa atggaggctt cgtggagctg cttttcataa
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300catacaggaa ttttctgtg gtggaggcaa gttggtcaat gctgcatgat gagaggccat
360atttatgtaa tttcttagga acganttatg gaaaatcacc cagacaggca ctaatgaaca
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453

<210> 2345<211> 423<212> DNA<213> Homo sapien
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60ataagaacat tacagggttg gtttttcttg catgggtggc cacctaattgt ttaaggagtt
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240gtattttaaat aatgtatgag tgaccaccca attccaacat taaaagtgtg atctgggccc
300ataatttata gtgaaattgt atcaaaacat agggaaactg tattactggc cattttgaaa
360atatgaaact tgagtattga aaatattcca acatggaatg gcagtattct aatttcagtt
420agt

423

<210> 2346<211> 425<212> DNA<213> Homo sapien
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180atgtgctcag aacttttttg acaggtattt tgagaagagt tgcggaacat tctggtaatt
240tgtagagatc tgttggcatc tctgttccac aaactggaaa aaatcatttg taagtcttgc
300taattacttt tcttggagaa gaaaaaaaat gctacagctg caacaaatgt atagttttca
360aaaagaaaac acttttttgc tccccagtt attcttagtt tccagcccac gccttgcat
420agcgg

425

<210> 2347<211> 429<212> DNA<213> Homo sapien
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60tatctctgtc cttgatcttc ttgccaaaa tgtgagtata cagaaatttt ctgtatattt
120caacttaaga catttttagc atctgtatag ttgtattca atttgagacc tttctatgg
180gaagctcagt aatttttatt aaaagattgc cattgctatt catgtaaaac atggaaaaaa
240aattgtgtag tgaagccaac agtggactta ggatgggatt gaatgttcag tatagtgatc
300tcacttagga gaatttgcag gagaaagtga tagtttattg tttttcttc gccatattc
360agntttgttc tacttctcc ctttcttcc agatgataac atcacatctc tacagtaagt
420gcctctgcc

429

<210> 2348<211> 425<212> DNA<213> Homo sapien
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60gcattctttt aatgtgttct ttctttatgt gattatttga ttaattctctg cctccccac
120tagactgtaa gctccctgaa ggcaagaatc ctgtgcttat gctcaatatt agctctcct
180tggcacagag taggcactca acaaatgctc cccaaaaggc tgagtggctg actgaattaa
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300cagactgaat aagttggaga ctccctaaa ggggtggcatt tccccagggt aacaacgcaa
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420gcaa

425

<210> 2349<211> 423<212> DNA<213> Homo sapien
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420aga

423

<210> 2350<211> 425<212> DNA<213> Homo sapien
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120tagtctggc cggaggagtc tcagagctgt cagaaagaat aagactgatt ttatgggaaa
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240caagatgatt tatggtaata agatataaaa ccaaggaaaa taacctaaag tctgaaaaag
300accagaatcg aagtttcctg attcatattt taatgttttg aaatttatac tccaggctgg
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420gaagn

425

<210> 2351<211> 429<212> DNA<213> Homo sapien

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120acgctggggc agcaagccag ggtttggttg gtgcgggtgc tgctcaacct gctggtggtc
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300tccatcttca tcgctggggt caattttgtg ctgccggccc ggtcaagct cattgcttca
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429

<210> 2352<211> 428<212> DNA<213> Homo sapien

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120attgtgccct ggagagttgt acacatgttg aaatgtaatc tgggcttacc tgatccattt
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300gtcttatcac agaaggcagc caccatttca ccaaaacaaa agttcacggc attcaattcc
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428

<210> 2353<211> 432<212> DNA<213> Homo sapien

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432

<210> 2354<211> 437<212> DNA<213> Homo sapien

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180ttacgggcag tggaacagag ggtggcttcc tatgaggagt tcaggggtat tgccttgca
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437

<210> 2355<211> 431<212> DNA<213> Homo sapien

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300cctggggacc gngtgcacc gcttagctcg gccccattc taaggggctg gtttggcagg
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431

<210> 2356<211> 427<212> DNA<213> Homo sapien

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120aagtcaccc ttaatagacg agatcaccga agtggccttg gaggacaaca actgtcatgg
180ggaccaggtg gtggagcgtc tcttcagca cctgcggcgg gtggatgctc cagtgcagg
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300ctgctgcaac actgtggtgc tgccccagtg gactccttc tccaggaccc acaacgtctg
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427

<210> 2357<211> 427<212> DNA<213> Homo sapien

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120ccctcaaggt tttttgcttt tctcctgtgc acctggcgag gctgaaggcg aggggtggag
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427

<210> 2358<211> 439<212> DNA<213> Homo sapien

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300gtttctgag tgtgcaaagc ttctctctcc ttccttgcc attcttccct tlcacgtga
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439

<210> 2359<211> 429<212> DNA<213> Homo sapien

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120acctactac tgacgaagac acccattcca gtggaccact gtgaccagg aggcattcag
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240ctttatagtg aagacagagt cctcaagcca aatagctaaa gctgtttat cacaacaaag
300gcctagtgtt ttccatgagt gtgcatttca tttcttcagt taaagcctc agagacacac
360aataaattg gaccagggga ttttttagtt attaatgtc tctgaagaaa ggcaacatct
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429

<210> 2360<211> 424<212> DNA<213> Homo sapien

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120gaagacgac gtgggcctcc acatcgatt ctggtttcat aaatcaaacc aggagcaggt
180gcagcccgga ggccccccc gtggggagaa gcggctggg ggtccctgca tcttgactg
240cggccctcc aacaagtcgg tggatgtcct ggcaggactg ctccagagaa ggatggagct
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360gggcagcagg aagctgtca ggaagagccc ccgggagggg aggccgaacc agagcctcag
420gagg

424

<210> 2361<211> 415<212> DNA<213> Homo sapien

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120ctgacctcaa gtgatccacc cacttcggcc tcccaaagt ctgggattac aggcgtgaac
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240cttatgattg ggggtataac gtgtattct tactaatct gtgccttggc tcttgctac
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360aaattaactg atgtaaagga cttctcctta cccctgtggc ttatatattat catct
415

<210> 2362<211> 413<212> DNA<213> Homo sapien

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60gcctataacct tatttttagca tgagagcata atcttacact ttcagctaa aataaggat
120aggctaaggg aaatactgta aatgggttg ttagaattaa agtttagaac tctaaatctt
180atgcttattt ttaaagaaaa aagttgcctc actgtcatga aatcctgtta ctttcattaa
240aaaaaaaaat cttgtaaaat ggttaaatg gataatgtaa gacataatga aggctttgag
300gcatttcata ctttaccagt ttacatttgg ctaacatact ggtaaggatt agggttctct
360ccactattgg aaaattaaat gctaaacgct ctaagaatta cggtgatttc aan
413

<210> 2363<211> 422<212> DNA<213> Homo sapien

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60gagagagaga gagagagaga gagagagaga gagagagaga gagagagaga gagagagaga
120gagagagaga gagagagaga gagagagaga gtgagagtgt gagagacaga gagagattga
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420cc
422

<210> 2364<211> 414<212> DNA<213> Homo sapien

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120ttaaaagaaa tgggaaattg cctacggagc atattgctt tcagatcata ggtatctttt
180ccaataactt tattgtaa ttaagggag tttcgttga ccttagagcc atacctcac
240tgacatctca tccgtttgtg tttccaaaag ctgctttac aggtcttagc cgccgccccg
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360aacttggatc tggagtctg aaaaacacaa accttataaa tgcattctt tttg
414

<210> 2365<211> 405<212> DNA<213> Homo sapien

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240ggggaagctt ttgtttttt tgaaaccctt aaaaccgga aaaaaaagt aaaaaaaca
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405

<210> 2366<211> 406<212> DNA<213> Homo sapien

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360tattttttta tctataaacc tctttaagg gacgcagagc attcat
406

<210> 2367<211> 406<212> DNA<213> Homo sapien

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60gcactgagtt tccatagaac ttcaaaacaa ttggttgatt tcaacttaaaa aaaaaaagtc
120attcaatata cagaaaatta ctcccctggc cagtactgtt agccccaat aatctgaaaa
180aatttgttct taaaaaaaaa acaatttgg aggccaggca tgggggttca tgctgtaat
240cccagcacat tgagaggtca agttgtggc atcacttgag ccaggagtt tgagaccagc
300ctggacaaca tggggaaacc ctatttctac aaaaaaatac aaaatttacc cgggcatggg
360ggcgcatgcc tgaagcccca gctactcggg aggctgaggc ggaagt

406

<210> 2368<211> 407<212> DNA<213> Homo sapien

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120acatcacaaag gttāatattg gtttggtgta aagaattatg cagtaaaggt atttataagg
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240gattatttca taatccctta tacatgagcc aatgaaatat tttgagctct acttaagaag
300catgaagtct atattataaa tctāaacaaac aaaagcactt gtaacttgtt tagtaaattc
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407

<210> 2369<211> 407<212> DNA<213> Homo sapien

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60attgtgtgac tacgcaagta taggtcctgt tgtattgcat taatctttac cagtaactaa
120acatcacaaag gttāatattg gcttggtgta aagaattatg cagtaaaggt atttataagg
180gaacatgatg actttattca atatttttct tctttgaaac atctcattac taacttttaa
240gattatttca taatccctta tacatgagcc aatgaaatat tttgagctct acttaagaag
300catgaagtct atattataaa tctāaacaaac aaaagcactt gtaacttgggt tagtaaattc
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407

<210> 2370<211> 407<212> DNA<213> Homo sapien

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120aagaaatag agatcagaga aatcaaagat tattattaaa ttacatttct tttggtatct
180cctgagattt ctgagttatg cactacttgt attcattcat ttattcatca aatacaatat
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300aaatagtatt tatatttata aatgatgaaa caaaaagaaa aaatagaagg tgaatcggtā
360ggtaāaaaaga gacaatagac taccagccaa tctcaatgtg tgaaccn

407

<210> 2371<211> 422<212> DNA<213> Homo sapien

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120agccaggtgt ggtggcgac acctgtagtc ccagctactc gggaggctga ggcaggagaa
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300atataatgaa atatattttg aactāaatt atattctata tgtgtatctt cctaggcaaa
360agctgtaatt tccagagaga ccattaggaa caggtagcat ctatttttct ccattattta
420tt

422

<210> 2372<211> 168<212> DNA<213> Homo sapien

taaaggactt aaacacctat gcgcgatgat aaagagggtā ctattatagc gcttgāaaaa
60taccaggaag ttgagagagt taacagaagg gcgcācgctg gattggccac āaatcgaat
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168

<210> 2373<211> 410<212> DNA<213> Homo sapien

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410

<210> 2374<211> 422<212> DNA<213> Homo sapien

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60ctggaagaaa gggggāaaag ggagcagaga aggcaaccaa caacagctat tatagatgca
120gattttggag gcagaccgcc tgggatttaa aactttgctc tactactttc gagccatgtg

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300gtccacagaa gggactcaat gactgtgttc cctttgttct tgctaggatg tgcattaggt
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420tg

422

<210> 2375<211> 406<212> DNA<213> Homo sapien

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300tttgaatttg gatttttttt ttttttgag gggggaaggg tataaggggg gctaaaaatt
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406

<210> 2376<211> 420<212> DNA<213> Homo sapien

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120gaacatgacc taatttaaca ggtaatttg aagtgcattc gccaagtaga agaccagcaa
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420

<210> 2377<211> 420<212> DNA<213> Homo sapien

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420

<210> 2378<211> 411<212> DNA<213> Homo sapien

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120tttttagttt tggaagaaag ctctgcagggt gaggagaagg acgtacgtgt gtatggatg
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240tttttggcac cgaaagtgtg atgaactata ctttttaaga attgctagct ttgtttttct
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411

<210> 2379<211> 409<212> DNA<213> Homo sapien

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300agtcaccaacc ttctgtaaca taaccactct tggcattggc gtgttccttt ctagtctctc
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409

<210> 2380<211> 411<212> DNA<213> Homo sapien

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180aaagtccttg attggcatct tcattcggat gatggagagc ctttgtggta gtgtttgctt

240atgtgaacag caggcctttc agataagaga agtggcctttt ccttgggtgat gaaggggtag
300agattgagcc atggggatgg tttaggttaa agaagctttt tttttggcca tcatgaggat
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411

<210> 2381<211> 417<212> DNA<213> Homo sapien

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120ttcagttttt tcattgttat attgccaaaa accattcttg ctatatatat ttttaaaaga
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240cttttaattat cttcaaagta tgatgaattt ttcattgtgt gaattgtgtg tctgataatt
300tttttaggaaa caacactcca cttagagagc tagaatctta gaattcatct acttcattct
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417

<210> 2382<211> 410<212> DNA<213> Homo sapien

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120aggtgacctc agcttgggct gcggtgcagg ccatgggact ggcaggaggc ggctgggggt
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240tgctataaag ggctgggtgg ctttcttccc cacagctact cagcctaatt ccattgcaga
300gcacatgtag ccatggacaa cacaaggggc gtatccgtgt tccaggacag ccatattgac
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410

<210> 2383<211> 414<212> DNA<213> Homo sapien

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120gggtactgagc tcctgttaa ctttctttac tcttggtttt agcatttcca tttccttgaa
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240atttccaaac ttttactta actaagaatt gcaggcctca gcattaatgc tacctgaagc
300tttctctaat cctcatttaa attagttctg ttacaaactt tcaagttgcc atattcttcc
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414

<210> 2384<211> 416<212> DNA<213> Homo sapien

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300aagcccggga gtcaggagac acagggcagc tggaggaggg tctttactga ggctactgag
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416

<210> 2385<211> 405<212> DNA<213> Homo sapien

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120ataagtgcct tgtccacatt ttgcgagaga caacagtaaa atactccaaa atacgttctt
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240aagatgagtg cttttatgcc catagtcttg tggaactgaa agtctggata atgcaaaatg
300aaacaggtat ctacatgat gctattgtc aagagtctaa acgatattgg cagaatttgg
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405

<210> 2386<211> 416<212> DNA<213> Homo sapien

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240ggaggggagga ggtgctgact gaagaggagc tgaccaccac actaaaggta ctgtgcatgc
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416

<210> 2387<211> 411<212> DNA<213> Homo sapien

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300tcacccaaag ggcacactgc agagtccca gtgtcttcct cgctatccca tcggcagctc
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411

<210> 2388<211> 411<212> DNA<213> Homo sapien

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120ttgaggcagg agagggtagt tgtgcttccc taggaagagt gtcttccaaa gtgttcttca
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240aattattctt cataggcttt atcatcatgg gattcttctt ttatatactg attacaagac
300tgacacctat caagtatgat gtgaatctga tctgacagc tgtcactgga agcgtcggg
360gaatgttctt ggtagctgtg tggtagcgat ttggaatcct ctcgatctgc n

411

<210> 2389<211> 417<212> DNA<213> Homo sapien

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120tgccaagacc aagtgaaga ggcttctgga cctccatcct tgcttcagcc agagcagcgt
180gggttcattt catttttggg ttttggtttg tgggaagaaa gggttctctt gccggtgtgt
240gtgtttctga taaacaaaga agtgtggaag tggctgaatg agatgaccca aggactctt
300ctgggaagat gcaggaggaa gtaggtgagc tgaggggaag ctggtgggga taggcctgtt
360ggggcctggg gagaaggatt tgaaggctca agtcacacgg tgcaggatgg gactcaa

417

<210> 2390<211> 413<212> DNA<213> Homo sapien

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300tctccaggta gggctgtgag ctgtgagttg gatccttttg gtgaaatggt ctctctcatc
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413

<210> 2391<211> 407<212> DNA<213> Homo sapien

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60tccctgatgt gctgcagagc aatgacgagg tgttggctga ggtgacttcg tgggacctgc
120ccccgttgac tgaccgctac cgcagggcct gccagagcct ggggcaaggg gagcaccaac
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240ccctggacca ggcccagctt acaccctgc tgcgggcct caagctgcac acagcactcc
300gggagctgcg cctggcaggg aaccggtg gggacaagt tgtggctgag ctgggggctg
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407

<210> 2392<211> 405<212> DNA<213> Homo sapien

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120gagaccagtc tacagtttga acatcactca atgaaaggga taattccatg aatcagaaaa
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240atgttaaaga gataaagtga tcgagacaag gactgactgg gtatagaagg aagacagact
300cctgtcttca ctctaaatg cagttctttg gaatcaccct actgtggtgg gcgtagtagg
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405

<210> 2393<211> 411<212> DNA<213> Homo sapien

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120ccagaacatc caggagaccc atcggctcta ccgcctgaag ctggaggagc tgaccaaaact
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300ggagaaccag atgaaagagc gccaaaggcct cttctttgac atggaggcct atttgcctaa
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411

<210> 2394<211> 411<212> DNA<213> Homo sapien

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180tggacagggc agctatgaaa caattggacc cttgagtga ggagattcag atgaagagat
240attttgtaagt aagaagttga aaaacaggaa ggttctacaa gacagtgatt ccgaaacaga
300ggacacaaat gtctctccag agaaaactac ctatgacagt gccgaggagg aaaataaaga
360gaatttatat gctgggaaaa atacaaaaat caaaaggatt taaaaactg t
411

<210> 2395<211> 406<212> DNA<213> Homo sapien

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60tccctagtgg agcgcagggg aggcagaagt catgacaggc gaggtgggtt ctgaggttca
120cctagaaatc aatgaccaa acgtcatttc acaagaggaa gcagatagtc cttcagatag
180tggacagggc agctatgaaa caattggacc cttgagtga ggagattcag atgaagagat
240attttgtaagt aagaagttga aaaacaggaa ggttctacaa gacagtgatt ccgaaacaga
300ggacacaaat gtctctccag agaaaactac ctatgacagt gccgaggagg aaaataaaga
360gaatttatat gctgggaaaa atacaaaaat caaaaggatt taaaa
406

<210> 2396<211> 415<212> DNA<213> Homo sapien

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300tagaaaggag catcgaaacc agcagcactc tgcatagcag gctcaaggaa caactggcaa
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415

<210> 2397<211> 407<212> DNA<213> Homo sapien

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360tgatcatctc tgacaacgca gttgacaatg acagcttcta cgtggag
407

<210> 2398<211> 409<212> DNA<213> Homo sapien

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240gccgctggtg cagtggctcc tcccctctgc cgggtgggc cctcgggtt tcgctgtctc
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360gtgtgaggat gtccctggat agtccactgt gtgcagaggc atgggagtn
409

<210> 2399<211> 410<212> DNA<213> Homo sapien

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240cggaggatgc caaggcccgt ctgctggcag agcagcagaa caagaagaaa gacagcgaga
300cctccttcgt gcctaccaac atggctgtga attatgtgca gcacaacaga ttttatcatg
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410

<210> 2400<211> 412<212> DNA<213> Homo sapien

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120aaagtattct caaactagac ggtgatgttt taatgaaaga tgttcaagag atagcaactg
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300atggacagta cccaatatgg atgaacaaaa ggcaaagaaa aaggctgaag gcaaagcgag
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412

<210> 2401<211> 405<212> DNA<213> Homo sapien

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405

<210> 2402<211> 421<212> DNA<213> Homo sapien

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360tagacccatt cctgataaag aatttgtaga aacttatatt anagcttatt acctaactga

420g

421

<210> 2403<211> 408<212> DNA<213> Homo sapien

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408

<210> 2404<211> 411<212> DNA<213> Homo sapien

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411

<210> 2405<211> 397<212> DNA<213> Homo sapien

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120agagagcgcg cgcgcgcgct ctctagagtg tgttttctct ctcccgtcga ttacgcccc
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397

<210> 2406<211> 402<212> DNA<213> Homo sapien
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402

<210> 2407<211> 390<212> DNA<213> Homo sapien
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390

<210> 2408<211> 392<212> DNA<213> Homo sapien
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120agaaaaataa tcacctagaa actataaata gaaatgtgct gctgaggctg ggcagggtg
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360aattgctcga acccaggcgg cagagcttgc an
392

<210> 2409<211> 385<212> DNA<213> Homo sapien
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385

<210> 2410<211> 404<212> DNA<213> Homo sapien
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180tataaaggat ttcacagaa gttttcattt tttctaaatc ctcccctact caattttcac
240attggaaatt actcttgtat ttgtagaaga ttgtctctaa aattgtggtt taactcacgc
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360gaattctctg gtgatgattc tagcctaacc ttcaacataa aata
404

<210> 2411<211> 403<212> DNA<213> Homo sapien
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120agtttccgtt ttgcaaggcc taggtgactt tttcatgggt tttgtatgtt tagctctttt
180gaaaaggaa tttgaaatct ccatcaactg aagtaaatga tgtctgagt ttacagtaaa

240ggtgaccaag tctctttctt aaagtcacaa tgactaaagt attagttgaa tttttttttt
300ttttttgagg gagcctcgct ttgtccccag gctggagggc agaaccacaa tcacgggtca
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403

<210> 2412<211> 386<212> DNA<213> Homo sapien

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60tgttttgaga gattacagaa taggaggcct gctccacttg cagataagtt tattataatt
120ctccagaaat gtgcaggatg tgcattagca aattgcactg tactttttcac tccagcctgg
180gggacagagc aagactccccg tctcgggggc ttaaaaaaaaa aaaaatgctg tttctaaagg
240aatctgagta tcttggggccc aaatgtgggt ttgtccaat ttatttataa agggcttgtt
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386

<210> 2413<211> 404<212> DNA<213> Homo sapien

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120aatcttctaa atatgtaaaa tgaaagcaac agcaacagca aacacaatta tcgtattctt
180tgggagtaac aaatactgggt tttcatttta aaactaagga aaattttatc agtacttaaa
240ttcaatccaa aaaagggtttt ataacaccca aactgtacat ttaaaattat gctttcttaa
300ggtaatggct agcattacct agttttagt tttcttgagc tgtaactttt tataactgaa
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404

<210> 2414<211> 388<212> DNA<213> Homo sapien

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120cttgagtctt ctacagcttg ggcatgcacc tcaggggggag ccagcatcag tgtccagccc
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388

<210> 2415<211> 389<212> DNA<213> Homo sapien

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389

<210> 2416<211> 398<212> DNA<213> Homo sapien

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398

<210> 2417<211> 388<212> DNA<213> Homo sapien

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120ttagtttgtt gatttaagaa tattcccaca agttaacaa tgaaagtgat agttatatta
180cagatatgaa tgactaatta ttctgccc ccacctacat cattttcccc ccagcttaat
240ggaggtttta ttgacaaaca aaaattatat atacttgcac ccagtcataa aaaagaatga
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388

<210> 2418<211> 387<212> DNA<213> Homo sapien

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120taaattgaaa ctttaagttag tcttcaggct ttttaagggt ttcaaatttg aactggaatg
180caattcagaa tgtgctagaa taacatttct ccatttctcc agtgtcaaga tgggaaggca
240tacattctaa gcgtctgtat ctccatctat ttttcttttt tttttttttt ttgaaaaaa
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387

<210> 2419<211> 385<212> DNA<213> Homo sapien

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120tttccagcat tgtaaagac agcaggaaat actcaatggg ccacaggaaa taattaacat
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240taaatctagt tctaacatat gttgattctg tggattagac gagtttctta gtcctctga
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385

<210> 2420<211> 389<212> DNA<213> Homo sapien

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120agtagattat gtccgaagca gttgacctaa aaactgcctt ggactgacat ttgttaggtg
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240catccctctg gtgtgtttgg ttttttagcc accaaaaatt taacaaattt gataacctgt
300cacgtgtaag ttcagaaagc actttgtgtc taattggtga cttgggggtt atttgggtata
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389

<210> 2421<211> 161<212> DNA<213> Homo sapien

gaatgttccg gtcggtcttc agcataagct gaaatatatg catgtaaaaa ctttgacatc
60ttttttttta attttccact ttcttcttaa ctttacttct cttttgtcc cccccccat
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161

<210> 2422<211> 397<212> DNA<213> Homo sapien

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397

<210> 2423<211> 404<212> DNA<213> Homo sapien

cgctgctgctc gcttttaata tggaaatccac ctcataacaa ttaagtctaa atttctggaa
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404

<210> 2424<211> 399<212> DNA<213> Homo sapien

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399

<210> 2425<211> 389<212> DNA<213> Homo sapien

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389

<210> 2426<211> 387<212> DNA<213> Homo sapien

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120gactgagtgg agcggaaactc tgtctccaaa aaaaaaaaa aggggttttt ttaaaataac
180cacttttgggt aagggtaggg gaaggtaagg ggggcccaaa aacaactttg tttttttaa
240tataggcggg aagggaataa aatggaattt ccttgttttt tcccaaaaaa gacaaccccc
300caatttgga gggctaataa ccattccccg ctttggaata aaaagaaac ttcaactttg
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387

<210> 2427<211> 385<212> DNA<213> Homo sapien

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240cataagaaaa acggtgaagg ggttttgttt acttttaaaa ccgcacacac acaccacac
300accacacac acacacacat ttttttctat actcttaaaa aaccgtagag ttttaacaat
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385

<210> 2428<211> 387<212> DNA<213> Homo sapien

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387

<210> 2429<211> 388<212> DNA<213> Homo sapien

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388

<210> 2430<211> 390<212> DNA<213> Homo sapien

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360gccaacacat tttaaagctg atctcatcag
390

<210> 2431<211> 395<212> DNA<213> Homo sapien

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395

<210> 2432<211> 390<212> DNA<213> Homo sapien

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390

<210> 2433<211> 388<212> DNA<213> Homo sapien

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388

<210> 2434<211> 391<212> DNA<213> Homo sapien

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391

<210> 2435<211> 404<212> DNA<213> Homo sapien

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404

<210> 2436<211> 393<212> DNA<213> Homo sapien

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393

<210> 2437<211> 389<212> DNA<213> Homo sapien

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389

<210> 2438<211> 387<212> DNA<213> Homo sapien

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240gtaaaccag cgagagtatc tactcagccc tgagtgttaa tgactatttc agtgaaagga
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387

<210> 2439<211> 391<212> DNA<213> Homo sapien

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180ggagctctga ggctcacagc tggcagtcta gtccactca gtctctactt gagaattct
240ttcttttgaa gtacagcaga ggccttagag ctgactcttc taatgtatta gatcttcag
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391

<210> 2440<211> 402<212> DNA<213> Homo sapien

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300cctgtaatcc cagcactttg ggagggttgc ggtggatcac ttgaggtcag gagttcgaga
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402

<210> 2441<211> 387<212> DNA<213> Homo sapien

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387

<210> 2442<211> 391<212> DNA<213> Homo sapien

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120ccgcttccctg ctgccatgga agccaacagt ttccaccggc gggagacctg gcacagacct
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240ctcctcagcc tctgggctcc cgggcccggc cagatggggc agctccacag ggccctcgcc
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391

<210> 2443<211> 404<212> DNA<213> Homo sapien

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404

<210> 2444<211> 395<212> DNA<213> Homo sapien
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240aaccactgcc aggaccaatg ggaaaggaaa tccaggtgag cagtcgccga gccctgagca
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360tgggtgttggg gaactggatc tagacaaagg gccag
395

<210> 2445<211> 393<212> DNA<213> Homo sapien
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120agctgacaca gacactccca agaaactaat gtttcgcaga ctgaaaatta taagtgaaaa
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240ggatcttgat caattagaaa atgtccctgt agaggaaagag gaagaattgc agtcacaaca
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393

<210> 2446<211> 404<212> DNA<213> Homo sapien
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404

<210> 2447<211> 402<212> DNA<213> Homo sapien
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402

<210> 2448<211> 392<212> DNA<213> Homo sapien
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392

<210> 2449<211> 402<212> DNA<213> Homo sapien
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120tgaggacag acagagacat ggggctgatg aatgccattg ggcttcagcc ccggaaccct
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402

<210> 2450<211> 393<212> DNA<213> Homo sapien

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120tgagtcattg gaggagacat cccaaaggcg ccagctcccc tctgccctaa actgaaatta
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393

<210> 2451<211> 392<212> DNA<213> Homo sapien

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120tcggagggat cacgagacac agaacttggg ggggtgtgca cgctggcagg tggcctctgc
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392

<210> 2452<211> 404<212> DNA<213> Homo sapien

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404

<210> 2453<211> 394<212> DNA<213> Homo sapien

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120gaggggtctg gttactgggtg ccactgggct tcttggcaga gctgtacaca aagaatttca
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394

<210> 2454<211> 396<212> DNA<213> Homo sapien

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396

<210> 2455<211> 393<212> DNA<213> Homo sapien

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60ggagagctgc gatgtgaact gccctcccc tcgcatcccc caggccacca acggcagctc
120ttctgccttg tccatggcat aggccataga ccaggctcct gctgctcaca cctgggcctc
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393

<210> 2456<211> 392<212> DNA<213> Homo sapien

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120tgcacccaag accaaagaaa agaatacga gaaagtggat cacagggcgc ctggcgctga
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392

<210> 2457<211> 401<212> DNA<213> Homo sapien

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401

<210> 2458<211> 403<212> DNA<213> Homo sapien

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240aaggaacgct tacatcaact tgttatgaac aagaaagata agaaaatagc tatggacatt
300ttgaattatg tcgggagagc tgatggaaaa agaggctcct ggaggactgg taaaactgaa
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403

<210> 2459<211> 399<212> DNA<213> Homo sapien

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120gaattcaaac caaatgctga aggaaatggg ggagagatta aaacaagaat gccgaaattt
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399

<210> 2460<211> 397<212> DNA<213> Homo sapien

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240aaacctcggg atctgaattt gaccatcaca ttgtatcatg gctccgttgt ggagagagac
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397

<210> 2461<211> 386<212> DNA<213> Homo sapien

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120agtgtcaca gaacaagcag agcaagagag gaaagagcag gttctacctc agctggaggc
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386

<210> 2462<211> 392<212> DNA<213> Homo sapien

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120ggaggggcatc tccagggtta ccatcattga tcttgatgcc catcagggca atgggcatga
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240cccaggggac cgctttgcc aagcaggccat caggcggaag gtggagctgg agtggggcac
300agaggatgat gactacctgg ataagggtga gaggaacatc aagaaatccc tccaggagca
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392

<210> 2463<211> 385<212> DNA<213> Homo sapien

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120ccacatccaa cagtattcgg acatagagga ctttcgacaa gccacggcag cctcttcctg
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385

<210> 2464<211> 386<212> DNA<213> Homo sapien

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120agagtacacc aaatgtgaca tcctttcacc aatatagatt acttcatacc acattgtcaa
180ggaaaggact agaagaattt ttgatgacc caaaaaactg ggggcaagaa aaagtaaaat
240ctggagcagc atggacctgt cagcaactaa ggaacaaaag taatgaagat ttacacaaac
300tttggtatgt cttactgaaa gaaagaaaca tgcttctaac cctagagcag gaggccaagc
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386

<210> 2465<211> 391<212> DNA<213> Homo sapien

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120agagtacacc aaatgtgaca tcctttcacc aatatagatt acttcatacc acattgtcaa
180ggaaaggact agaagaattt ttgatgacc caaaaaactg ggggcaagaa aaagtaaaat
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391

<210> 2466<211> 397<212> DNA<213> Homo sapien

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397

<210> 2467<211> 397<212> DNA<213> Homo sapien

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120atgctgaatt gattgaagat tatcggtatc aacagcagca gcaatgtgca atggccccac
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397

<210> 2468<211> 390<212> DNA<213> Homo sapien

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390

<210> 2469<211> 387<212> DNA<213> Homo sapien

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387

<210> 2470<211> 383<212> DNA<213> Homo sapien

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383

<210> 2471<211> 371<212> DNA<213> Homo sapien

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371

<210> 2472<211> 383<212> DNA<213> Homo sapien

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120tattttcaagg aaaaacacaa agaaatttca caatgaatta aattaacagc cttggtagct
180aggttaaaaa atttaagca aagaaataaa agttgatacc aggttagcaa agacaaggta
240aaaaatagta ctaagacact tcaggacctt taaggatatt tgaagaggtt tcaatattta
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383

<210> 2473<211> 383<212> DNA<213> Homo sapien

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180gcaattaccc aatgacttt ttaaaagtat gagaatttgc ctggctgaac gttttttaat
240taatgccgtg agttaacatt aataactatt catagcttag tgagctgggc ttgaggtggg
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383

<210> 2474<211> 381<212> DNA<213> Homo sapien

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180aggtaaagaa ttaaggggtcc tgtttcattt acttcttctc tgccttgacc tgtccttcat
240taattccaca aatacttact gaccactgca tggcaggctc tatgctgagc actgtgaata
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381

<210> 2475<211> 374<212> DNA<213> Homo sapien

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360ttgaagatgc ttag

374

<210> 2476<211> 381<212> DNA<213> Homo sapien

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120gtaattccac ctattcggga ggctgaatca agagaatcac ttgaacccgg gagggcgagg
180ttgcagagag catagaagga gccactgcac tctagcctgg atgacataat gaggtcagc
240ctatcatggt aatagtagcc tgaacctatg tgaaatctaa gaacatataa cactaatttt
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360tctctgtatt gatagactgg c

381

<210> 2477<211> 380<212> DNA<213> Homo sapien

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120tattaccatt taactgcagc aagtaaagac gttaatagt aggtttttgg gaatgtggta
180aaaccgggag gtatatttga ctttgtccaa gttatctgat gaggcagatc agctaagca
240aaatacagtg ggttgctccc tactatcact gggacctaga gatttcatct acatctctga
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380

<210> 2478<211> 374<212> DNA<213> Homo sapien

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120aacactaact ctctttaagc ctgatcacct cccacattct aatagggctt ccattgccag
180ttgttttcta gaatctttcc ttccattttt cagggagcgc tgaatgttgc tttaaatgca
240gcgtttttaa gtgggtataa gctttttatg tgacttaaat tacataaaca tttcagttgt
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374

<210> 2479<211> 373<212> DNA<213> Homo sapien

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120catgtgcagt tttggctgat aattgaagga aaaatatcaa atactttgaa tttttttct
180cttttttcaa accctctgca gaggtaggaa ggtatgaatt tcttttttat gtcaagatgc
240aaaaacaaat catgatgctt ttgttgggag aatttttgta ttcagtattt tgtatgtacc
300tttttttttt ttaaattgga aagcccaatt aggttaaaca ttttaacttg cttgactcca
360gtgtaaaatg aan

373

<210> 2480<211> 367<212> DNA<213> Homo sapien

ggcacgaggt gactctagct tctggtacga gcccttcagt tcacctctc gccctgctca
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120gcccaccag gactttccga ggctcacaga ttctttgaaa tggacgtgag caciaacgcc

180cagccccgac agccagggat cagatcgggt ttcacttctt aggagggagg atgtactgca
240ggggaggccc acgtggctgc cccaggcctg gccagcctct gtgacccaac aggactgact
300gttttacggg atggccacac ggtaccctgc aggtcatcc atggtgggac cttgatgctc
360cttttgtg

367

<210> 2481<211> 384<212> DNA<213> Homo sapien

gtagcacgaa ggcccactcc aaggttctgg ccaggctgga ctgtaacagc agtaccagca
60ccaggaatgg ggccaccatg tgatctttgg gtagaaatga cttttttggg cttgagtttg
120tcttttctaga atgcacgtga tcccttatcc cagggaggtt gtaaagacca cactgtggag
180atccttaaat tgatgacgat ggcctatcga agccttgta ccgcacagcc cctaacagtt
240tacaaaacgc gtccatgatg aggacgggtc cattagagcc cccaacgttc tgtgaagtgg
300gcggcacagg ttggggaagg ggacttaatg gggttatgta atttgcata aatcacaga
360acctgaagtg gtgggtgaga ttca

384

<210> 2482<211> 383<212> DNA<213> Homo sapien

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120gggtagacag agccacctca gcatcctgat ggatgataca agaaattgtt acttcttagt
180atggaagtgt ctttaaggaca cgtctccatg atattttggg gaacccaaag tgctttatcc
240tcaacaaaat gttcctctgt tcccagttaa agtaatatc cctgcttcca agtaagcaag
300actgttcact aaagaaggaa ctttttagaa aactaatctc ctttatcatc caattttagt
360tctgcatggt ccgaggtagc cag

383

<210> 2483<211> 379<212> DNA<213> Homo sapien

cgttgctgtc ggtctcccca gtagctggga ctacagacac acaccaccac gcctagctaa
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120gacctccggt aatccgcaca ccttggcctc caaaagtgtt gggtttacag gcgtagacca
180ccatgcctgg cccattagg ttactttcat tccaccttca tgcttatggc cactcctctt
240atgctgctgg gtggacatag agcttcacca ccctcctccc gcatgtcctc tgtgtctgct
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360ccagcaacct gggagggaa

379

<210> 2484<211> 377<212> DNA<213> Homo sapien

cgttgctgtc ggaaggtttg gtattgtaaa tgtgctgttg ttccaaagaa aaattagcag
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120aaaacatgta aaagccaaca aaacccttga aaatattttg catatggatg tctgtttcac
180gtttcaactg aagatgtata gagcacctct gatgatgagg aagataccat gctaggcagt
240actttcaaga acgtgagttc ttatttctgc aggccttttg tgcccccttt taaatgttag
300catttattag gtacaaaacta gtggggaagg tttttttaa aagttttgca gtcttgtaat
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377

<210> 2485<211> 375<212> DNA<213> Homo sapien

cgctgctgtc gtatagaact aaaatgtctt aaaccacgct tagtttcata tttagaacia
60aaaaatccct aaaccattct gtttaactgt tagaaacct tctgtaaaat gaagaaaatg
120ggagacatgg aaactgattg ggggagttta gctttactct catttttctc agccattaag
180aagctggaag tatgtttctt taaagaagaa aaattcacag tgtgccatct tatttctctt
240ttctgccact ttttaaaaat cttcttattc agaagttcag caaagtaaac caagtctggc
300ctaatacttt gatttacttg aatacctcta cgtatcttaa taattccttt aattttacat
360tgtgtaaaata tttat

375

<210> 2486<211> 372<212> DNA<213> Homo sapien

ggcacgagat tgtactggga agaatgaaga ggtgatacct ttactagatc cttcagacac
60atctatgaga agatttgctt atttaaaagt ctgcccactg aggataggga aaggattaag
120gattttttcca cctcctctta gtaactcctg aattaccaac atcaacttct ttctctccgt
180tcttgaagga accttgggga atcatcttca tccgtagtta cgctttcctg aaccttctca
240gtgggtttaca tgccctctgaa actatgtgca atatttttg ttgacacttg tatccatcct

300taagaaatta gtgcagattg cagatgttct gtcttccatc ccaaacaagc ctgccatgag
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372

<210> 2487<211> 155<212> DNA<213> Homo sapien

ggcacgagct ccgcgcggcc tcgggtccctt gcgcgcggccg cccacaaca aaactcagcg
60cagcgctccc gggcgcccg ttcagagcga cctgcggctc agagcggagg ggagactgac
120cggagcgcgg atcgggacag cggccgggac agcgg

155

<210> 2488<211> 375<212> DNA<213> Homo sapien

cagctcatat ctggctaaca gtggcactat gggagtttat atgatctgtg cattattctg
60tggcatcacc ttctaagagc agagatgtga cccaataccc cttgttttcc ttaaagataa
120ccattaaatt atatccatga atttatatca ccgtccttga ctttatacgt agatttttct
180aattctgtca acccttaggg taatgaataa cttaaattggc caatgcctct gaataacatc
240atacttctt ttgtttctcc aaaaattgaa tcaagatgcc agggcaacta agattttctt
300caatttgcta agttaagggt cagtgtattc attagccaat ggttctgtat tttattcatt
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375

<210> 2489<211> 379<212> DNA<213> Homo sapien

gcggattgtg acaaaatctt tcattaacaa ggggagtttc ggtgaagtgg aggtttgggg
60aaaggcgagg aagtcggtct ggagcaagca agcaaagtgc ggaagctgta ctgggattct
120tctagaaagt ggggtgggaa aggaggtagg gagggcgtgt gcagggacga gatctgtgtc
180agaacgtgcg tgtgagcggg taaaaaccc gagagaggcg tgagcagcgc tgtgtttgcg
240agcgggagcg aggggcgccc gctgggggtgt gtgctcctga gctcttcaga aaccaggctg
300ctttcaggaa cattgctgtg gattcccagg gcctattcca ctagaagcaa gatggctgaa
360ctcaatactc atgtgaatg

379

<210> 2490<211> 372<212> DNA<213> Homo sapien

catctttggc gtaggccatg aaagacagga tgctcattgg gtgttctgct gagtgaggaa
60tgctgcctat tccctgcag tacgccctac ccagggatgt gtgttgaaga gccctggagg
120aaatggaccc agttttgcca catatcagta ttacgctgaa gatcaggtga ctggtatgcc
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240cctgagaggt ttgcaatttg ggaagccatg aaaaaggctt ttatatcttg gaaagatgga
300gagagggaca taggatcggg gactcctaca tgacatgaat aggctggaga ttgggaatcg
360gccatccacc an

372

<210> 2491<211> 375<212> DNA<213> Homo sapien

ggcacgagaa actgtcagcc cattaagtgt tcattcttaa tgtgaaattt ctgatgaag
60gcaatttagc ttaatttgcc aagacatctc ttcattgtct ggagggctgc tgggggaagt
120agagctggaa tccattggag ccaccaatct gcagaagtct agaacacaaa ggacacagag
180tgggttttgt gggtcattgt ggcatttgtc aaggaaaagc aacattgccc tctaaatgac
240tcccacttct gttctggaaa aaacgcatca tcattcatgc caccatccca atagacatag
300gaagcaattt ctcttcaggt tttgagatgg tgcaagcatt gacttttctt tctacagagg
360gctgggatgg ggggg

375

<210> 2492<211> 382<212> DNA<213> Homo sapien

accgcacgag ggaaaatcaa acttcttggg tgttctagct ttgaagcttt tgcttcagta
60atatttgttt aaagaaccag atcacatacc atttatcaaa gtctttactt aagccagact
120actttgcaga catacatatt tggaaaacag actgtttctt gttactaga tagaatctgt
180attgtagtaa gaaactactt acaagggtggc ttctttcttg ctttgctact ctatgtataa
240ctcaataata tatgtatggg cacagggtcc ctggagatgg ttattttctt tatgacagac
300acatgagtat gcacctctct ctagtctct gatgtcactg cagctacagt ctcttctcac
360tctgtttttg agagccttca aa

382

<210> 2493<211> 375<212> DNA<213> Homo sapien

cgttgctgtc gtgagaagc aatgtcaggt gtgggactcc ttctgcccct gcagtgggtg
60ttacgggcgg tgtgccctgg cgagcaagct ttgattcttg gttctttgag ctcgtttcag

120aggctgagtc cccacatcag ctttagttct tggacttccc tgtattaagc aagaattagg
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240cttctcttct gttttctttg gctgtatcag ccgaaccagg agaggcctgg gctgcgacta
300aggagaaaaga aatcggggggt ttctgagagc agatggtgcc ttgtgggtg cagggctttt
360gtggaaattg tcacg

375

<210> 2494<211> 371<212> DNA<213> Homo sapien

cgttgctgtc gaaagttcca tataatgaat taaaagaaaa gtgctgtgaa gaaaacaaat
60tcaggatggg aataggaggt ccaagggagt gcaaggtgtt ttcattttga atgtgggtgg
120ctgggaaagc ctactaaaaa tttagaaaag acttgatgaa agagaggagt gagccatgca
180gccatttggg ggacaacttc caggcagacg gccggaggca gcagtgcag ggctgagtcg
240gggcagtgtg tatgcctcct gtgtagcaaa cccagggcac cttttattaa gccaactatt
300agggtttcca ctgtttggag gtggctcctg ttcttggaga cccccaactc tgatgttttt
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371

<210> 2495<211> 368<212> DNA<213> Homo sapien

ccgttgctgt cgggcgagtc tttaaaggag tggctcatct ttcctctccc tggggcattt
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120agagaggtta gggccctggg aaaggtggga gatcagccag agacaggttt ccagaacag
180aatgtctggc ctttgtgggt aggagggact gtggtatgag ccgcagaagc gggccagggg
240taaacctccc tgtgcgtcct tccttcagcc tggctcctgag ggtgacctt tgatcctggg
300ttctccaggt agggctgtga gctgtgagtt ggatcctttt ggtgaaatgg tctctctcat
360ctggcctg

368

<210> 2496<211> 378<212> DNA<213> Homo sapien

ggcagagcc aaggcctggt ggccctcggt cccctgccc tcgtcaccat cctgtccttg
60gctggccgtg aggactcccc tctcaccac tgggtccac agggctgagg tgggcagtag
120agggcatagg tyggtacatg tcccgggcaa ggtctctcgg ggggacagaa gtgagtcag
180ggagtgggtg ggcctgggag tccctcactc aaaatgccgt ggggtgagga cggtagggac
240aggggtggga ctgggttctg gtttagagtc agtaatgtta gggcgagtg ggcagggggg
300caggacatct ccagccggtg gtgaggaagc atgggtgggt ctcctccaca ggacgggagc
360tgggngaggg gtcctggg

378

<210> 2497<211> 384<212> DNA<213> Homo sapien

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120gaggtgctgg ccacctatgg aactgataaa cctgacactc gctttggaat gaagattata
180gatatcagtg atgtgttag aaacacagag attggatttc ttcaagatgc acttaataag
240ccccatggag ctgtgaaagc catatgtatc cctgaaggag caaaatactt aaaaaggaag
300gacattgaat ccattacaaa ctttgcagct gaccatttta atcaggaaat cttacctga
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384

<210> 2498<211> 371<212> DNA<213> Homo sapien

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120gaggttgaag atctctatga gcttttgaag cttgttaagg aaaaagaaga agtagagggg
180atatcagtag gtgctatact ttctgactat cagcgtattc gagtggaaaa tgtgtgtaaa
240aggcttaatc tccagccttt agcttatctt tggcagagaa accaggaaga tttgtcaga
300gagatgatat catctaacat tcaagcaatg atcatcaaag tagcagcttt gggtttagat
360cctgataagc a

371

<210> 2499<211> 377<212> DNA<213> Homo sapien

gtccaagctg ctgcgcttgg agcaatgacg tccatggtgt gtaagggttg caaagattct
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120cagactaaag atgctgctac aggaactgct tctataattg tcaataatga aggccagaat
180atcattgtca tagtggctgg agcaaattha cttttgaata cggaggatct gagggcagca

240gccaatgtca ttagcagagc caaagtcattg gtctgccagc tcgaaataac tccagcaact
300tcttttgaag ccctaacaat ggcccgcagg agtggagtga aaaccttggt caatccagcc
360cctgcccattg ctgacct

377

<210> 2500<211> 346<212> DNA<213> Homo sapien

tttcgtttgc gagaagacga cagaaaggca aggaactagt gtgtatcaag ccataactaag
60ctggagttta gcaggacaaa ggcaactaa atgtagaaca taacatatca gctgaatatg
120tctatccagg actgtttttc tagaacataa atcatggagc tccttgacag tgtatccact
180gttttttggg tttataaaaa ccaactagaa tttagactta caaagaaatt attattcctt
240ttgggtgtcc acataaagca gtccagggct atcatatggc taaaatcaag atatttggtt
300catctctggg atgtatttat aaagtcaact tatcagccat taagat

346

<210> 2501<211> 344<212> DNA<213> Homo sapien

tacttttctgc gagaagacga cagaaggggg cggaggggca ccttacttac ctcagggcaa
60ctcccccaac actggagaca gtctgttcca aacaggagtg ggagacgaga ctgaatggag
120tttgataat gaaaaagaat gtctgggacc aatttaatat tcatatccag ttagtgagga
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240cagagacaga cttcatgctt taggtgtttc aaccagggc ctctctggct cctcggatgc
300ccttttccat tgggcaggct acaatgccc tggttatgcc cagt

344

<210> 2502<211> 338<212> DNA<213> Homo sapien

agggctatgg ctgctagaag acgacagaag ggataacca acctcctaga ctaacaacac
60agtcattcat cttacctcca agaaaaacat aacccaacc agctatttgc cctgtccca
120gtagaggcag acacacctga atgtgctatg aagagacaag ccttagggga gaaacagtgt
180gatttggaca aatcattcta taacagcga acctttcgat gtgttcaacg gctgcagaaa
240gcacaccaca ggtgagagac cagaagtgc ccaaggggtt ttatacaaaa aaactatatt
300taggtatagg gcacagtcta cgtagaaaac ctttcaag

338

<210> 2503<211> 335<212> DNA<213> Homo sapien

tacggctgcg agaagacgac agaacaaaac ccctctgctc tcctctcgca gaggtcatcc
60ctgagtcagg gtggcagtc cttcccgagg ggcagaggag agtgccatg gttgaggctg
120gggactctgc aactggggga ggcacggtaa aattaacacc tgctgatccc atgggccttg
180gacagggttc ttgacttttt gggggccgct gtcaaagggt gagtataata acctcctccc
240cacagcaaat taataaatgg catgtgcaca tacagcgctt gcctcatgtc tcacatgata
300aacctgattt ctgggcactg gctgagcgac tatgg

335

<210> 2504<211> 475<212> DNA<213> Homo sapien

acttgaactt nnaaggatc ccctcgatc gctcagatct ccaactcctc ctcttcttc
60taagccatca agtattcctc ggaaatcatc tgtggatctc aatcaagtta gcatgctttc
120tccagctgcc ctatcacctg ccagctcatc acaaagatct ggaactccta agccatctac
180tcctacacca accccttcat cgaccccaaca ccctcctgat gctcagagct caactcctag
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300aactcagttt gctcagcagc aaaggctctt gagccaggca atgctgttaa caaccattcc
360tctttccacc atggtaacat ctataactcc aggaaccacg gccaccacag tcatggcaaa
420ctctgctgga cttaacttca tcaatgtagt gggctctgtt tgtggggccc aggct

475

<210> 2505<211> 446<212> DNA<213> Homo sapien

gacaattctc anggcctttn tggaagatcc catcganncg gttgcggcac gagaatgctt
60ttgccattat acctatattt tttagaacag caagccctat ttgaccactc tcttcagcct
120gtgtgttctt gctgttttga agtaatcaaa tgctgtgcat ggtattttac ctgagctgca
180acctgttatg gacttgaact tctgtttaag ttgaaagcaa gactccctga gtataaagga
240aaaacagcaa aacaaaaagc aaacaaaaaa aaactgcaa agtctaaaat acccattggg
300gatgtttttt aaaaaaatct tgctttcagc tttcaggagg taatattctt tgttttaatt
360tgataattgg atatggttga ttatatttgg gtttaactg cggagcttcc atgtttactg
420gtaattagtc ttaaaatatt ttttac

446

<210> 2506<211> 444<212> DNA<213> Homo sapien

tagctccatc ttatacgac gacccgctcg attccaagat cgctgctgtc ggcattggaag
60gatgcatgta tgactgagga aaagtcattc agtattgagt tcatttgcat tagaggaatt
120tcatagtttta aaacttgat atctttacct atccttcgta tgtttcttc ttaagcatat
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240ttttccttac ctattattat tttcttccat gctttacaac acatttttta aactaccttg
300ttcttaata attacacgga cctgcttctg tgtactttca cagaatcttt gacagttaaa
360aattgtatgt tatataaaaa ttgacaagc ttctacagtt aggaaaagcc tttagaatc
420tgccctcccc aaaccgtatg ttat

444

<210> 2507<211> 431<212> DNA<213> Homo sapien

ttcaaggacc acatgtgttc tctattttgc ctttaaattt ttgtgaacca attttaaata
60cattctcctt ttgcccctgg attgttgaca tgagtggaaat acttggtttc tttctttact
120tatcaaaaaga cagcactaca gatatcatat tgaggattaa tttatcccc ctacccccag
180cctgacaaat attgttacca tgaagatagt tttcctcaat ggacttcaaa ttgcatctag
240aattagtggg gcttttgat cttctgcaga cactgtgggt agcccatcaa aatgtaagct
300gtgctcctct catttttatt tttatttttt tgggagagaa tatttcaaat gaacacgtgc
360accccatcat cactggaggc aaatttcagc atagatctgt aggattttta gaagaccgtg
420ggccattgcc c

431

<210> 2508<211> 433<212> DNA<213> Homo sapien

cgttgctgtc ggccggcagg aaatttaaac tgaagccgcg gccgaaaacg ccaagagatt
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120gcgaatgtaa tacggaggcc tctgaggaag gactacggag gccgagaagg agccggcatt
180tgatgagcga accgggaaag ggagacgatt gcctcgagct ggagagttcc atggctgaga
240gtaggctccg ggccccggac ctaggagttt ccagggtgtc aggaaaatgc cagaagaact
300caccaggtgc caggaagcat cccttttccg gaaagtcctt ttacttggat ctgctgctg
360gcaagaatct ccagtttttg acgngggcca ttcagcaact gggtagggta attgaggggt
420ttctgagcaa aga

433

<210> 2509<211> 425<212> DNA<213> Homo sapien

tagatatgca tgcttgagga aacttgcttt tactgttttc ctacttgat cccagttca
60gttgaattta caaggaccta caagatggtc atgtttgtct tggtagtgc taccacaatt
120ttagtgtttc tttctttatt ttaaatcagt aattattcag ttgattgttt atactatata
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300gctaggaaga gggtcagaaa gaagctagag ggaggtcagg agaagggtaa caggaggat
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420gaatn

425

<210> 2510<211> 423<212> DNA<213> Homo sapien

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120tatcaaaaaga cagcactaca gatatcatat tgaggattaa tttatcccc ctacccccag
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240aattagtggg gcttttgat cttctgcaga cactgtgggt agcccatcaa aatgtaagct
300gtgctcctct catttttatt tttatttttt tgggagagaa tatttcaaat gaacacgtgc
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420ggc

423

<210> 2511<211> 421<212> DNA<213> Homo sapien

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120agagagagag agagagagag agagagagag agagagagag agagacacac cctctctctc
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300tattcccccc cccctctct ctctctcaca caaatttttt ctttttttgc tctgtgtgcct
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420c

421

<210> 2512<211> 422<212> DNA<213> Homo sapien

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240gaaaatgggg aacaaaagaa aaaatttgga gcggattttc tttttcctg gtaagggggg
300gagattttcc caaccggag gggccccccc ctggtttgga acctggaacc acatccccgg
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420gg

422

<210> 2513<211> 422<212> DNA<213> Homo sapien

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120tgggctcggc ctgctctgc ggggacttct gtatgcaccc cgtgcagtgt ccccgacagg
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240tcccagccgt gcaactggcg cgaattcggc gctgagagcg ggagaggag agaaaaacac
300tttgtatttt ccaggttgcc tttgcaggcg cccgcatttc taacctgttc ttcctcttgg
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420at

422

<210> 2514<211> 422<212> DNA<213> Homo sapien

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240aagttcattt aagtcaccag acacagtgtg ttttaagcaga ggaaaattat tagttgaaaa
300agctatcaag gaccatgatt ttattccttc aaatagtata ttatcaaag ccttgtcatg
360gggagtaaaa attcttcata ttgatgacat tagatactac attgaacaaa agaaaaaaga
420gt

422

<210> 2515<211> 166<212> DNA<213> Homo sapien

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166

<210> 2516<211> 415<212> DNA<213> Homo sapien

ggcacgagga gagagagaga actagtctcg agagcagnnn nntttttttt tttttttttt
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120cctttttacc ctttttttcc ccccggggtt aaaaggggga aaactcttgg gggttttccc
180ccccctttt aaaaaaggaa accccccctt tttaaaccgt gtttttttcc cccctccga
240ggagggggaa tttactcca aaaaccctt ttttttaaaa aaaaaaacc ctgggggaat
300tttttttttc ccgggtttta aagaccccc aaaaaaaaaa aagggttttc cccacattt
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415

<210> 2517<211> 416<212> DNA<213> Homo sapien

cgttgctgtc gaagaatagg agagaataga ttatgctctt ttaaacctga gagagggttg
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120acagaaatag ccagaggtaa tggatttctt ctaccaaatt tgaaggatta gctctgtaga
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240tatattgagag gcagtttaag gtgcttcatc aactgtggat ggaatcctca aagtcagtc
300tctgattggc tgccaggggc ctaaacaggt tgaatatatt aatcaactat acaggagtca
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416

<210> 2518<211> 413<212> DNA<213> Homo sapien

ccatcgattc gaattccgtt gctgtcggcc tcatttgcta tcccagcatc tcttaaaact
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120aaaacatgaa tcttgggagt ctacattttc ttatcaccag gagctggact gccatctcct
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240aggcctgagg tcggcggact gcctgagggtc aggaattcaa gaccagcctg gccaacatgg
300caaaacccca tctctactaa aaataaaaaa attattagct gggcatgggtg gtgtgtgcct
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413

<210> 2519<211> 416<212> DNA<213> Homo sapien

ggcagagat tttaatcagc tatgtcattt ctgcgtctcg ttgtatactc ctggaaggctc
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120gcactgtcag caagtatctg ctgaaacaag tatttttgaa tcittagctt ttctgtagct
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416

<210> 2520<211> 413<212> DNA<213> Homo sapien

cgttgtgtc ggaagaattc gcggccgcag gagttttcca gtcccagcta cccgggaggc
60tgcggcaaga ggattgcttg agcccaggag ttcgagtcca acctgggcaa aagagtgaga
120ccccatctct aaaacaaaa aggtacctta gaaggcacc tgggtggcta accttttaa
180ggcaggggag tgacacgtag gacacattgg gaatgtcttg gctactacat gtacgttct
240gggatatatg tgcccagagg gagaagcact gagcctgaag aaactagatg agtctcagaa
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413

<210> 2521<211> 166<212> DNA<213> Homo sapien

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60tcaaaggaaa tcacactatt aagcagcttg gttttgacat gttatgttg ggatcatctt
120tcatgtcaat acatagatta atcttttatt tcaaagtct acataa

166

<210> 2522<211> 413<212> DNA<213> Homo sapien

cttttgttac ctaaataatg agtaggatct tgttttgttt tatcaccagc acacagattg
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300gccttttat ttcataccat ctctgcctta taagtggntt agtgctcagt tggctctagt
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413

<210> 2523<211> 416<212> DNA<213> Homo sapien

ctgggggtgaa tgcacgtcag tggaggcaga atcattctgt ctgaatgaat ggagtttcca
60ggcccccaact ggccctctgt gtgagggtct gcagggttg gcaggacagg tctttctctc
120cggcgagagc acccaccctg accggctgct ggatgagggc accaaagctc gctaggaggg
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300ccacctgcca tagtngcag gtgcgggagc cagggcggca gtggcctcg ggctgggtg
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416

<210> 2524<211> 414<212> DNA<213> Homo sapien

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120ctatgattgc accactgcac tccaggcaac agagtgcagc cctgtcttaa aaaaagaagg
180gagaaagtgt caaatggtga tgaggctctg gggggaaata gagaatgggg atcacagtg

240tggatggtgg tattccctca ccaagatgtg acatgtaagc acgccgctgg gaggagaggg
300tgcgacccgc gtggaatttc cacaaccacc ctccgtcgtg aggccacacc caatgcagag
360gccgagaggg gggcacccca atcccccgga actgggattg tgaaggctag gtcc
414

<210> 2525<211> 413<212> DNA<213> Homo sapien

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60aagtccactg cctttgcccc agcacagaag agggccctgc caccctaggg acgggccaag
120ggctggtcag gctgaagtgc cctccttagc agggccctt cccactcagc ccgcggtgtg
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240tgcattctcag caaagccctt cccaggggtt gatcgattga gcaggacagc cctgctcctg
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413

<210> 2526<211> 416<212> DNA<213> Homo sapien

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360gggaacgctt cagcccaatt cgggtcctcc aattactgag gcatacgtaa cagttg
416

<210> 2527<211> 408<212> DNA<213> Homo sapien

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180attttccaat aagagaatat aacaatttct gtacactatg gaagagtttg acttgggtgaa
240aaccttacac aaaacttcat ctctctgtagg atctgatgaa aattctcttc attctcttgg
300actgaactta aatactgata ggtaagaatg ggatttaaaa aaaatgtacc aaatcagaat
360aaccttattt gcatacgttt atcaacttat ccaaatagtg tcgtagtg
408

<210> 2528<211> 409<212> DNA<213> Homo sapien

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120ttgtgtaaat acttctgcaa aggtactgat gctgtaaagt caaacagtt ttgtggaact
180gtgaattttt tttctttttt cttttttttt tccttttttt tttggaataa accccttga
240aaaaccaatt ttgctgcctg aaaaagaagg gaaaaaaaaa cccagtgct ttttttaaaa
300aaaaaccttt tgggaagggt ttttgggttt tccttaacat gaacccctt gaaacgtttg
360gcggggccaac ctcaaagctg ggacaaaatt tttttttttt ggaaatgga
409

<210> 2529<211> 408<212> DNA<213> Homo sapien

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120gaggcacctt tattgctgag gaaatggaag agttgaatag gatttaggga tgaggatact
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300ctattggagt gtgacagaag agagaatgtg aggttagtt gtggcacaga ggagaacctg
360tggagtgagg ttgtgtctac ccgtctaggc ttcaggggagc cgaagact
408

<210> 2530<211> 165<212> DNA<213> Homo sapien

ctcccttggc gatctgcagg aacactagta atgactggaa ttactccgtg atctttgatg
60actattacac ataacagcac tctagcact tttcttactg gcatggactt cctcatggac
120tgctacttca tggatgatag ctccattgct ttgggtaggg attta
165

<210> 2531<211> 409<212> DNA<213> Homo sapien

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60gtaagtcttg tgtcaaagca ggaatctgat cagaggttca gaattggaag tacaatttca
120ttgcttttgc aatttctaca aattaatttt aaagtgtcag aaaaagggtga cggcaaggac
180atgcattgca atttgcaggg ggaattgtca agtgaggact tcatcacata tgacacgaga
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300aatttggtg gagcagagtc gctttgaagc cttggtccga tctaattcta ttgtattggt
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409

<210> 2532<211> 409<212> DNA<213> Homo sapien

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120ttttcatccc atctagcaag cacagtgtta attttagaaa ttatagaaga aaaaatcagc
180aaggagtgtg ggaaaactgc atgccccagg cctccccgc cccaggtga attggaagcc
240ctggaatggg ccgaggcaca ccaggcagct gatctgggtg catgtgggcc acagaccact
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409

<210> 2533<211> 412<212> DNA<213> Homo sapien

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120gagagagaga gagagagaga gagagagaga gagagcgcgc ccccccccc tctatacacc
180cacacgcgcg cgccccccc tatctctctc ttctctctca ctgcgcgcgac ttttgtgttt
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300ctttgcgcgc cccccccat atatctctc ccccccccc cctctctttt tctgtgtgtg
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412

<210> 2534<211> 411<212> DNA<213> Homo sapien

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180gaaccgcgtg cgtgccaaagc caggcacgag gaggtggcag gcatcccgac ccccggtggg
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411

<210> 2535<211> 406<212> DNA<213> Homo sapien

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240atatagcaga atattattta aatattttc atctcgtgac ccattagcca ccaagtatgc
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406

<210> 2536<211> 404<212> DNA<213> Homo sapien

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120gtttaccccc agcccccttt tttttgggaa aaaaaaaccc ctccctcttt ttaaaaaaaa
180cccttttctt tttttttttt ttttaaaaaa aaaaaagggg gggggggaaa aaaaaaaa
240aagggggggg ccccccccc cccccctttt ttttaggggg gggcttttgt ttttttaaaa
300aagttttttt ccgggggggc cctttttatt ttccccctta aaacccccat tgggggggga
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404

<210> 2537<211> 403<212> DNA<213> Homo sapien

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60ccagacctca gaagcaccag aatacgttta gtttcaaaaa tgacaagttc gataaaagt
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180ttcttgagtg gcgtgtaaaa tacagcaaat acaaaccatt atcaaacct aaaaagtgtg
240ttaaatgttt acaaaagaca gtgaaggatt cttatcacat aatgtgcagg ccatgtgcct
300gtgaacttga agtttgcgca aaatgtggaa agaaagaaga cattgttatt ccgttgaata
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403

<210> 2538<211> 403<212> DNA<213> Homo sapien

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240gttgggtttg gaccaaccac acttaaatgc cggcgaaaa accgcttttt tgggaaaatt
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403

<210> 2539<211> 406<212> DNA<213> Homo sapien

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120cggggccccc agaaaaaccc gagaaaattt ttgtgttaaa aaacacaaga ttttggcccc
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300cccccccgcg ggggggtttt aaaaaagat atgggggggg ggccccctcc tcctaccca
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406

<210> 2540<211> 405<212> DNA<213> Homo sapien

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120aagattgcac cactgcactc cagcctgggc gacagagtga gactccatct tggggggaaa
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300gtgtggagt tttcagaaat tttgatccta aaagcctttt cagaaactca aagctttcag
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405

<210> 2541<211> 403<212> DNA<213> Homo sapien

ggcacgagct atctttattt tgggcacact atagcttttg ttaattattt ctttgcactt
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403

<210> 2542<211> 407<212> DNA<213> Homo sapien

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120acccttgga gttggaagga cttttcccaa gggccaaagg ggagtggaag tccaaccggc
180cttggttaat aaccattact tttccccag ggaaggacca aacggattct tttttctct
240cctcaagcct cccaaacaaa aggtaaacca gcctgggcct attttaagtt ggacctggcc
300aaaccaagga tttttttaat aaaaaattta aaaggtccac cattagaacc cggataattt
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407

<210> 2543<211> 406<212> DNA<213> Homo sapien

ggnangagtt ccgagccgcc gtaagactgg ttccggcggg ctggtgagga atggagccgg
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120gtaacctggc ggaggtgggt gagcgtgtgc tcaccttctt gcccgccaag gcgttgctgc
180gggtggcctg aatgttcgca tcttaccaca tacagttctt tacatggctg attcagaaac
240tttcattagt ctggaagagt gtcgtggcca taagagagca aggaaaagaa ctagtatgga

300aacagcactt gcccttgaga agctattccc caaacaatgc caagtccttg ggattgtgac
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406

<210> 2544<211> 403<212> DNA<213> Homo sapien

nnctcggcac gagaatccat tcccagggc cccccggctt gtcccagccc ctcttttgc
60tctgaccacg gaggctttct cacagcccag cctgcctgaa gcaaaggagg ctcccgtgct
120ctgggcagct tctgtttccc tctgctgcct gggagctgag gcacccgtgc cagtggcaga
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240agggctctgtg ttctccagga gaatgagggt gttggtccca gaattgggac cggggccccg
300ctggccagcc ctgggccact tcccgggtct ccattgtgctg tgggtggcgt gttccaggcg
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403

<210> 2545<211> 403<212> DNA<213> Homo sapien

cgttgctgct gaagacctgc ctcccatcct ggcagcccag cctgagaccg ttgcattgag
60gcaggcagga gcggcagggt ggctgctctc caggagccca cctgccttga gttcctgccc
120cactgggccc cctccctgct tgggcaatcc tgggaaggct tggaggttcc tgtggacctc
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240ctcttttccct cccctctggt ctccattctc ttcagctccc tacatgggct ggggaggaga
300cacctggtgg gcagagctca ggcagagggt tggatttcag ctccctcact tccggggctg
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403

<210> 2546<211> 404<212> DNA<213> Homo sapien

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120atttcaacgg ccaaaaaact tttttgtata acgagctcta tgtctacaat accagaaagg
180acacctggac caaagttgac ataccagtc cacctccag gcgctgtgct caccacgcgg
240gggtagtgcc tcaaggtggc ggacagctgt gggctcttgg aggggagttt gcctctccca
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360gggaacaagt caactggcca gtccacgac caaatctgcc tta
404

<210> 2547<211> 402<212> DNA<213> Homo sapien

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60gtgcaattgt gatgaaagtc agtgggaacc agtctgtggg aacaatggaa taacttacct
120gtcaccttgt ctacaggat gcaaatcctc aagtgggtatt aaaaagcata cagtgtttta
180taactgtagt tgtgtggaag taactggtct ccagaacaga aattactcag cgcacttgtg
240tgaatgcccc agagataata cttgtacaag gaaatttttc atctatgttg caattcaagt
300cataaactct ttgttctctg caacaggagg taccacattt atcttgttga ctgtgaagat
360tgctcaacct gaattgaaag cacttgcaat gggtttccag tc
402

<210> 2548<211> 399<212> DNA<213> Homo sapien

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120tcagtctcct gccggaagaa atgggttgag cccgaaagga ggctgtctga ggaagggaga
180gggagggcct ggggtgttnn tnnnnntntt tntttnta ctttctttt ttttcttcc
240ttcccttatt tcttctctt tcttttccac tctccctt ctcttactt ctatctcccc
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360ataattaatt ttctctttcc ataactttaa cccatgtat
399

<210> 2549<211> 398<212> DNA<213> Homo sapien

cgttgctgct ggccatgttg ccagactgg ttttgaactc ctggcctcag gtgatctgcc
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120cttccacttgt aaaagaaatt aggctaataa gaagggtgag tttttgagaa atgaaattta
180acttttagcct tttcactagt aaatagtcac atctcatttt cttccttgtt aaaatgggg
240tactactggc cctacctcat attctatgag aatgagtttg tagctgtttc aaatcatgaa
300gtgcatagta tcacatgtga tagaatattt ataacttttt attagatgct taatgttcaa
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398

<210> 2550<211> 401<212> DNA<213> Homo sapien

ggcacgaggt actgcttcct ccaaccaggt ggagaatcct ggcaagcact acctcagcca
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120ggaaaacatg attcttttac tttttttttt tttttttaag ggaaggggct aattttgtca
180cccaggtgg agggcagggg catgatctaa gtcacatggaa agggcccttt cctaggctaa
240aagggccctt ccacctaagc ctcttgaaaa gtaagggata aatggaaagg ttttttttta
300ttggatcttc ttattgggac acgggggacc ctgaaaaaaa ttttcggggc gggctggggg
360gttaacacct ggggccccac cacttgggga ggctggggcg n

401

<210> 2551<211> 395<212> DNA<213> Homo sapien

ggcacgagga ggcattgtgt atagtgtgt tctgggtctt cccacgaaac tctggctctgc
60acagtggagc ctcatcttct ggtctgttt gatgagtgg cgaatgcaca tggcagggcg
120tcatgtccct tgggcctgtg aggtgaggaa gggctccctga gccctgtggg gatagagact
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240tgggagacag accatctctc tcagcgggtc cagccatgag ccagcagact gtttccatt
300ggcccccatc tttcagagtg ggatgatctt tctaacaag aaaccacac aggaatttgg
360cgtgtgtgt catgtgtgta ttaccttga ggatg

395

<210> 2552<211> 396<212> DNA<213> Homo sapien

gagtgataga acataccaac gttaccaaga aatttacaag ctgctggctt taagcttatg
60caagtggtag ttgggaaagt aggaggtgtg gaagagggtt tgcattttgg attaatcat
120gcaaaatgaa ggaggaagcc tggcttaaga agatactgtc tttcaataga aatgatttct
180aaactgctac agattaagaa tagataatct gattgtgtgt gttttgtttg tttgaaaaga
240aaaaaaatgt ctggcttctt ctactatttg ttttactac caaactgtgt tactaaattt
300cttgtcatcc ttgtatgtaa aatgggtgct gggggtggag ggggtataaga ggaggagag
360tcatagagag tgtgtatggc tttgatggca ctgggt

396

<210> 2553<211> 398<212> DNA<213> Homo sapien

ggcacgaggg aggtacaga tgccctgag caagtggagg agattctgga tcacagtgg
60cagcaggcac gccctgctcg tgtaaatgga ggcacgatg aggagaatgg tgaggagctg
120cagcagggtta ataatgagct tcaactggct ctgacaagg aaagaaagtc tcaaggagct
180ggcagtgagc aagatgaggc tgatgtagac cctcaaagac caccaaggcc agaagtaaaa
240attaccagtc cagaagaaaa tgaaaacaac caacaaaaca aggactatgc tgccgtggct
300tanaacattt ttaaaaagag agtatatgga tcgcaagaaa aatgaagggt tatcatactt
360gaaagataag cacatagtta ttgctgaata taatgtgg

398

<210> 2554<211> 395<212> DNA<213> Homo sapien

ctcaagtttc ttgagttgct gcttggttaac acccagcttt taactgagtg tttgctcctg
60atggttttagg agattttcat gttgtatcac actgtcaagt tttattttgt ctttttatcc
120ctccgtggat gtgagtttga aacaagcacg gtacagtaat cctgcctgat agagtgtct
180ggaatgagaa ttactttttg ggtgagagag ttctccattt taatgtttct aaagttttcc
240atatgaactt ggcattggaa aagggaggta aagaaaaagg acgtttacta aaagcagtg
300ctactcttcc cctttgtgag tgtttattca tggctaata gaaaagagaa ggactcttgg
360gttttgtgtt gccatgttaa gcatggagag ggatg

395

<210> 2555<211> 398<212> DNA<213> Homo sapien

ggcacgagcc aaccccgaa cccctggtgt gtacgggtca ggcagacaca tgtggctggg
60cggctgggct ggggagggga cagccgccac ctgagggtta tattccctc tccccttccc
120tccccgcaa gagctctgcc aggggcgggc aaaaaaaagt aaaaagaaaa gaaaaaaaaa
180aggaaccaac cccctctac atattatgga aagaaaatat tttggccgat cctaattctt
240ttataattat gcggggaaaa agtaaaccca ttaaacgatt ccagttggaa acaaaaaaaa
300aaccctttaa aactataggg ggccggtttc cgtaaaccca aactggataa aaaccttga
360ggagttgggc caacccccac ctaaatggcg gggaaaaa

398

<210> 2556<211> 398<212> DNA<213> Homo sapien

ggcagagacc accatgcccc gccaatccat gaaatcttaa tggctcaact aaacaaacat
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120ctcagagatc tagacagatg gagtctttac tatcttatga tgttgctgtc tcaacacaca
180gcttctagag ttctgtgggt gggataaggt gtaaaaaact taaactttct cttaaagtct
240ttggccctgg ctacatcag tcctatgaat ctctctcagt gctagggagt tgggatgtgc
300agtcctccct gatgccccaa cagaacaggc aaaccagata ttactgagtg caagaaatcc
360ctactatgtg tactgaggaa caggattcaa gctgtatt

398

<210> 2557<211> 401<212> DNA<213> Homo sapien

cggtgctgtc ggggtattatc ttttaagttg tcagcaagtt accaaggtat tcattaaga
60acttgtaata tcaaattact atttattcat acaattgat ttgatgctaa taataatttt
120cttttaaaactc taccattcat tatgtggtaa ctgtattgaa cttactttat ttggatttta
180ttttaatgtg actagatgtc accacttcaa aaaatcaatt tgttcttaga acctgggtga
240aaataaccagg aaactgttac agactccatt tcaaaaaaaaa aaaaaacccc
300ttggagcctg ggggggggtc caaaaaaac cccattttg ctgaaagggg ttttttaaaa
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401

<210> 2558<211> 400<212> DNA<213> Homo sapien

ggcagagac ctggccctct gggaagtcta ccagtggcaa aaaggacaga tgcagaagca
60gaacggaggg aaggccgtgg acgagcggca gctgtccac ggcaccagcg ccatttttgt
120ggacgccatc tgccagcaga actttgactg gcgggtctgt ggtgttcatg gcacttccta
180cggaaggagg agctactttg cccgagatgc tgcataatcc caccactaca gcaaatccga
240cacgcagacc cacacgatgt tcctggcccg ggtgctggtg ggcgagttcg tcaggggcaa
300tgctccttt gtccgtccgc cggccaagga gggctggagc aacgccttct atgatagctg
360cgtgaacagt gtgtccgacc cctccatctt tgtgatcttt

400

<210> 2559<211> 400<212> DNA<213> Homo sapien

cggtgctgtc gataattttt tattatttta gggtagaatt gacatcttta taacaaatga
60gtgtttatct ccttttgttt aagtaatctg ttatttctgt cagtaggttt ttatgtttc
120ttcatacagg tcttatacag ttctagtgtt ttatatctac agattttatc tttttgttg
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240cacccctccc acatttgatt gatagacttc ttgatccctt ttgattcctc ttccttacc
300ccaagcaggg atttgaatat taattttttc attgagatat aattcacata ccataaaatc
360aatcctttta aagtatgtaa ttcagttagt tttaatatag

400

<210> 2560<211> 396<212> DNA<213> Homo sapien

cgctgctgtc gatggcggcc tcctggctgc tcttggttac cctgcgcccc ttagcacaga
60gcccgtgag agggagatgt gttgggtgcg gggcctgggc cgccgctctc gtcctctgg
120ccaccgcccc tgggaagccc ttttgaaag cctatacggc tcagacatcc gagagcatga
180ccccaactgc cacttcagag acttatttga aagctttggc cgattgccat ggacctctgg
240accactatga ttttctgac aaagctcatg agctaaagga tgatgaacat caaagaagag
300tcatacagt tttgcagaaa ttacacgagg accttaaagg atacaatata gaggcagaag
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396

<210> 2561<211> 397<212> DNA<213> Homo sapien

cggtgctgtc ggcgcctttg gccttatgac ccaacttctc tcaccgccat ggagttcgac
60ctgggagcag ccttgagacc cactcccag aagcccgggt tgggggaggg ccacggggga
120gatcccaagc tcagtcccca caaagttcag ggccggctcg aggcaggggc aggtccgggt
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240accccgagg cctgccttag gcctccaact tcagggggct gggtaaaggg cgccgcctca
300ctgccacacc ttcacccagc aaggacacca cagctcttcc gactccagca gcagctccag
360cgattcggac acggatgtga aggtaaaggg ctctcgc

397

<210> 2562<211> 401<212> DNA<213> Homo sapien

ggcagaggg accctcagtgg aaacacgccc ctcatattat cctgctccgg tggccatcac
60gagcttggg cactgctgtc acagcaggg gcctccatta acgcttctaa caataagggc

120aacacagcgc tgcacgaggc tgtgattgaa aagcacgtct tctgtggtaga gctgcttctg
180ctccacggag cgtcagttca ggtgctgaac aagcggcagc gcacggctgt agactgtgct
240gaacagaatt caaaaataat ggaattgctt cagggtgtac caagctgtgt tgcttcatta
300gatgatgtgg ctgaaactga ccgcaaggag tatgtcactg ttaagatcag gaaaaaatgg
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401

<210> 2563<211> 391<212> DNA<213> Homo sapien

ggcacgaggt taatacaagt aaaatactta agacagtaca tggcacatag taaatactgt
60ttaaatatta actgcaatta ttattattat catcattatt gcagtctgag atatctggcc
120tgaattttatc aagttaggaa gctctgtcat tgcacagaaa taccttggtc tcaggagagt
180cactaaccga agtgcttctg taaacaaggg acataagcag agaaggggta tgttaagtaca
240gaaaactcat gattacctgg ggaatagtta aatagatttt aggtattagn tggttttttt
300ttcctctctc tctctttggg ggaatttttc tgtttactga gtcattcttc attaaggggt
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391

<210> 2564<211> 394<212> DNA<213> Homo sapien

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120gctaattttg tatttttagt agagatgggg ttctctccatg ttggtcaggc tggctcacia
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240agccaccgcy ccggctgcct taaatctatt tatctgacgt tcccaactag gaaatttttt
300gtccaaatga gtatatgtga ttttaaagta gaaatcgaag gtaaaatagg atttatctca
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394

<210> 2565<211> 393<212> DNA<213> Homo sapien

tacggctgcy agaagacgac agaaggggta atcccagcac tttgggaggc cgaggcgggt
60ggatcacctg agatagggag ttcgacacca gcctgaccaa catggagaaa tctcgtctct
120actaaaaata cacaattatc cagggtgtagt ggcgcatgcc tataatccca gctacttagg
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240tgccattgca ctccagcctg ggcaacaaga gcgaaactcc atctcaaaaa caaacaaaca
300aaaaaattgc aaaatgtagt caccctgtta tgtttcatga ctctgaaagt gttatgtgtt
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393

<210> 2566<211> 394<212> DNA<213> Homo sapien

atccgttgct gtcgattcag aaactgattt tacttttatt gcagtacaaa ttatattatt
60aagcagggtt cttgttcagc catgaaatgc agatgggctg tttaatatgc acatacatga
120cattttttat taattttggt ggtcattaca atgagttgaa tttaaaaagt gggtaaatgc
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240cagaaatatt acaatttcat gtttagttaa gcaaaaataag caaaactggg agaatttaag
300gtggcatctt atttactgct ttccagtagg attataatta aaaatttact gaatgaagtg
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394

<210> 2567<211> 391<212> DNA<213> Homo sapien

ctgaggtrac ctcttgaggt gaggggtctg agtgaagccc agcccggcag ggtcatctgg
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120gtcactgggtg tggctttttc ttctatgcag cgagtctgac agtgacctaa agcctgtggg
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240agagagtggg gacatcgtct ctctattca tgactgagga agtgccctgca ggaaacaagc
300cctgtctgac cgccaaggct tcatactcaa ggatgtctat gcttccccgt gagcttctctg
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391

<210> 2568<211> 392<212> DNA<213> Homo sapien

ggcacgagcc aaccccgga cccctggtgt gtacgggtca ggcagacaca tgtggctggg
60cggctgggct ggggagggga cagccggcac ctgagggtta ttttccctc tccccctccc
120tccccgcaa gagctctgcc aggggcgggc aaaaaaagt aaaaaaaga gaaaaaata
180aagaaccaac ccacctctac atattatgga aagaaaatat tttggccgat ccttattctt

240ttataattat gcggggaaaa agtagacca ttaaacgatt ccagtgggaa acaaaaaaaaa
300aaccctctaa acctataggg agccgtttta cgtaaacca aactggataa aatccttgga
360ggagttgggc caacccccac ctaaaaggcg gg
392

<210> 2569<211> 393<212> DNA<213> Homo sapien

ctcgggaggc tgaggcggca gaatcacttg aatcatagag gtggagggtg cagtgaagctg
60agatcgcgcc actgcactcc agcctgggca acagagcaag attctgtctc aaaaaaaaaac
120aaaacaaaac aaccccccaa aaaaacccaa ttaacattct ttcaccccggt atttcctaga
180ctttattttta gctataacaa gcaaaacacc tctttccatc cttctaaaag cgtgttcctg
240aaacctcact tggagagttt tacggaaatg cagcgacagg actggaaata atgacagcaa
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360cgacctgacc gtgtcgctat aaagacggga ggg
393

<210> 2570<211> 393<212> DNA<213> Homo sapien

ggcacgagtc tagatcacat tttatatatg ctgcatgcc aaaaaaaaaa aaaaaaaacc
60gccttttttg gggggggggg gaaaaaaaaac caattttcc ccttcctag aaaagtcaaa
120acaagggtttt cctggaaacc ttttcaagaa aaagtaaacc aggttggttt ttgaaccttt
180ggccattttt tttttttaa aaaagcaaaa ttcagcccc aatccttttg aagggtttg
240aaacccccaa acccccggag aagccctcca ttttgaagg ggaatttg agaaaaacct
300gtttttcccc gaatttgcc aaataaagg aggtttttt caattcgggc cctaaaaaca
360agggcccccg tttgttctaa ccataacaa ttt
393

<210> 2571<211> 391<212> DNA<213> Homo sapien

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60aatgtgtgac tgaagtccaa gtctgtggca tcagggtctg cagagcccag atgcgggaga
120ggttagaatg tacctggtga tatgaggcaa ggacagggga gctggggcag gtgatgcagg
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391

<210> 2572<211> 394<212> DNA<213> Homo sapien

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120aaaccagggc cctctttttt aaatatcccg ggtaccccaa gcggggccagg gggttttggg
180gtttgccctt tggggggcag gcttaataaa acaaaaccct atttttggcc ccccaaaaaa
240ccccgcccta aaaaaattgt ttgagggggg aaaggcccaa aaaggcctgg tggtttattc
300tccatagacg ggaaagccag ccccttcccc ttgtaaaaag ggggagccaa aatttcctga
360cctcttgggg gttaaaaaaa ctcttacggg gggg
394

<210> 2573<211> 391<212> DNA<213> Homo sapien

cgttgctgtc gaatacctgc ctcccattct ggcagcccag cctgagaccg ttgcattgag
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120cactggggcc cctcccctgc tgggcaatcc tgggaaggte tggaggttcc tgtggacctc
180aggggaagcca ggggcagctg tcaggcctga ggaagacctg tggagctcct ctccagcctc
240ctctttccct cccctctggg ctccattctc ttcagctccc tacatgggct ggggaggaga
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391

<210> 2574<211> 391<212> DNA<213> Homo sapien

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120gaactttcag agaaaccagc tgagtctgtc acttctaaaa agacaggacc ccttagtgcc
180cagccctctg ttgaaaaaga gaacttggca atagaaagtc aatcgaaaac tcagaaaaaa
240gggaagatat ctcatgacaa aaggaagaaa tcaagaagta aagccatagg ctcatgact
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360aatattgggt tgcctgaatt cgagaaaacc g

391

<210> 2575<211> 392<212> DNA<213> Homo sapien

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120ggaggcctct ctgcgcttca ctctgccggg ctccggcact gaggggcccc ccaagcaaga
180gaacttcac ctaggcagct gtggcacaga ccaggtgaag ggtgtgctga ctctgcaggg
240ggatgccctc agccaggcgg atgtgaacct gaagatgcc cggaacaacc agctgctgca
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392

<210> 2576<211> 391<212> DNA<213> Homo sapien

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120acatgtctaa ttatgatgaa gaaggagcat ggcctgttct tattgatgac tttgtggaat
180ttgcacgccc tcaaattgct gggacaaaa gtacaacagt gtagcactaa aggaaccttc
240tagaatgtac atagtctgta caataaatac aacagaaaat tgcacagtca atttctgctg
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360aggatacatc ttggaccata tcgtatttca t

391

<210> 2577<211> 392<212> DNA<213> Homo sapien

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120accatgtgtg gctacaaaac tatcgacaag gagcgtttca gtgtgcagga tgtcatctac
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240ggcatcctcc tgggcatcct gcttccccag ttcttggggg tgctgctgac gctgctgtac
300atcaccggg tggaggacat catcatggag cactctgtca ctgatgggct cctggggccc
360ggagccaagc ccagcgtgga ggcggtaggc at

392

<210> 2578<211> 392<212> DNA<213> Homo sapien

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120atcgcaacct tgggtgtggc ccagctgctc ctgggtgcagt ggaagcagag gcacccacgc
180tcctacaata tggtgaccct ctttcagatg tgggtgtgtc cctctatctt cacagtgaag
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300accttccgag ccacccgaaa acctctagta cagacaacct caaggttggg ttataagtgg
360gtcctgctaa tctataaaat cagctatgcc ag

392

<210> 2579<211> 384<212> DNA<213> Homo sapien

gcacgagaca gtttatattg acctataacc aagaggcagg ttcattatgt ttaattgcat
60taaaagataa aagaagtaga gaaattgaaa ggaaaaagag cccagagatt gttacctttt
120tatcaagcaa cagcatgcca caaactttgc ataaataaaa aataataacc tgagcctttc
180atcttgggaa tctaataaaa taaatgtgtg ctgttttccc cattagccct caccttagcc
240agcccttaca ttgtggacag aggagtgatg tcattatttg tgagctagat gactggctca
300gtagggtgccg tgtggttcct aagaagattg taggtcttgc cattgcgtct tgtgtctctt
360gtgtgacagg tggaacatc tgtg

384

<210> 2580<211> 385<212> DNA<213> Homo sapien

gttgcgtcgc ggtttggcct gtgggttttt aagtggttat tgaattggta tcaggagatc
60ctgaggctgg taggggaagg tgattctttc taagttacct ctgtattttt caagttttct
120ataaggaata cacatacacc cacatgcaca cccatagtt tttatacaaa cagcaataac
180aaaacaaaa agatgcccct tttttgtag ggataagaaa tacatttgtt ttatacttct
240atgctatatt ttgctattca aaatttagtg ggcattactt aacattgttt ctaattattt
300tgtggctgct gtatgtttta tgtgttggga gccattgta ttaggccgtt cttggattgc
360tataaagaaa tacctgagac tgggt

385

<210> 2581<211> 388<212> DNA<213> Homo sapien
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60cattcatgca gcatgaattc atatttcccg agcttatggt atgcacaata ctaggaaaag
120ttcaaccatg agcaacattc cttacatctt aatggaggga aacagagctt aaacaaatga
180ctacagattt ggaaggaagc agtgctgtaa ggaaacctga agtagtgtaa agagagaaag
240cttagtgagg aagggccttt ctttccattt ggtgtcttgt tttctactct tgctcatgaa
300atgttctgag tagcttcaaa tatgttttaa attgaattgt gtagagtcca gtacctctga
360gaggtaaactg agtgcagcta ttctaggg
388

<210> 2582<211> 384<212> DNA<213> Homo sapien
ggcacgagga tacaagtgtc tccttgtcat aacccaagag caaaagcagc cttcacttac
60tgtcccatga aacaaaaatt ggatcttttc taagcaacag aacttttagat ggcaaagaca
120aagctggcct ttgtccagat gaagatgata tggaggaga ttctttcttt gatgatccca
180ttcctaagcc agagaaaact tacggtttga ggaaggaacc taggaagcaa gcaggaagtc
240tggcctcgct ctcgatgca ccccccttaa aaagtggact cagctccctg gcgggagccc
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360tcagtataa aattggatca cttg
384

<210> 2583<211> 156<212> DNA<213> Homo sapien
nnctctgatt tgagaaaagg gaggagggga agatagtctg aatggaaatc tgaaatacgg
60aatgttttag agaaatatgt cacttgcata tagaatgtt taattgaggt ataaaataat
120gagacaaagt gaaaaagaaa ttatattcag ataggn
156

<210> 2584<211> 389<212> DNA<213> Homo sapien
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60ctggagtccc agactcatag gtcccgcccc agccccgaa gagccgcctc agccgggggg
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180ctgaggccac catggagcag tgtgcgtgag tggagagaga gctggacaag gtcctgcaga
240agttctgac ctacgggcag cactgtgagc ggagcctgga ggagctgctg cactacgtgg
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360tctctctggt gatgtcacag tgctgccg
389

<210> 2585<211> 386<212> DNA<213> Homo sapien
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120atgggggatg gggagttgag caaggaaaa aattgcata atggtgttg ctccctgggtg
180aaactgaaac ccagcctgtg tgggtggggc cttgtttcca aacgtcagcg ctgctgcccc
240cgaaggcctg caccaacgca cgggtgcctc cggggcggcc acagaggccg gcgtctggcc
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386

<210> 2586<211> 385<212> DNA<213> Homo sapien
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120ctaaaagtta tttcaactaa tttgaatatt atcgcaaaaa gtttacttga gaaaacaagt
180tgaaattgaa attttgactt gctaaaatta cattttttaa acggtagttt tgaatgacat
240tctaaaggta atttagttgg actttgtgtt tatatggcca atttgggaa tggccctgta
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385

<210> 2587<211> 387<212> DNA<213> Homo sapien
ggctcgagac ctggcctctc tgggaaggct accagtggca aaaaggacag atgcaggggc
60agagcggagg gaaggccgtg gacgagcggc agctgttcca cggcaccagc gccatttttg
120tggacgccat ctgccagcag aactttgact ggcggtctg tgggtgttcat ggcacttctt
180acggcaaggg gagctacttt gcccgagatg ctgcatattc ccaccactac agcaaaccg
240acacgcagac ccacacgatg ttcttggccc ggtgtctggt gggcgagttc gtcaggggca

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387

<210> 2588<211> 384<212> DNA<213> Homo sapien

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60gaggagagtg agaaggccat gcaggagcgg gtgcagaggc tggaggcggc gcggctgtcc
120ctggaggagg agctgagccg agtgaaagca gcggcactca gcgagcgtgg ccaggctgag
180gaggagctga tcaaggccaa gagccaggcc cgcctggagg agcaacagcg cctggctcac
240ctggaggaca agctgagact gctggcgag gcacgggacg aggcgcaggg cgcttgcta
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384

<210> 2589<211> 389<212> DNA<213> Homo sapien

ggcacgaggg caagtggta agatgagatg ataacaatgg ataatgcaga agaatatgtg
60gatttgatgt ttgacttttg tatgcatacg ggtattcaga aacaaatgga agcctttaga
120gatgggttta ataaagtttt tccaatggag aaattaagtt ccttcagcca tgaagaagtc
180caaagtattc tttgtggaaa ccagtcacca tcctgggcag cagaggatat tatcaattac
240actgaacctt agctgggtta tacacgtgac agccctgggt tcctgaggtt tgtgagggtt
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389

<210> 2590<211> 379<212> DNA<213> Homo sapien

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60acaattaagc aaccatatac aatttaacat acctgaatat gagaaacaca tttaaattca
120ttgttggtt aaacacattt caaaatggaa agacaaatat tttatttact gacctaaaac
180aacactacct atgaattca tgcactattg ctttcagatt acttacagga ttatatcaat
240ttaacatttc tttgtgagat taagcatttg aaatccatag tcagagaact attttaata
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360tctagagact acatgacct
379

<210> 2591<211> 379<212> DNA<213> Homo sapien

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60tggtttacag actgatttag aaaaccagaa cggatttcat ttctaattgga gggggccaga
120gatgggaaaa tttcttggtc agtccgggga aacacaccta ggtgctggtg atgggcttat
180gaaggagct aagcacggt gctcactggc cccactttg tttcttggtt aattcacagg
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300ctgtatgtac acatgcatat atctgttaca gaagatactc ctggcagtga ggtgctaagt
360catcactgag gctgtgtgc
379

<210> 2592<211> 380<212> DNA<213> Homo sapien

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60cagattgctt tgtaaacttt cttaggcctt cccccacc ctttgcccca gtgctttaag
120cccttctttt tcttcttgct gtttctttta ttcctcacgc ctgcggggcg gggcggggt
180ggcgcccagg acgactcccc gggtcagct tggctgcctg cctccttctg taagtgttt
240ttttttcttc acctgggacc ctctanaggt tggaaagaga agagaggctg ggagcggatg
300gaaagcatga ctgcatctgg agccccctggg gggagtggg aagagggagt ggaaggacag
360tggtgaggg gcttctgtt
380

<210> 2593<211> 381<212> DNA<213> Homo sapien

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120gtaaaccaag agagtagaaa tatacccatc ttattttaag ttgggtttat ggcacgctc
180atatatgtaa aagcactaca aactctttaa agaaaattgg gaaactacag agaagtcaaa
240gaaaaaaaaa agtaacccat atttctattg cccaggcata atccttgta aaattttggg
300ttggcctcct cttttcccc caatatagtt gcaaataaat gatgtcttct agagttgaca
360ttaatcctgg agcttgatg g

381

<210> 2594<211> 380<212> DNA<213> Homo sapien
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60aggaacagag ctgacatctg agcctcaaaa atccagccca ttgtacta gactaccaga
120atatacctccg cttctgaaa acattcagta tttcaagat ccaaggactc agataccctt
180tgaagtccca cagtaccac agacaggata ctatccacca cttctcctc tgttcagtgt
240aaactttctt gcggatttct cagagagtgt gagtgggtaca aactttgaag aagatcatct
300ttcccattat tctccctggt cttggggcac catcggtcc tgtataaatg ccattgattc
360agagcccaaa gatgtcattg

380

<210> 2595<211> 382<212> DNA<213> Homo sapien
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120atgggtcaact aaatgtttcc ttatgaaagt gaaattggga aaagtcaaga taaatcctag
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240atttggttg ctgtggtgct ttgcaaactt ttggttgta tttatcctgt cattcataaa
300ttatggcaca tatgctggag ccaaactctg cattaaataa attctcatat aattccctac
360attcatttat ttcactaatc at

382

<210> 2596<211> 379<212> DNA<213> Homo sapien
ctccttcaga accccaccca gtgttgaga agcttcggtc cattaataac tataacccca
60aagattttga ctggaatctg aaacatggcc gggttttcat cattaagagc tactctgagg
120acgatattca cgttccatt aagtataata ttggtgcag cacagagcat ggtacaaga
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240tcaacggcag tggacacttc tgtggcgtgg cagaaatgaa atctgctgtg gactacaaca
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379

<210> 2597<211> 375<212> DNA<213> Homo sapien
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120taagataaat tccttgaaat taaaatgatt acgttctctt ctgtggatct tagctggcac
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375

<210> 2598<211> 378<212> DNA<213> Homo sapien
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120taagtgtagc agttcaaagt tccagctctg gaggcagagt cctgactctg ttaggcaggt
180tcttaaatctc aactataaaa tgaagttaca aacattgagt gcctcatagg gccagtgtta
240agattaaatg aaataaatat aaaccatttg gcatgggtcc tggagcgtgg ttaagtgtc
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378

<210> 2599<211> 374<212> DNA<213> Homo sapien
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120tttaactttt ttttttaaa atttgaat taatgattaa aaatgttact tttataaaag
180tgtaaatatt cagtatttaa aagataattt taaaaataac cacaatacaa ttttctacc
240taaaaaattt taatgagttt ctagcaaat atccaagcca ttttgtatt tctctgatag
300ttttataaat ctgtatgtat gtgttttagt acttttttga attaagattg aaataagatt
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374

<210> 2600<211> 375<212> DNA<213> Homo sapien

ggcacgaggg gagggcccca ggaggggtctc aggcagcttt gctgggagtg tccacatcac
60cctgaccccc gtgaggcctg acaggacccc acgcccagcc agcccaggac ccagcctccc
120agccaggtcc cctcccccac cccaccgcag gagactggcc gtccctgcca gcctcgacgt
180ttgtgacaac tggcttcggc cggagccccc tggccaggaa gcccagatgc agagctggaa
240ggaggaggag aagaaacccc accttcaggg caaacaggag agacccttgt ccccgccaa
300tgctccctgct ctgcctggcg agacgngnac ctcccagtc aggtgcacc ccgactacct
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375

<210> 2601<211> 377<212> DNA<213> Homo sapien

ggcacgaggt cctgctccgt gtcattatca agcgtaata aagcactactg gcaggcacca
60gactacaggg ccttggaac agccttctga gccagcattt attcacactg cattaccgtg
120tcctccatgt caagtcccta ttcctacgga atgacttggg aaacatgagg tgagtccact
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240tcagaatcac acatgtatga cagaatgccaa caaagtaact catgctgatg gctgcactgg
300ataaaacaag gctgtgccag aatgccttca ttgtgaggaa gggagctcca agtcacggcc
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377

<210> 2602<211> 372<212> DNA<213> Homo sapien

gtgggcatgg tgggtgtaac cgacctcaag gtggccacct cctgctgct gctgctcttc
60gccatcttca tgggcctgcg ggcctccaag atgttcgggc agcggcgcaa cgcgcaggcg
120ttggagctgg cgcacatgct gtactatcgc agtacgtcca acaactcgga gctgctcagc
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240ctggcccggc ggccaggggg cactcaaggc tcgcccgaag agacctccag gtggctccgg
300tcggaggtgg agaactggct ctagccaag tcaggctgtg aggtgacctt caacggaact
360cgggccctgg cg

372

<210> 2603<211> 371<212> DNA<213> Homo sapien

ttcaattccg tgctgcttac attttctatc ctttatagga ggccgagctg cagggggggg
60cctgtcttct ggggggagag ggtcctcaaa ggagcggagg cagctggaga cccctggagg
120aatcttgca ggtggggac gtaagacagt cccatggaac aaataagatg gaaacagctg
180caacatata ttttctctt tagagatcca accttattcc atttataata aactgagaag
240ttctatatca aatataactg cctgtaacat tttaaattgc ttcaatctga gtttaacacc
300cacctttcct ttcattctct agcaaataat cttaaagctg tatctaact gacgtcagaa
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371

<210> 2604<211> 353<212> DNA<213> Homo sapien

tatctgctgc gagaagacga cagaagggtta ggtgttacga gattgggaga cttttctcag
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120gcagttctaa tactgaatgt tetgactgtg gtttactatg tatttcaggt tattttgttt
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240taaggctagt aagtagtgag gctggattta aacttaagtc tccagcttcg tggccagggt
300tctttatact tgactccaca ctgggcttat taagtgaatg acaaggagtt tgg

353

<210> 2605<211> 342<212> DNA<213> Homo sapien

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60aaagtttttt tggcggtaca gggaaattat aggatgttac tgtgcccccc accccatta
120ttagctgcgc tatccgcagt gacatgacca tgtgtccttt cttgatgggc taagtaccag
180cagatcgat catcagtgt aactcaagac aatatctgaa ggctgggggt gctgcttttg
240ttcacatttt ttttttttaa ataggaaaaa aacttgggaag cttgcagaaa tcttcctgta
300acattttatt ggctggatta taccacatgc ttatttctat ac

342

<210> 2606<211> 335<212> DNA<213> Homo sapien

tacggctgct agaagacgac agtagggctc atgaggaaga ggaggaaaag agcattaccg
60ctgtttgtca catgaggatt catttgca tagtatgaaa atggaggcaa tttttccagt
120ctcaagaatg gtaaaaggca caggtgggac ttgaaccag actcttggct tcaagtccag
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240ggaagtttag tccttgggac gcttggcctg ccagtctctg aaaaaaatat gatggggatg
300gtggtggtgg tagtgcacgt tgggttgagg ggaca
335

<210> 2607<211> 331<212> DNA<213> Homo sapien
ttacggctgc gagaagacga cagaggggat gagccactgt gcctgaccta gggtatcatt
60cttgagaaaa gtttaaacat gccatataaa tcaaatatt gatgacatta attaatagca
120cttaattctg actttgactt tttttcaatc ccattagttt actttcattt cttacctaaa
180atttgtttag tgggttaatag aattctgaac ctaatatatc atcttattat tttctgctca
240atgtgtaaca ctagtctgac tattttattc tttttttttt tttttttttt tggaaaaaag
300tttccacttt tggccagggt tgaacgccc g
331

<210> 2608<211> 457<212> DNA<213> Homo sapien
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457

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120ttttagatt tatagcaaat agagactcgt tatttaaaag ttaaataaca atttgttctt
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429

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120acttgaaccc gggaggcggg ggttgctgctg agccaagaca gcaccactgc actccagctt
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300caagagcagg cttgcgggtg tggaaagtgc aaatgtaagt gttcgatttt ggataactt
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425

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419

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420

<210> 2614<211> 414<212> DNA<213> Homo sapien

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414

<210> 2615<211> 414<212> DNA<213> Homo sapien

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180cataaaaagaa aaataaatgt ggaaatttca tcttggaaa aaaaaaaaaa aaaaaaaaaa
240aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaanaan nnnnnnnnt tggggggggg
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414

<210> 2616<211> 402<212> DNA<213> Homo sapien

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120ttctttattaa aaagaaacat tctaagtaaa cataacgaaa tattaattct ggggtggtgt
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240aagtccagat aggagtgagg aagctgtaca tgaaacataa tggacttaca ttctagtca
300gatactaata ttctgtagaa gatatttcta aaatcttctc tttaaaatat gaaataattt
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402

<210> 2617<211> 409<212> DNA<213> Homo sapien

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120ttaattaaaa acataccttt actctgttcc ctttagcatt tcaacctgat gttaaagat
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409

<210> 2618<211> 406<212> DNA<213> Homo sapien

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120ttgcttttaac taatcctatc attaaaaatg aaaatgattt tgctttttta ttgcgcaag
180tagcactaaa gatagaagct taattaatga aagctaattg caataagggg tagatagagt
240agtatatgtg ggggtgggag ggtatgggag tntnannntn nttnnncnact gatgttctgt
300gttattggaa tgttgaacta aatttaatat agctacttaa tatagagcgt ttctgagaca
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406

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402

<210> 2620<211> 412<212> DNA<213> Homo sapien

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120ttaacaaaaa gctgctgcat gccaaagtcac tgtgctaggc attgaggatt cagctctaca
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240acatatagtg tgacacattc tacagtgggg gaatccaggg ttctcaggca gattgtagga
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412

<210> 2621<211> 403<212> DNA<213> Homo sapien

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120atttcaattg caactcaaac aatgaatctt ccaaagatgg ttaccctcac tctacaaaag
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240ttaattttat ttttctcaca taaatgttaa ccaaaaacta aatgataatt tccttctgtc
300acacagcaat tccactgtgg tggaaacaaag tgttatctca agtttcacag agcaattgtt
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403

<210> 2622<211> 404<212> DNA<213> Homo sapien

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120aataacagac atctgctcta gttcatgata aaatgttgat agattttatc aggtgggttag
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300taattattgt ctaaatttca taatcgaagc gatttttagag tagttaactt gagatttcac
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404

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408

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120tcctagctgt agctacagat atagaaaatt ctaccattga agatcttgta taaccttact
180tcagccactg aaataattta aattataaat attacatgtg ggtttgacta tcacagaaaa
240taaaaatgatt atagatccta aaaacataaa ttcctgaact ttgcaaccat taattcatag
300gtactactaa tactcttact acagatttta taagtacttc cacttataga cagaagagca
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409

<210> 2625<211> 416<212> DNA<213> Homo sapien

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416

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300ctggcctcat atgggtaagg agatttgggc aaccttttgc aggctgatga aattttggag
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414

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120aattcagaat tgtttaaaac attgtgcttg ccaaaacaaa aaacatgttt gccagccagt
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300cttttagatg tatcttctc ctcatctcta aataatctc agggattact tttcttact
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418

<210> 2628<211> 407<212> DNA<213> Homo sapien

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300actaacccaa ttaaagcaac agccatgaat aatattggcc ctgaccttgc tgaattcaa
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407

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405

<210> 2630<211> 403<212> DNA<213> Homo sapien

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240aaacaatgat aaggttgctg agtcattagg aatcacagaa ttctacgga agaaagaaat
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403

<210> 2631<211> 411<212> DNA<213> Homo sapien

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411

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413

<210> 2633<211> 402<212> DNA<213> Homo sapien

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300cccaaattggg ggctgcagca tgggccttgg ttgaagcctc taatcctgta agggctgctt
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402

<210> 2634<211> 418<212> DNA<213> Homo sapien

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120aaacgtaggg agcaggttgg aagtgaagga actttccaaa gagatgatgc tctgtcatct
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240aagaaaggag agggcctggg gaaggatggt ggaggaatga aaacgccgat ccagcttcag
300cttcggcgaa cacatgcagg cttggggaca ggcaaacat cctcatttga agatgttcac
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418

<210> 2635<211> 409<212> DNA<213> Homo sapien

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409

<210> 2636<211> 403<212> DNA<213> Homo sapien

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403

<210> 2637<211> 389<212> DNA<213> Homo sapien

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240aaccacttaa tcttggagtg ggaggagagg ggggtggggtg ggagagaata taagatgtat
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389

<210> 2638<211> 396<212> DNA<213> Homo sapien
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396

<210> 2639<211> 393<212> DNA<213> Homo sapien
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120cagttaggcca gttacacca tttataataa ttaataaaat cactatgttt gacttcaagc
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240tctatttttg ttttaattgg tactttgatg taatactttt ttttctgct ctgagcatt
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360ttccatcata taacttgaaa gattatcctt ttt
393

<210> 2640<211> 393<212> DNA<213> Homo sapien
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120aaagagaata aaaatttctt aaaagactgt catattaagc ccttttacct tttccttgtg
180ccacctcatt acatagatag atcatcattg tatcagaaaa atgttaattt atattattaa
240tgatcacttt gtaagtatgt tttttcaacc atcctaaaca cattttcaga aatgtttttc
300tttaaaagggt gataagtttt aaaaattttt ttataaagag ttaggcttgt gttattactt
360aatgaggaga acctcattcc ctattaatgt taa
393

<210> 2641<211> 384<212> DNA<213> Homo sapien
ggcagagga gagttatagc cttatttttt ttacattctt aggaatttat gaaaatgtat
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120atatttttgt cttttgaatt cattaaacct taaaattatt ggagttctga tttagtctt
180cagaactatt ttggtatttg tgtatcttgt tttggacagg gttagcatgt atttgacacc
240cttttagccct ttaagggata ttttgcctgt gaagattttc tttctttttt tttttttttt
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360tcccctgcta aagaaatttt ctgg
384

<210> 2642<211> 392<212> DNA<213> Homo sapien
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60cttaaaggta atatccatat attcctatta gactcaccct ttccctatag ctaaaattaa
120attcttagag aagaaactta catcagttta atgaatacac agcctgtcta taccaatttc
180ctctctaga gtcactacat tcaaagcttg gtgggtctca atagggattt actgctgact
240gggtaacttg ggttctctgt tgcagtgaac tcaagcaaga gatttaccac gagaagtga
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360tttccctctg tgaaaacaga agcctgtttg ca
392

<210> 2643<211> 391<212> DNA<213> Homo sapien
ggcagagtg ataatatagt aagccaaaat tggctcagtgt aggataagca agatggaata
60agtgcgaagt tagtaatttt ctcatctttc attatgacaa gtcacactt actatataag
120aaatttttaa atacggtaaa atagtacata aaattacaaa gataaccacc aaaagatcct
180agaatagact ataaaccttt ggaactatca gaataaaaac acacaataaa gaaaacaaat
240accatagggg aaaataattg tgtgtatttg tgtctttaat ttgtttgtga gtgtctttta
300tttatgtgtg tataacatta taaaggaaaa atataactaa acataatccg tatgattaaa

360tattttctcct atatccagaa atgtaaattt a

391

<210> 2644<211> 389<212> DNA<213> Homo sapien

ggcacgagga tccccccagc actcatatgg ttctataacc aacagttatt gatattacag
60gagagtatgt aattagtaat gctaaaaaaaa tgcactttat taccctatgg acttttccaa
120atgccatagc taccaataga gtcatttgca ttacacatac taatagtatt atttcttctg
180aggagatcct agctgtagct acagatatag aaaattctac cattgaagat cttgtataac
240cttacttcag ccaactgaaat aatttaaatt ataaatatta catgtgggtt tgactatcac
300agaaaaataaa atgattatag atcctaataaa cataaattcc tgaactttgc aaccattaat
360tcataggtac tactaatact ctactacn

389

<210> 2645<211> 387<212> DNA<213> Homo sapien

ggcacgagcc catctctact aattatacaa aattagccgg gcatgggtgt gcatgactgt
60aatcccagtt acgcgggagg ctgaggcagg aaaatcggtt gaaccaggga ggcggaggtt
120gcagtgagcc gagatcgcca tatatatata ttcatatata tgtatatata cacacatata
180tattcatata tgtatatata cacacatata ttcatatata ttatatata cctatattca
240tatgttttca taatatacga atatacctat atgttcatat atgtatatat aatattcata
300tatgcatata tgtatatata atattcatat atgcatatat gcatatatac ctatatatgc
360gcacatacat attcctatat gcatatg

387

<210> 2646<211> 386<212> DNA<213> Homo sapien

cgttgctgtc ggtgaactgt gatcatccag attttggcag cttatagggt cttagtgtgat
60ataaaaaaga atgccaaagc atgggtaaaa atacatgaca taactatgta aacaagtaga
120agaacttagg gttcttctaa gtagggtcag agccaagatg agctagcaaa aaaccttggt
180actttttttt ttttgaaagg gagtttggtt tggccacca agctggaggg caggggaggg
240atttcgggta attgaaacct ccacctctgg ggttaaagca attttggggc ctaacctcc
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386

<210> 2647<211> 396<212> DNA<213> Homo sapien

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60gtagtaacat gtttcattac agtatcaaat atataggtaa aatttggtga catgaaaaca
120cttggtgtct gtatgtctat caaacattca tgaaaaattt gaagactatc aatttggtac
180ctacaaaaga tgatgcggta gccatggaaa tgcatacccc agatctcttc ctgtgagaag
240cagagttgac agaaccctag ctgctacccc atgggatcta ccaactgtatt cctgctgttc
300ccagccaatg agtgagaatg gcaggactat taacactgac ccagtcacct gatgggcaac
360attgggtcaa ggatttccca ttgattgcc cagaat

396

<210> 2648<211> 387<212> DNA<213> Homo sapien

gacttgctgt tcttaaccta ccaaagcagg catgtagacg cacatgtgtt ttacacacgt
60cattggagga aggttgcaa taccagcttg gttgcaagga aagaggcaat tgagaggact
120cctttctaca ctgcagtaat ttgctgagtg acctgaaca aggatcttaa tgcataaaag
180tctgttttct caacccccaaa atgaagggtt tggaccagat gccctcaagg ttctcaagg
240gtcagctgtc acagttctcc aaagtgagtt ttcaggcaca catagagta gccagtgtcg
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360cgggactggg ctcataacta cctgaag

387

<210> 2649<211> 398<212> DNA<213> Homo sapien

cctcaccca gctgctgt gttctgacg gatcttggtg ctgaggctgc ctggctctcc
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120cccagggttc tccccctgtt gattctcgcc tgctttctca tctcaggga ggcagtggca
180cctccctctc cctgctgaca tgaagagagc tatgatagc cactgctgcc aactcatcct
240ctgccccac ctcgaaaccc acagtcccca gtggagggcc actactcctc ccattgggtt
300tcccagggga ggggtgttgt ctggaagggc aggttcagat gcagccttc agatttagag
360gcactgggag gacagtggct gagtggaggc gccacac

398

<210> 2650<211> 387<212> DNA<213> Homo sapien
cggttgctgctc ggtttgatga tggatgatgat gatgatggca gtcataaact gaggagtgaag
60attcatgccca ctctacattt gaggttcttt ctccagccat gtaactctgg caatggagta
120gaatagggag gagggggaag gtgagaacgt aggtagaaag agctgttggg caactgtagc
180aataaaacag aaaagagatg aatgtttgca cataggcagg ggcagcagga atgcagaagg
240gcaggtgtca gagagcgtcc acgtggtagg acccacagga ccaggtggct gaatgcagag
300gctgaggctg agcagggcgg ccagtatggc tcctgtgttc tgatggcgtg tagtggcgtg
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387

<210> 2651<211> 400<212> DNA<213> Homo sapien
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60tgctgtaaga taatttaaca ggtggttttg cttagtttga ggggaaaaac tttaggggca
120tgaggaatta gaaagagcta gtgaaaagaa agtgtagcag ccaaagagtt aggtgaagaa
180acaaatctgt ggtacattaa gaaaccaaga aggaggaatt tccagagcat atttgtggtc
240atgaaagtca aatgctgccca agatggaaag gaagatggga gttgagactg gtttgcata
300tatggtgatg aaaactgttc tagaaaagtt tcaagttaat aggaccaaac acagcttaca
360ggtgattaaa aaatgagaag gtggtgaaat cctaagtact
400

<210> 2652<211> 389<212> DNA<213> Homo sapien
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120tggcgctctcc aaggggaggc tcctcagagt gcactgagat ccagaggaga tggccacatc
180cccccgggct acatctcaca gctggtgggc gtgatcactg tgcccgtttt acagacaagg
240ccactgagct ctgagagggt atgtgacttg cccaaggtca ccccgctgc aggtctcaaa
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389

<210> 2653<211> 397<212> DNA<213> Homo sapien
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120ggcgaggagg cgcagggaga agtccccagc gctgggggag aagagcctgc cgaggaggac
180tccgaggact ggtgcgtgcc ctgcagcgac gaggaggtgg agctgcctgc ggatgggag
240ccctggatgc ccccgccctc cgaaatccag cggctctatg aactgctggc tgcccacggt
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360gaagaggaga gatccgatga ggagccggag gccaaag
397

<210> 2654<211> 398<212> DNA<213> Homo sapien
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180ggcagagtct ccatacagca gctgggggtt ctggtggcac tccctgtgcc cctgctgctg
240ctgggctgtg ggtctgcctt gcacccagga gccccacggt ccatacccca caccatgccc
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398

<210> 2655<211> 386<212> DNA<213> Homo sapien
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60cccaactatct ctgtaaaggc tctctctctc tttttttttt ttactaacc gagctaaaac
120caattcctgt tgataacaac taaacaacct cattaccgga gaggactttc gtttactttt
180tgcccttttag gttccacttt ttttttggga aaggggattt aatttgttcc ccagccccga
240catcgactgg tataattttg ttaagagca cccttgagcc tcctagggaa acaacattcc
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386

<210> 2656<211> 399<212> DNA<213> Homo sapien
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60tgggatctcc cccgtggccc gccccacac cgggcttctg ggaggtgggc tccagggctg
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180ctccagtcca cactccccag gagctcacct gctcccaggt cgaactccat ggcggttaaga
240gaagttgggt cctaaggcca agggcgctg ggccctgcag aggagcggag cagggggagg
300agcgtgaga cctgcccgtt ggaggaatgc tgagacgccc caccacaact ctgtcctggt
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399

<210> 2657<211> 395<212> DNA<213> Homo sapien

ggcacgagga aaaaagagct gttgaatggt agatcatgaa catcagtatt tatctgagga
60acatcctgcg gaggaatccc ttcccatt tattaaacac aaaattgccg gtgtttcaag
120tagttctctg atcgatagac caacaactga aattaaatgc ttttagtctc aagtgcccat
180ttttattaaa atgtaattat catgaacaga aaaagcaata caaggcgtgt gttcttaata
240attctgccat tctctttttg acatttaaag gaagagccta ggctggatgt cttgatcaat
300aacgcaggga tcttccagtg cccttacatg aagactgaag atgggtttga gatgcagttc
360ggagtgaacc atctggggca ctttctactc accaa

395

<210> 2658<211> 388<212> DNA<213> Homo sapien

cgttgctgtc gatcgggcaa cccaaggact tcctcactgg catgtgcctc ttcctgcaga
60cgctgaggca aaaacagcct gagcggctgt gctcatgccc tgccttgag ggcaacgtgc
120tgccggagccc atttgcccgc atgcggccat aactgcatca ttggtcccaa tgggagcctg
180ggacctgtcg tgcgtgtcga agatggtgtg tgtatccggc ggtgcacgat gctgcgggat
240gcccagatg cgtcccat actggcttga gtctgcatt gtgggtggc gctgcgcgt
300gagtcaaaga gtactcatgg agaactgac agagctgagt gaggacgtca taattaatga
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388

<210> 2659<211> 378<212> DNA<213> Homo sapien

ggcaccagga gagagagaac tagtctcgag agcagnnntt tttttttttt tttttttttt
60tttttttttt ttttttttgg ggggccccca aaaatttttt tttaaaaaaa aaattggggg
120ggggcccccc ctttttttaa aaaaggggtt ttaaggggg ggattttttt cccaaaaaaa
180aggtgggttt ttttttccc gggggggttg gggcccccc ccaaaaaaaa aaatccccgg
240gggaaacccc ccccccccc cccggggggg gggcccccc tttttttggg aaaaaacacc
300cccccccccc cctttttcct gggggggggg ggaatcctcc tcggagaggg gggggggggg
360ggcaacaaaa aaacaaaa

378

<210> 2660<211> 382<212> DNA<213> Homo sapien

cgttgctgtc gattttccag ttgttttgct atattctgca aataaaaaacc gtgtttcctt
60tttttactta aacttttgta ggaaacaaac taaagcagac aaacatttct tgttatgttt
120gttgctttct ttaatccaat ggataaaaaa agtaaaaccc tgtaaacatt attttatttt
180tttatgcaat accatgctgt aaatatggtt catcaaataa ggatgtacct atgattgaat
240ctttaattct gcacagttag agtttatata taaacgtgtc ttgacaatca aggactttta
300tgtgagtctt cctttatgat gtttattaat gttatgcatt ccatttggtt tgaagtgaat
360accaatgtgc taatttgat tg

382

<210> 2661<211> 373<212> DNA<213> Homo sapien

cgttgctgtc gggaacttta aaaattatgt ctgtagttaa ataactaaat gtaagaaagc
60ctttaatatata ggtagaggtt attaaatagc acaattaaaa aaattttaga acttacaaat
120acaaaggatt attattttct caaaattatt atctttattg ctataatatt tatttaattg
180agcttttttg ttcaatgcac ttttgaatt tttctttgga aattactaca tgatgctttg
240gacagctttt aaatattttg tatatattca gtcccttaga ttttaaatat ttctgtttct
300tcactttttc ctctgttaca tgggtttcca tgtaacctct tcactatctt ggttgtcttt
360ttcttctaata gct

373

<210> 2662<211> 373<212> DNA<213> Homo sapien

tacggttgcg agaagacgac agaaggcct tattttgaaa tcagaataat ggaaattatt
60acaattaaaa agtccactaga aaaacagacc tattgtacaa agattccagt cttacctttc
120tcaagctgc ttactgattt ttctcttatg tctctattct tccccctcc ctttgcctt

180ccttttctccc ttctgctctt tgaccccaaa ctcatctttt cttcttagtt tattaataaa
240aaaccaaact atattactat caatatattt ttactatatg cagttcatat agtctcgtga
300ttggccaaag tctaatgggt cccaataggt cctcaatctt taaggcccag tccaaacctt
360ccacaatgaa ggg

373

<210> 2663<211> 378<212> DNA<213> Homo sapien

tacggctgcg agaagacgac agaagggaaa cctcgtctct actaaaaata caaaaaaact
60agctgggctt ggtggcatgt gcctgtaatc ccagctattt gggaggctga ggcagagaat
120ttctttaaacc tgggaggcgg aggtttcagt gagccaagat tgtgccactg cactccatcc
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240ttcttggaaac cttgtgcaga gggaagagta aaaagacctc cacacggccc actctgtcca
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378

<210> 2664<211> 378<212> DNA<213> Homo sapien

cgttgctgtc gattcagggg tcaactttgga acttgctgga ttatgggtgat ggtttttgga
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120ctacactttt ggtactattt tctttttaa tttttgggtg ctaagattta cactaatta
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240agggtaaatg tgtcttttcc tactattgag attttaaaag gctgtgatta agagagactt
300tattaatttg atctgaaaga agtagaaacc tctatgaaac aatttttatt ttcctttgca
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378

<210> 2665<211> 373<212> DNA<213> Homo sapien

tacggctgcg agaatacgac agaagggatg agagtgagga tgacatgtga tcccatgcct
60ccaagagcaa agccactgag gatggtgaag aagacgaatt aagtgtgga gaaaaggagc
120acgatagtga tgagagttat gatgactctg attagacccc agataaattg ttgcctgctt
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240tcttactggt aggatccttt ttggccctc ttttttttt ttttttttt tttaaaagag
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373

<210> 2666<211> 376<212> DNA<213> Homo sapien

ggcacgaggg ctggtttgtc tggggagaca gacaggatgt tgtggagctg ggggtggaacc
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120ggcaggctgg ctggccttgc tcccatcctt agaactgctg cctctccctg gatattccag
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240ctccccatgc aacaaagcaa cttacttctg gatttctct ccaaggagag gacacagaca
300cagttgtttg ctgtgttata tgttagctcc gaacaatggg tctcaattgg cttagcatca
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376

<210> 2667<211> 382<212> DNA<213> Homo sapien

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120gtgggcctcc ctgagtgcc tgagttaggt ggcataaggg gtgagaggcc atggtgtctt
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300tgttgtgaag gtcccggctt agcctctggc aggaaggagg tgctcaggag gtgggcacag
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382

<210> 2668<211> 371<212> DNA<213> Homo sapien

tcgaattccg ttgctgtcgc atttcacggg ttttctgtgc agttatggga gcatgacagg
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120gagacatggg tgtgcacaga ctgagaggca agaaagttgt atgatgaggg tgggggggtg
180tgcggataga ggttgaagcc caaaagcctt gaaagttcag tgttgaggct cagggtgggg
240accctagaga ggcaaaagat gccagccag atggaattgg tgggtgtgaat tgccaggact

300ggaaagagcc cagatggggg ctgcagcatg ggccttggtt gaagcctcta atcctgtaag
360ggctgctttg n

371

<210> 2669<211> 378<212> DNA<213> Homo sapien

ggcacgaggc ggatcagggg gattcagaag cgcttcagag aacaggagcg cagccgggag
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120tcccgggtca agggccagct ccaggagcct ggcctgcct ctgggacaga gtctgccac
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240cagccaaccc caccaggtcc cgaagctaag gagccaggcc tgggggtgga cttcattcgt
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378

<210> 2670<211> 373<212> DNA<213> Homo sapien

ggcacgaggc ggatcagggg gattcagaag cgcttcagag aacaggagcg cagccgggag
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120tcccgggtca agggccagct ccaggagcct ggcctgcct ctgggacaga gtctgccac
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240cagccaaccc caccaggtcc cgaagctaag gagccaggcc tgggggtgga cttcattcgt
300cacaatgcac gagctgcaa gagagcccc cggaggcatt cctgctcact gcaggtcctg
360gcacaagtgc tan

373

<210> 2671<211> 376<212> DNA<213> Homo sapien

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120tgacgcca gctgtgtgga ggacagccag gcctccatga agcagggtga ccagtgcac
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240ttccaggacc gcctggcccg gtgcaccatg cattgcaacg acaaagccaa agattcaata
300gatgctggga gtaaggagct tcagggtgaag cagcagctgg acagttgtgt gaccaagtgt
360gtggatgacc acatgg

376

<210> 2672<211> 370<212> DNA<213> Homo sapien

tacggctgcg agaagaccac agaagggggg gcacagccct gatgatggag gggctgctca
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120acatgatcgc cggactctgc atgtgaagc tctaccagaa gcggcaccg gacatcaacg
180ccagcgccta cagtgcctac gcctgcctgg ccattgtcat cttcttctct gtgctgggag
240tgggtcttgg caaagggaa acggcggtct ggatcgtctt ctccatcatt cacatcatcg
300ccaccctgct cctcagcacg cagctctatt acatgggccc gtggaaactg gactcgggga
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370

<210> 2673<211> 355<212> DNA<213> Homo sapien

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60tttcaaaaca aaatggtttc aatagagcgc catgatattt tctgacatt ttctttgaaa
120tagttgatac tccttctgca aattttgttg acagtgcctc taggttccaa aaagaagggt
180aacgccacta cagcaccttt gccatctgac cagcagcaat tctaagatgt cattgattct
240aagatgcac tcaattccca agatgttaaa atgaacaaaa tacatcactt aggatcataa
300acacatttta gttggaatag acacatttga agaccagatt tgaacaatga tcctg

355

<210> 2674<211> 361<212> DNA<213> Homo sapien

gcctacggct gctagaagac gacagaaggg atttaaaaga aaagcatata acataaaata
60aaaaagaaga ttcaatacgt aaccatagga gatacaaaac ttcaaagagc aggttaagga
120aagaagcctg agaaggaccg ttcagagaga cagataaaa gaaaaccag aagagaagtg
180taaactctgac gtcacaagag gaatgcactt tagaaaatag gagggctcaa tattaccta
240cagagagacc aaataagact aaattgcaca aagttcttga ggaagtgaag actcagatta
300tagactatat ttttgagaat attgggtatg aaaaagggtg acttgccac tcaccagttt
360t

361

<210> 2675<211> 356<212> DNA<213> Homo sapien

tatccgctgc gagaagacga cagaagggta cagtttacac ttttttctta aaatcatgaa
60agcggtttc tatcttaagc atatattgtg actactatta acagactgat ttgtgtagat
120attaaatgct ttaagctatt ttaccttttc aagaagttgt gttttttttt ctccaagtca
180taaccaattc ctgcaaagag gttcccatg acttgatgatt ataaagtaga caaccagggga
240attgcgcgag acacattttt atttaattct tttttttacg gaatgccctt gagccggaat
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356

<210> 2676<211> 366<212> DNA<213> Homo sapien

cgttgctgtc gaaataatag agctaaataa tgtcctgtca cttccattat aagaaatctg
60gattcatatc taagtgtata tgtataatac tgtacagtta agagttcaga acaagtggga
120atgtttttctc ttaatttaac tcattttgtg ctttctttac tcattcaaac acacatacat
180tttaccatata gtttattttt ttatgaaatg ctaatcttca gcccgtagga aaaagtagag
240tggagcctct ttgactact actatcaata aatttttaaat cagttggatt ttaagcatt
300ttttaaaagc tgacattaaa gtaaatctaa aaaaagttta acaaactggc caagacacta
360attttt
366

<210> 2677<211> 367<212> DNA<213> Homo sapien

ggcacgagcc ccagtcctat cccaggacgc cctgagggat ggacgcagcc atgcaccccc
60catctggggc ctctccctgc tccctctccc acctggcagc tgggagttct ggcttctagg
120cctgcccctgt caccaggcct ctgagtggcc aggcccttcc acctcccat ctgtaaaacg
180aggcagctgc ccggacagcc ttgggtcctt tagtggccct gcaggctctc tggcagctct
240gctgacccca cctctctccg gactgcctt ctgtcccaga ggggtcacc tgacccggcc
300caccttgcca ctgggctttg gactccagcc ctgacagggc ccagccacac tggctctgcc
360cctcgaa
367

<210> 2678<211> 349<212> DNA<213> Homo sapien

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60ccttctagta gcaatcacac cccagcagc ctggaactag agtattctgc caaagcagaa
120accctgtcac tctactcacc tatataatga ttttctgtga acttaggtat gaagttgaaa
180atcctcaact tgtcatacaa ggctctttat gttgtcctg ctttagtggc caccaatcta
240ccaccccatc cactctccca ctcccaacct tacacatgca caccctctc acattcaatt
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349

<210> 2679<211> 337<212> DNA<213> Homo sapien

gctactgttg ttagaagacc acagaagggg tctcaggtgt gatgcatttc tagcaagacc
60aggctggaat ggagaggggg taaggacatc cttcattcat gaggggaaca aagagtgttt
120cccatcccc catccctcc tcataaaaaa ctgaaaata atgcataaaa taaacaatcc
180atcaatcatg gggaaatttg aatcacatgt agcataatgc agggcatatc tgtaaaagta
240tcagtagagg atactacaaa tccccaaag cccacatag ccagagtgat cgtcttaaac
300cactaatagg attacttctt gaccgcttc aagcttt
337

<210> 2680<211> 470<212> DNA<213> Homo sapien

gttctttttt nnaatcccat cgattcgaat tgggcagag gtgcaacgct ggcaagtctc
60aaagtgcga cagaaacatg ccctgattc agtgcctctg cttagctgta acatgttaat
120cagaactacc tggcatcttc ctgaacaaga ctttcaatag gggccagtat gcttcgcttc
180atccagaagt tttctcaagc atcttcaaag atactgaagt actcttccc agtgggacta
240agaaccagca gaacagatat actttctctc aagatgtctc tccagcaaaa cttttcccca
300tgtccaaggc cttggctttc ctcatcattt ccagcgata tgagcaagac acagtgttat
360catacatccc cctgcagctt taaaaagcag cagaagcaag cacttctagc cagaccctca
420agcaccatca cttacctaac tgacagccca aagccagcat tatgtgtaat
470

<210> 2681<211> 420<212> DNA<213> Homo sapien

cgcacgagag agaaaacagg tggngagggt ctgattaaaa actatgcaca agtaggttta
60acaaaaatac tcatgaaaat gtctggaaac tgaaatttaa acaactgtaa tattaaggaa
120accagaatca ataatcact gtcttgccag cacagctaca gagtaacatg attcagggga

180ggaaaagtctt cttacagtta cttttataat tctttttttt ttttctctt aggttaaaaa
240ctctaactaa ttttaacttt atctttttta acttatttga acatacttta gaattattgaa
300cctctaaacc caaatgttta tagataccct cttatccata aacaaaaccc tgctaagcca
360tggctctatt ttttttttgg cttatagagg ccggtaacag tttttttgca ccaatatatg
420

<210> 2682<211> 440<212> DNA<213> Homo sapien

gcaggagccc atcgagctgc ttgtttgggc cgaagcggcc tacggctgcg agaagacgac
60agaaggatcc tgaatgtgtg tgctactttc caccttcacc accaccaccc tagtccaagc
120ctccacatca ctctctgcta cgatcctcca gcctctccca tgatggcttt ttttctgtcg
180ctcagctccc agttctctgc tcttcacact aatcataaca tatcatttct acctccatgc
240ctctgtgtga tctcttcccc aagtctagat tgcataacc ectggccac acacagctct
300tcttgacact cagatcctca acagtgactt tctgaccac ccaaactaat aaagatacta
360gaaacttttc tcattctccc cccaccacct ttttttgaga cgcttttttg gggctctcact
420ctgttgccca ggctgggtgtg
440

<210> 2683<211> 427<212> DNA<213> Homo sapien

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60atccaaatct cgggagatac gccatcgcca caggtcccgc tccagcagcc gtagccgag
120ccgtagccac cagagaagtc ggcacagttc tagagatagg agcagagaac gatccaagag
180gaggtattga tgtgtcaatc agaggatatg gagctacctt aatgttttag agttgtttat
240gtttacttat gttacttatg tttatagcta cagattattg gtttgaatct ttcgcatacg
300gtgctatgtt cacatttatg tgcgggtgca caacattttt ctgtgattat atgggtaact
360atgactgaat atacttatga agccgagcac gacattgtaa ccaatatgtg tagaggttat
420tgctttt
427

<210> 2684<211> 468<212> DNA<213> Homo sapien

gcaacagaga tgtaccngnt tnnncgaaga tcccagcat tcgttatttc gttgctgtcg
60ggaaaactgt aagaagttta cccactctg attattccac cattgccaga gaagtttata
120gtaaaaggaa ttttggacg ctttaacgan gacttcattg agacacgcag gaaggcttta
180cataaatttt tgaaccgaat tgctgatcat ccaactttaa catttaatga agacttcaaa
240attttttctca ctgcacaagc ttgggaactc tcttctcaca agaagcaagg tcttggttg
300ctaagcagga tggggcaaac cgtcagagct gttgcgtcct caatgagagg agttaaaaaac
360cgcccagagg agttcatgga aatgaataac tttattgaac tatttagcca gaaaataaat
420ttgatagata aaatatctca gagaatttat aaggaagaaa gggaatat
468

<210> 2685<211> 419<212> DNA<213> Homo sapien

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60aaagataaac gaagttatga agctctttat cctgtacctc agcatgaact gcagcaagga
120caaaaacctg atttccattg cctagaatac ttcaagtctt tcaattttta cacactgctt
180ggagaagagt ggaaacaacc ggaatcagac ctgtggctaa tagagaaatg tgatatatag
240gagtaataga taaccatacc gatcattttt tctctatac cttttaagat aaacaaaaaa
300taaatatcaa ttttttaaga tgcatgcat acatttcaac aacaaatatt ttcatagaag
360tcaactgaaa tatagtatct gtggcaaat gtatatgatt aacaagaaaa tatatgatt
419

<210> 2686<211> 428<212> DNA<213> Homo sapien

ctcagaagag cttacggcat tggggatccc cttcttgagt cgtggggctg gcttcttcat
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120gcgccgcttt ttggacaaca aggtgctgct gtcttttggc aaggccttcg agtgtaaaga
180gcctgggttg tttcgctttg tcttctcaga ccaagtccac cggctttgcc tggggatgca
240gaggggtccag caggtgcttg caggcaaatc ccaagtggca gaagaccccc gtccctctca
300tagccaggag ccaagtgacc aacgcagggt agctggctat tgtctcgtgg ccagagggcc
360cagcagccac tgtggacctg gggcgttctg gcgctgcaca agactgactg tggatgtgcc
420atttgcca
428

<210> 2687<211> 426<212> DNA<213> Homo sapien

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60gccggggctcg tggccggggc cagttgacct tcaacgcgga ggccgtgggc attgggaaag
120gggatgcttt gccccaccc accctgcagc cttctccact ctteccctcc ttggagtcc
180gcccagtagc tttgccctca ggcgaggaag ggaatatgt cctggcactg aagcaagagc
240tacgaggagc catgaggcag ctcccctact tcatccggcc agctgtcccc aagagagatg
300tggagcggtta ttcagacaaa tatcagatgt caggtccgat tgacaatgcc atcgattgga
360accctgattg gcggcggtcta ccccgaggc taaagatccg agtgcggaag ctacagaagg
420aacgga

426

<210> 2688<211> 397<212> DNA<213> Homo sapien

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60cacatagttt acaaatcatt taaggcaagc ttaccatctt aagacaattt aatacataga
120agtgtccctc ctaaaaatct gagtttgatt tagaaatcca gttatacctg caggtagtga
180tgactaattc cttctttgaa gacaaaataa gcagctgtgt agcttcagtg gctctcaaat
240ggataataga ttcagtgtat actcgctttg aactttcctg ttttttgatc agctagataa
300atgactttag tgggtaaatg tctgctcca aaaccaaatt ctgacctga tctaagtatt
360ctaactgcacc gctgtcactg gaatatcaaa gttggcg

397

<210> 2689<211> 391<212> DNA<213> Homo sapien

gtttaaaact tttgacaagt ggtagtccta ctgtttacac tcacagttta tgttcatacc
60tagttttata agctgttctg taacatagtg tagcaaaaaa aaaagttcaa gtcattgtat
120acagggtgtg caaaagggtat cttggtcatt aagtattgtg cagtgcatta tttattatcc
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240tgcttttttt tttcttttgg acccatgggt attataataa aaagcatttt gtacctgagg
300ggccctaatt gaaaaaagtg ctgctcaaag gaagtatgaa gttatatatt aaatttttta
360attttaattt ttaatttttt tgctgtgaag g

391

<210> 2690<211> 416<212> DNA<213> Homo sapien

ggcaccagggt gtgtgtgtgt gtgtgtgtgt gtgtataaaa ccaaaatgtg tgacacaata
60aatgctggca cagctctgat ttctttttaa aagaaaatta aaataggagt tctggttcta
120attattagct attagctact tctgaaattc agaaagtacc ataattaggc taaaggggta
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240ttagtttgtt tacattagta accaggccat gccaacacaa gtattccagt ccattgtgat
300atattttctca atgtaaatga ataaactgaa attctaattg taaacatttt ttcataaatg
360tagttagaga cccctctgaa agacaaagca gcttttgcca tgctgaccaa attaga

416

<210> 2691<211> 412<212> DNA<213> Homo sapien

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60gaggagcagg ggaggaaaga accctgagga accaaatcat attaggagac gaggtgaaaa
120tggtactgag ggagtctgta ggaagcttag caggaaaatg gtgtataaga acttagggag
180gagagtttcc tgaaggaggg gcagtaattg cagtatcaaa tgctacagag aggagaggga
240tgatgagacc ttacaataag cttttcattg tatttgctct ttgggggcca gtgagaaggg
300aaaactgagg gtggtggagg ctggaagcta gatcatgat agctaaggag tgagttggag
360ttgagctatt tagactagtt agagctttga tttaaatatt tggtagtcat gg

412

<210> 2692<211> 368<212> DNA<213> Homo sapien

tacggctgcg agaagacgac agaaggagg aaaggctcagt cagcctgcac ttgcaatatc
60agaatcagct tgctcctagt ctagtacaa tcttctcac tgggagatct gggctgcctt
120tctgagggca cactgcaaag gccaccttct catctccctc tggcctgcct gtcagctctc
180agagagctga atgggcccctg ccaccaacag tctgttgtgc ctttctgact gtgacacgaa
240tgactacca cgcaaagaag ggctccgtgt cacgagcgt cctagctggc tctccgtctc
300gggtgtccca ccacgggaac ttgagaagaa gctgaacctc tcaaggcttc cggtagtctg
360cttttaaac

368

<210> 2693<211> 388<212> DNA<213> Homo sapien

gtgaaaagtg ctcatctgtg aactctatag caaattatat tttagaaaat actttgtgag
60gccgggcatg gtggcagagc gagactccgt ctcaaaaaa aagaaaagaa aagaaaatat

120aaggatgttaa aagaagcaat ttgcttgac atctgaatat ccttcttggtg tctccatttt
180cactcttgaa aactgaaagc aatttgactt ttatttttgt tttctaaag aacagctagg
240tgaaaggagg ttaagctgat tgtcactctg cctgcccact acctactccc caccatgggtg
300tttcatgaaa catccccacc acctgaagtg atctttttaa tccttgatgat agtaaatagca
360ttgataatta acaggaaaaa catgtttt

388

<210> 2694<211> 377<212> DNA<213> Homo sapien

tacggctgcg agaagacgac agaagggatg aacagcagaa gagaattatt ctacaataag
60aaatcaattg gtctctcaac tgagaatcac tagcaagaaa ctggtaaacc aaccaacaag
120tgggtaaagg aaatgtgaaa ttatataact aaataaatac acacaaacac acacacacac
180acacacacac acacacgcac acacacaagc acacaccata gaatactact caaccacaca
240aaggaaggaa ataatagcat ttacatttgc agcaacctgg atggagttgg agatcattat
300tctaagttaa gtaactcagg agtggaatac cacatctcgt atgttctcac ttataagtgg
360gagctaagct ataagga

377

<210> 2695<211> 380<212> DNA<213> Homo sapien

ggcacgagag acagtctccc cctcagatgc catgctccca ctgtaccacc atgtactgct
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120actaattaat tccagctaag ggaattgact ggaattagtg acattaatat ttactgagca
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240gcaaccctat gacataggtg ctactatgcc cattttgtag atgagacagg ttcaggggag
300tttagtatcac cttcaagtca tacagtggct aacaatctgt ggtctcgtg aatgctgggc
360gcctgctctg ctaagtctac

380

<210> 2696<211> 399<212> DNA<213> Homo sapien

atcggcacga gattgattgc tgttgcgaa acttgaggtt acttacagaa tgaagcacat
60tttttacata cagtacaaat gagtgtgtgc tttttaaatg gatttaaat tcaaatgcaa
120atctgcagtt taatctccca agtgctgatt tttctatgta taaagtagga gagtgcaca
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240cagacactca gtattacact cctgctatct ctccagagca ggtgaaacag acggccagga
300agcacacgaa gagacactca gcatcactgc ttgttaagga aggtgcaaat caaaaccaca
360gtgagacgcc acttcacacc tacaagttcg gctagatan

399

<210> 2697<211> 408<212> DNA<213> Homo sapien

cgttgctgct gctggagaag cagccttata cagttgattt tgtgtatgtg gctagtctta
60ttgtcactat gtaagtaac caatggtttt agaaactaaa ctttctagag caataaaatg
120actataatgt taagtaaca taatgttgat ttctaattat gttttaaaaa atgaagtctt
180gaattatata aagaaatttt ggcagctgaa gtcattgtta ttttgaagct gttagttttt
240tcctataatt taaaagatc ttttagattt atagaagagt cagaaatgta caagagagtt
300tttttgttgt tgtttttgtt ttttgagaca gagtctgtct ctgtcgccaa ggctggagtg
360cagtggcgca atcctggctc actgcagcct ctgcctcctg ggttcaag

408

<210> 2698<211> 406<212> DNA<213> Homo sapien

ggcacgaggg aagcatttac agttttaaat ttcccagtc gaataaattc ttattgaggg
60caatacctag cctgtcttca tcaaactcat aggtgaatct ttgtcaaacc tataggagag
120agatgcaggg catagagatg gtcttgctga aggtcttata gctaaattag ttcagatcca
180ggaaccagat tctggaactg attgcaccta tattatgttg tgtgtcagac actcccagga
240cctgttttgt aataattagg acagctgaca tacttgttgc taattttgag atctgggcaa
300caactgtgta ggctgttctt tcaacctctt tcttctact tctttacttt tccttcacag
360aggagaaagc cacccttggg gtatagccac cgctccaatt ctgact

406

<210> 2699<211> 374<212> DNA<213> Homo sapien

tacggctgcg agaagacaac agaagggtc tcaaactaat caatcaaca aacaaacaaa
60caaacaaaaa agacactttc tagaagagat agtaacgata tctacctcat gaattaaatt
120acttggtgtg aattaagtgc ttactaggga ttaccacatc attaactatt attagtaatc
180ttacagtcac tattatcaaa tatgtctcaa aattaatgca acctgtcagt ctagtacatc

240caaaagtgcc acagtgcttt ttggaatta aacaaaacaa ttgcttaaat gtgcatcata
300cattcagagt aattcttatt caagcaagct gggtttatat tcatgacaag ctttttcaat
360tttaatatgt ttgt

374

<210> 2700<211> 406<212> DNA<213> Homo sapien

ggcacgaggga gagagagaga gaactagtct cgagagcagn nntttttttt tttttttttt
60ttttttttt ttttttttg ggcccccccc cccctttttt ttttttttaa agtcccccc
120caaaaccccc cgggggggggg ggggaaaaaa aacccccct ttaaggggg ggggaaaaa
180aaaagtttt tgggaaaaaa aaaaaatttt tttattttg gggggcccc ccccccccc
240ccgggggggg gggggggccc ccccccccc taaaaccccc cccccgtgg gtttttggg
300ggcccccccc cgggggctta aaaagggggg gggggggggg ccccaaat tcccaaagg
360ggggctttat ggcccccca tccccaaat gtggggggcg gggggg

406

<210> 2701<211> 395<212> DNA<213> Homo sapien

ggcacgagat ggtctcaatc tctgaactc atgateccac tgcctcagcc tcccatagt
60ctgggattac aggcaattag aaggaccatg tgactaatct atatcatttt cttagagata
120aagctgagat ccaggaggct atgctaaaga gacataggta actgtggcca agctacagcc
180agattccatg ttttaagact ctcagtctta ttttctggg tggggaaggg gaatgaaatt
240ataactttgc aactatcctc acttctcct acctacccaa atagaaagta gtacacgttc
300acaggacagt ggtctcatgg acttgtttct ttttctttc aaatgaaatc ctttaagaaa
360tctaaaaaca aatgagcaca gatgctctgg ctcaa

395

<210> 2702<211> 394<212> DNA<213> Homo sapien

tcacaatcca atatctgtgg aattcattgt gtatgtttgt gtatttgtgt gtaggtgtgt
60atgtgtgtgt gtgatacata catacatcac gtatcacaa acattgacct tatatattat
120gcactgtgat gtttttccgt ctttaatttt aaaaaacata ctgacacaa ccacaatttg
180gaaaatgttg ctccatacca tcccatacca acatcacca cctgcaaata atagcattac
240taggagctgc agtcacaatg aataaatcaa caattcgcta caagatctag gattatttgt
300gtattttgtt gagagtgcga gcgcgttggc gtgtatctaa taccattgta tctcattgtt
360gagactttgt tacaatagg gtttctggtt tctt

394

<210> 2703<211> 376<212> DNA<213> Homo sapien

tacggctgcg agaagacgac agaagggt atcctactta ttatttatgt tttacctct
60gtgtccaaca cacacacaca cacacacaca cacacacacc cttagaattg
120gggctcctta agagcaggga ctttatgggt cttatggagc aagactttat gggctcctgc
180tcttatgcag ggctgttca cctgcacctc cagaacctgg aacagtgtta ggcacaaaat
240atctgattaa taaatttgcg ctgaaagaga gaatactcca aaagggtctc gtatgagtga
300agtggagatta ttatctataa agaattttgt ggaggcatgg caccacataa gcaccacaca
360cacagtattt ccagta

376

<210> 2704<211> 407<212> DNA<213> Homo sapien

ggcacgaggc cagtggagct aaagagctga gatattttg taaatagagt taataggatt
60ttctgatgat gtgggtctgg ggatcagga agagggacaa tctactgcta ctgaattact
120ggttttaagta actaggttagc ctttattggg aaagactgag agggaaactgg ttgtgggga
180aaaggactat gtttcaaggc atgttaagtt ttagatatct ttgagatatt caagtggaaa
240tgtcatataa gaactggaaa caaagttcag gactcagaag acagggttaa aattaaggg
300caaattttag agttattagc atacagataa tatttcaaat ttaaaagttt ttttaataat
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407

<210> 2705<211> 389<212> DNA<213> Homo sapien

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120gggaaccttt ggaaaaaaa gtaaggggtc ctttaaaggg gatcctgttt tgaaaaaatc
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240aaccaatttt ttttcccta agttttttt tgggctcgg catttaatat tccaccggg
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389

<210> 2706<211> 376<212> DNA<213> Homo sapien

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120ttcttatgga gtgttagtca tcaatggagt ggaaagaatg cagtcaaacc tgacacctga
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376

<210> 2707<211> 375<212> DNA<213> Homo sapien

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120cagaaatcta tacactccag accgagaata tatcccgaa gtcagcagttt atatgaggag
180tcaactggaa atcattgcaa gttaaagaaga gctagattaa tcgctatcct taaagaataa
240actaggcaga aacattagaa cagctgcttt caaatgtttt cagaactagg tataatgggg
300gaaagaagct caggtatttt agaggtaata ctctttttt attcctattc ttatttaaga
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375

<210> 2708<211> 413<212> DNA<213> Homo sapien

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120ctgcttgaaa ttttccatt ttaagagaa tatgggaaca tttcatatga tctccatcac
180gaagatagt aagatgctga agaaacatca gttccagaag ctccgaaaat tgctccaata
240tttggaaaga aggcagagt agttataacc cagagccctg ggaaatacgt tccccccct
300cccaagttaa atattgatat gccagattaa actcctagag aggaccagg cacacacaga
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413

<210> 2709<211> 395<212> DNA<213> Homo sapien

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395

<210> 2710<211> 383<212> DNA<213> Homo sapien

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120aaaatcccct tgcaaaggaa tgtgatacca agtgtgaccc gaggcttca gcagaccatg
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383

<210> 2711<211> 386<212> DNA<213> Homo sapien

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120actgtggcgc ggcactgctt gaccgagggg ctccggagcc cagctgcacc ggtgcggtt
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386

<210> 2712<211> 382<212> DNA<213> Homo sapien
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120actcctctc cagggtcttc tgacatccaa ggccctttga aatctctctc cacctgcgaa
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382

<210> 2713<211> 409<212> DNA<213> Homo sapien
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120gggcccctctt attttattat tgcctgaaag gttgcttgaa cccagggtttt cccccatccc
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360gttgccaaa aaaaacccaa tatcttctcc tgtggcgttc acccccccc
409

<210> 2714<211> 408<212> DNA<213> Homo sapien
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408

<210> 2715<211> 377<212> DNA<213> Homo sapien
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377

<210> 2716<211> 388<212> DNA<213> Homo sapien
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120gagggagtag ctgacaggct tccacaagcg gaaggtcgag cgaaagaagg cagccattga
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388

<210> 2717<211> 396<212> DNA<213> Homo sapien
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120ctcacttccc tgttctctg gtactgctac cgcctgggct cccaagacat gcaggcccta
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396

<210> 2718<211> 386<212> DNA<213> Homo sapien
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60gcctgaagca ggccgtggcg cagctggagg accaggccta gcactggggc cgccttcccc
120accccgtttc tgggaagccc gtggcagggc acagggttgt ccctccagtt ccctcctgag
180ggctgtgccca ggatgactgt ctcagcccc ctctgcattt tgcctggag tgccagcgag
240tgtgcacccc cagtttcctt ccctggaacc ctgcagagct cacagggccc aggacaccaa
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386

<210> 2719<211> 371<212> DNA<213> Homo sapien

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120atgctgagga caggtgcttc cctgcctagg ctacctctcc eggcctgtcc ctggctccct
180ccctgcccac ccctggctct ctccctgccc cagggtagag gtggaatgag ggtatgagag
240aatagcctga gacacaggca agggcatggg tgggagggca gtccaggagg gtgggactga
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371

<210> 2720<211> 389<212> DNA<213> Homo sapien

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120gagggatgaa gtcataggac aacgaaggcc tgttctcgac tacacagtgg ccaattcctg
180tttctgtggg agtgaccacc agccccaccg gctgggaggg agtaagtggg gatggtatcc
240agcagaagtt tcctgagaaa ccctggaggt gtctgatata agccttgtgg acctgctccg
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389

<210> 2721<211> 404<212> DNA<213> Homo sapien

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120tgccgtgttg agaaaagact gcaaggggga aggggtggaag cgaggagagc agtttgaggg
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300gcttttctta cctgtcacc tgtgatgtga aatcatgcat ttagagcaac ttggtaaata
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404

<210> 2722<211> 384<212> DNA<213> Homo sapien

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120ggaatacttg aagatgctgg cagagagaga agaggctctg gaggaggcag atgagctgga
180ccggttggtg acagcaaaga cggagtcggt gcagtatgac caccaccaacc acacagtcac
240cgtgaccacc atcagtgacc tggacctctc gggggcccg ctgctcgggc tgacccacc
300tgagggaggg gctggagaca ggtctgagga ggaggcgtca tccacggaga aaccaacca
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384

<210> 2723<211> 403<212> DNA<213> Homo sapien

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120gtgtgtcact ctgagtctgt gtctctctgt gcgcgagaga ccccccccc ctctcttctg
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403

<210> 2724<211> 397<212> DNA<213> Homo sapien

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60ggcacaggag ggattatatt cattgtatcc atttattaac tcattaatta ttactgtatc
120aatggaagat gatttgatac tgttcaccca ggaaaatccc ttttttagaa aactcagcag

180taagacctac agatcagcaa aggacctgac aaaggggaacc atcgtgctga agtatgaacc
240agattctgtc aatccagacg ctctgcagag tcccatcgtc ttatgcggat ggcatgaaa
300ggcctccatt ccaacttttg tgccctagaa tgaacggctt cattatctca agatgatgga
360gctggaggta ttgggagaaa agaacaatga aggagtg
397

<210> 2725<211> 392<212> DNA<213> Homo sapien

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120cccagtcctt gccctcggac cagccggtgg ggaccttcag cctctgacc acttcggata
180ccagcagccc ccagaagtcc ctccgcacag ccttggccac aggccagctt ccaggccggt
240cttccccagc gggatcccc cgcacctggc acgcccagat cagcaccagc aacctgtacc
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392

<210> 2726<211> 402<212> DNA<213> Homo sapien

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402

<210> 2727<211> 411<212> DNA<213> Homo sapien

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411

<210> 2728<211> 402<212> DNA<213> Homo sapien

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402

<210> 2729<211> 359<212> DNA<213> Homo sapien

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359

<210> 2730<211> 347<212> DNA<213> Homo sapien

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347

<210> 2731<211> 342<212> DNA<213> Homo sapien

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342

<210> 2732<211> 335<212> DNA<213> Homo sapien

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335

<210> 2733<211> 345<212> DNA<213> Homo sapien

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240ttctaaaaaa tccctaagaa atttcttggg atgagtcttt ggctcagag cctctcaaag
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345

<210> 2734<211> 336<212> DNA<213> Homo sapien

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336

<210> 2735<211> 356<212> DNA<213> Homo sapien

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240agaaggaaga ggataagagt aaaaggggga ataaagaatg tgaaggcac agagtacaga
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356

<210> 2736<211> 351<212> DNA<213> Homo sapien

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351

<210> 2737<211> 344<212> DNA<213> Homo sapien

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240tgcaagccag cagtgcaatg ccacatcaa gtttggtaaa tcaattctaa gtgagataaa
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344

<210> 2738<211> 353<212> DNA<213> Homo sapien

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120caattcagtg accgcagcag tcccttcaat gctgcatgag cctgggtgcat gagcctgtaa
180ctgttttccc tctcttaaga gcagtgtccg tttcttctc atcttagagt ctctgttgcc
240tagcacagtg tggctaatag aggtgtctca gaaacatttg ttgagtgaat tgcgtaaatg
300gttataatca catctgaatt aataaataac ttaaaatgcc actgccgagc ttg
353

<210> 2739<211> 342<212> DNA<213> Homo sapien

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120actgctcaac ctaaagaaa tcttcaaacc caagtatcca ctaaggctgg attcaacaaa
180tggttttagg gccacagtaa atatttcagg tttggcaggc catatagtca caattactaa
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342

<210> 2740<211> 336<212> DNA<213> Homo sapien

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120aacctgtca ctctactcac ctatataatg attttctgtg aacttaggta tgaagttgaa
180aatcctcaac ttgtcatata aggtctctta tgtgtctct gcttagtggt ccaccaatct
240accaccccat tcaactctcc actcccaacc ctacacatgc acacctctt cacattcaat
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336

<210> 2741<211> 341<212> DNA<213> Homo sapien

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240cctggcagtg tgcaggccca tgttgagcag ggccctgcc cttccttggc acctgtatg
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341

<210> 2742<211> 340<212> DNA<213> Homo sapien

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120ggaagaatca caggccaact gaatgtggag tcagaccacg gtgttcagt gatctttgt
180gtgcatgtt aaattgccac aagtgatgat ggaagtagtt agtgggtgtg gaaaggacag
240tgaggggata caggaattaa atcttgaagg aatgcttctg gataatgagt ttaatccaaa
300aactcattgg actaaatgaa ttttgtccat cgcttcaaag
340

<210> 2743<211> 420<212> DNA<213> Homo sapien

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60cttgggaaga aaacgtctat tttttcccc tctctgcat cacttttttg gtttttgttc
120tttttattct tttatttttt aaacccatga tctttttcc tgtgtccaag tgactgtgtt
180gcaggcggcc cggtcttggc agggactggt ggggacgcgg ggagcggccc agggccctgc
240cccgcggggc tcagcctccc atgcgctcgc gcttgctgt gtcccgggt tgtctgtgaa
300gtgggcgtga agatcgttgc caccttccaa cctacctac aggggtgttg tggggacacc
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420

<210> 2744<211> 438<212> DNA<213> Homo sapien

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60cagaagggct tgggtggttg aataggtaat cagacaaaaa ctaaatgaat tttattgtt
120atgaatatag actcactaaa tcagttagaa cctgtgtaga cacaaatcaa gattttgtct
180aaggatggtg aaaatacata tctgggcctg tggctgcctg aaagttaaag gagagttaca
240tatttttaaat actgaataac ttttgaaacc agcacgacac tacaactacc attattacta

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438

<210> 2745<211> 420<212> DNA<213> Homo sapien

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120agcttaattc tgaacttcaa agtaatattt tatacttaat ttaggagtt ttcatttaca
180tattgaaaaa tgccttgact gtattcacat aaatgggtgt aaaacattgt accccttata
240agaactgcag caatccacag taatgttggg tacttctgag tatttgataa aggaacaaag
300tcaaaatgaa tgtatttaac aagcttcttt ctcatctcca ttgtttttat aaaaatattt
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420

<210> 2746<211> 424<212> DNA<213> Homo sapien

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120acgaggcctc cggactggga cctgtcgtt tctgcagcac ctgggtgtcta agtgcctcct
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424

<210> 2747<211> 343<212> DNA<213> Homo sapien

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120acgatttttag tgacaaaac tatggataaa actgcctaag cataacatta atatatttag
180aatgycattc ttcagtgtc gtatttgaaa ttggaattag tacattgtgc attcttagta
240ggctttatcc ctagaatcaa ttctctcagc atcacaaaac tgaattgggtg aaatagtgtc
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343

<210> 2748<211> 337<212> DNA<213> Homo sapien

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120gtgggatttg aatgcccatt aaagacattt tattttactt gaatatattc ttgcttact
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240ttcctaacca ttcagtcagg aattaaaata tggcattgta taacaactgg gaagaagctc
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337

<210> 2749<211> 406<212> DNA<213> Homo sapien

ggcacgagga gagagagaac tagtctcgag agcagnnntt tttttttttt tttttttggg
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120ctgggtcccc ggggaaaacc ttttacccca aaggttttaa ccgtgggcaa ttaaccgaa
180cctaaaaattt tgggaacata aattgggtgg gggcccaaag gaagggaaaa aaaaaattcc
240tttctttttt tccccctt ttttttaaaa aaaaccccc cccccctt aatattttt
300ttagggggcg cctttttttt cggggccttt gaaaaacggc tttttttttt cctttcccc
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406

<210> 2750<211> 371<212> DNA<213> Homo sapien

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371

<210> 2751<211> 340<212> DNA<213> Homo sapien

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120tgatgtgttg ggtaagagat ggtttaaaag tccagcttgc tgtttttcat taagtgtctt
180gaaaatgagt aagtggcgtt cctggagggg aacaatcata taattccgca gggtaggtct
240aaacttgttt tctgatagtg tttagcagct catggctctg agggcacctg ataacacagc
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340

<210> 2752<211> 397<212> DNA<213> Homo sapien

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120ccgtggtggc tcacacataa tcgcagcact ttcggaggcc actgcaggaa gatcacttga
180gcccagaagt taaagaccag cctgggcgac agacacttcg tggcttattt ttttttaatt
240attaaaaacg aaattttaac caggtgtagt ggctcaccct tgtaattctca gcactttgga
300atgctgaggt gggcagatca cctgaggtca ggagttcag accagcctgg ctaacatggc
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397

<210> 2753<211> 350<212> DNA<213> Homo sapien

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60gccacctcc tcctgcagtg tgctactctg ctctgtgact gtcctcatg cagctcgcag
120ccatgtttcc tctctgcttc ttgatttgtc tcagctcctt ctagtgcctt gaaactgaag
180ctggcctgta gttgggatca aagatggagg gagaggggag attgtactat ggatagtgtg
240gggcaagaag tgaattctta cactggaatg ataaaaggaa cctgcttctt gagtttctta
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350

<210> 2754<211> 381<212> DNA<213> Homo sapien

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60caatagtctt ttctacaagc agaacattaa tattctgtc actctgaatg taggcacaga
120tttttgtcat cttttatctt ttttgtgtgt gtgtgacaga gtctcactgt caccaggctg
180gagtgcagtg gcgtgatctc ggctcactgc aacctctgcc tcccagggtc agycgattct
240cttgccctcg ctttttgagt ggctgggggt gcaggcgcgt gccatcacgc cgggtcatt
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381

<210> 2755<211> 388<212> DNA<213> Homo sapien

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120ggaagacaat tctaaatgca taactttctc atggtctaag gttgtgctgt tcactatggg
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388

<210> 2756<211> 368<212> DNA<213> Homo sapien

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120aaagacagct gcctgaaaaa gtccctgac taagcatgaa tgaaagataa actttatgtc
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368

<210> 2757<211> 369<212> DNA<213> Homo sapien

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120agattcagat cactaacttt ccattctcca ctttttccag tgggtggccat gttcccccg
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300gattgtctc aggtcttggg ctcttgccc atagaccagt ggctctgtgt tctgatgggg
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369

<210> 2758<211> 405<212> DNA<213> Homo sapien

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120aaaaaaaaa aattagccag gcatgcgaaa cgctgagggg ggaggatcaa atgagcttgg
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405

<210> 2759<211> 399<212> DNA<213> Homo sapien

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240aaaatgggcc tagtgaatc ataataaaa tgggtcagat taacttaatt cagattaaga
300aaattgtttc atactgaggt aagcgattga aaaattgtct atttaaaat gcagtgcatt
360ttaagagtt actatttgag gatctaaaat atacagaga

399

<210> 2760<211> 375<212> DNA<213> Homo sapien

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375

<210> 2761<211> 374<212> DNA<213> Homo sapien

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120ggggggggcc cccaattttt taatttttta aaaagtgttg gcccgggggg gggggcaaat
180ccctgaaacc cccccctttt ggaagcccag ggggggggga cccccggggg cggggatttc
240aaaccacccc tccccaccg gaaaaaaccc ccccttttat aaaaaaaca aattaacccc
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374

<210> 2762<211> 375<212> DNA<213> Homo sapien

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375

<210> 2763<211> 398<212> DNA<213> Homo sapien

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120cagtgatatt tacttagaat gggtaattc catttaaac ttttttttg ctgctcaggg
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240ctagtgactg cataatacga ggggctggag ccctgatccc tgcataagg catgtaacag
300cctgcatccc tagatttcag ggataactct ctgaagcctg gaaagggtca gtattccaca
360ggctgcgccc tctcatgctg tccattttga gtaacccg
398

<210> 2764<211> 376<212> DNA<213> Homo sapien

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60attgttcaca tgagaacatg tcctggcaaa aaaagaaaga gaaaataaga gaaaacaact
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300tttcataaga cactcttgtc tttgagtaag tttcttggtt gtaaacaaca caacacaatt
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376

<210> 2765<211> 383<212> DNA<213> Homo sapien

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383

<210> 2766<211> 373<212> DNA<213> Homo sapien

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120tttcccaacc acttccccct taacttgctt tccctgaac cgtagcaaat agtaatgcat
180gacaagctga taggagggaa aacatgacaa gtgaggttga gttagaaagg aaaagcaggg
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373

<210> 2767<211> 379<212> DNA<213> Homo sapien

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120acccactgcc catgactgct actccccgaa agcttccaga ggtgagagt gcaccacttg
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379

<210> 2768<211> 338<212> DNA<213> Homo sapien

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120ctgaggaagt gatgaaagaa tggaaatcaa tatgtaagag ctacaaagtc agagtgagat
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338

<210> 2769<211> 390<212> DNA<213> Homo sapien

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120tcttagctac tagggaggca gagggtggag gatcacttga gcccaggagg tctagggtgc
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240aaaaaaacca ccaacaggga aaggccagga cgacgaggag aagttggtat ctttttgta
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390

<210> 2770<211> 375<212> DNA<213> Homo sapien
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240acacatggag agatattttt aaaggtcttg tactacataa attgtactat tttttaattt
300aaaaatatgg gccaggtgca gtggctcaca cctgtaatcc tagcactttg ggaggccaag
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375

<210> 2771<211> 379<212> DNA<213> Homo sapien
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300tgcttgggtg ttgtaccagc gccaaccttc tgatgtttgt tgaattaatg aacaccatt
360tttcagatca ggaaagggg

379

<210> 2772<211> 330<212> DNA<213> Homo sapien
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60aatttaaatt tcaaaataag aatgttgaat ttttaaaaag caagttgctg aggtaataca
120aatgtatgac acaacttata tatagtttaa acataatata acaagagcaa atagtaaatt
180atgaatttga atgcatatgt gtggagagtg tgggggtgag tgtggatgtg ggggggatgt
240nnnnnnntnn tgnnnngntg tgtnntann ngtnntttt tttctttttt ttgntttttt
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330

<210> 2773<211> 348<212> DNA<213> Homo sapien
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60tttatgtata gataattggg ggcacaaaac attctaggga acctccaaaa tatttactag
120aataaataaa attagcaaag ttataatgaa acataatgtg gccaggcatg gtggctcag
180cctgtaatcc cagcactttg ggaggccgag gtgggttgac cactgaggt agggagttg
240agaacagcct ggccagcatg gtgaaacct gtcttacta aactacaaaa attagctggg
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348

<210> 2774<211> 408<212> DNA<213> Homo sapien
gtcttgctgt tcttaaccta ccaaagcagg caagtagacg cacatgtgtt ttacacagt
60cattggaaga aggttgcaa taccagcttg gttgcaagga aagaggcaat tgtgaggact
120ccttctcaca ctgcagtaat ttgctgagt accttgaaca aggatcttaa tgcacagag
180tctgtttcct caacccaaa atgaagggt tggaccagat gccctcaagg ttcctcaagg
240gtcagctgtc acagttctcc aaagtgagt ttcaggcaga catagagtta gccagtgtc
300cctcaccagg acattttgtt ttctgaacat tgggcctctg tggttgtca catacacca
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408

<210> 2775<211> 337<212> DNA<213> Homo sapien
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60aatgcttaaa catgcttcag tagcctcagg ataaaactct gtgtaaggc atcaaaggta
120ctcaaattgt aggtcccaga gttctacatg gggagcatct acttgttgct tgtatcatgt
180ctttctcaac ggtccctatc gcttagaaga agagttaatt gcttcttct tactgtcatt
240tcatgccttc agaataaatg tatagcatat ttcaccagg tagaaactcc acaaagggt
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337

<210> 2776<211> 338<212> DNA<213> Homo sapien
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60aggaggtccc tctgcccgt cagctgcccc tgcaactgca cgtcccatg ctctgcagt
120cccaccagac agacacctct taggaagcgg catgctccct gggacaggcc ctgaggcatc

180acggcctctt gtgaaattat caaacgtcac caggtgccag aggcaggtgg gcagaacgag
240gctgaggttc actgggatgc tgtgggtaag gcctctgctg acctgtgctg tgccggccac
300tgggagtgtg aaatgagcaa acgggaacag aaggggtgg
338

<210> 2777<211> 376<212> DNA<213> Homo sapien

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60tgttatataa cacatttact tttcataaat ggtgttatct ggcaggtatt ttttggcttc
120cagaataaaa gttttaaaat taaaaggggt atccaagtat ttttaggagc ctagtatttc
180ctcacttact cccaaactct aaaagtagat tggctttatg ttaaacagag aattcgtaca
240gaaaaaatct tcaggactgt attcattcca taaataatgt actttatttt attgcatatg
300gctattaagg agggcatcca tgatcaatac agactaaata caatgcacta ttctagtcca
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376

<210> 2778<211> 357<212> DNA<213> Homo sapien

tacggctgcg agaagacgac agaaggggtct attactcgac tttgaatttc tcacacagct
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120tgtcaatata tgtatctgca agaaactgcc agaaaacagc cagtatacct gtaaaggggt
180caagctaaat agaatttata aagacactat tacagagata taggcagagt tagggactgg
240caccagga ctcacaatag cagggaagccg ttagcacctg cgatgggctg aatcatgttc
300ctccgagact cacaagtga agccctatcc cccagtacct gataatgtga ctgtatn
357

<210> 2779<211> 375<212> DNA<213> Homo sapien

tacggctgcg agaagacaac agaaggggga gaggaccag atgggcttgt tgaagtacca
60tgtggtaatt ggtgaagtgg ccaaggggtat gaggagtga gggaataaaa gaaagagcaa
120tgggaaggaag ttgaggtgtg gtataagcag ggaaagctgt tggatgcaag gttggagtta
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240atgatttgtg tggatctgtg tgaattctg acttggctag cctatttcaa aatgcacgat
300gaggttgttt ttaaataaac ttacgaattc agtttttccc tatttccc:g accgtgattt
360gacatatctc acagg

375

<210> 2780<211> 337<212> DNA<213> Homo sapien

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120ctgggtccact ggcagtttga aagggaacct aattcacatg tctggcagtt ggctgaatgt
180tggctagagc aataggatga ctagaccata taccttttgt tctccaacaa acagttgcag
240gggaccaggg gagcaagtgg aagcatgcaa tgcttcttaa ggtctagtat cagaagttgc
300acactgtcat ttccactgaa ttatttagct gaagcaa
337

<210> 2781<211> 391<212> DNA<213> Homo sapien

cgttgtctgc gggacaaagc aaaacacata ccataaatgc ttatcattta gatcccaggg
60gccccaaatc tgaactggag catgagtttt atgaattaga acctctggct tcccacagct
120gcaactgccc tgagaagacc acttatgaag agaccacat ctgctctgaa tttttcaaca
180gccaaagcaaa gaatttaggg atgcctgtgc atgcagctta caacagtga ctcagcaaaa
240gcaactgaaag tgacgtggc tctgccttgt tacagcccc tcttgaacag catacgtgt
300gtcacttctt ctctctgaat cagagatgta gctgccaga tgctacaaa cacttgaact
360atggcccaca ctcttgccag cagatggggg a

391

<210> 2782<211> 378<212> DNA<213> Homo sapien

tacggctgcg agaagacgac agaaggggtgt aaggggaagg caaatactgg atcttgggaa
60ccactgtaat ctactttgtg tctagcctat ttcttatatc cattgatggg tctgacctg
120gctgtgcttt cctgttggct ctctttgatg ctggattctc tgtacctgc tcccacactg
180cctcctgctg gcttttctca gatatcaagg accaagtagt cacatttccc ctaccatgca
240ttgggtgtgc ttcttactg aagaaaacac ctagggactg accactctc cctccacca
300gatcttccca acccagtgtg ttctgaggct ttagggtgta gcagctagt aaatttttct
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378

<210> 2783<211> 362<212> DNA<213> Homo sapien

ggcacgagat gaaggcccat gaggcggctt ttattgaaca ggaacaaaaa gaagctgttg
60cgtgagctga gaaagcaccg ggagcgtgtg gagctgatga tggatctgcc tggggtttcc
120attgcagacg agggggagac tggcatgttc tccttgtgca ccattccggg tcaccagtta
180ttacaggaag taacacaagg ggatatgagt gcagcagaca ctttctgtc cgatctgcca
240agggatgata tctatgtgtc agatgttgag gacgacggcg atgacacatc tctggatagc
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360cg

362

<210> 2784<211> 336<212> DNA<213> Homo sapien

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60tcagagcctg ataagtgtag gtgcccaggg aatgtgggtc agtgaacata agagaggact
120tcatggagcc caggcgtggg cagggcactc cgtgggtggg tgctgagtga agaggcaagt
180agatgaaagg gcccaggtca tcctggccat gtcaggagca ggggaaggcc cacctgggtg
240aggggatggc cagaggagct gtggggcagc attgcgggca ctcacctggg gggcctctca
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336

<210> 2785<211> 378<212> DNA<213> Homo sapien

tacggctgcg agaagacgac agaaggcgctg tagtcccagc tacttgggag gctgaggcaa
60gagaatcact tgaaccggg aggcggaggt tgcagtgagc caagacagca ccactgcact
120ccagcttggg taacagagcg agactctctc aaaaaaagag caacaacaac acaaaaaaaa
180accatagcca tatggcttga gtaaggaaag acagagttgc ttttgttga gatggggatg
240acagtgaaaa gagcaggctt ggggtgttgg aaagtgcaaa tgtaagtgtt cgattttgga
300tatacttaat ttgaaacgtc attatacaac caagtggaga tcttgcattg acactggaga
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378

<210> 2786<211> 373<212> DNA<213> Homo sapien

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60gcggcgaaa gaaacggctga aggcctacg ggagaaaacc gggcgcaagg acaaggaaga
120tggggagcca aagaccaagc atctcagaga agaggaggaa gaaggcgaga agcacagggg
180acttaggctg cggaactatg tcccggagga tgaggacctg aagaagagga ggggtgcccc
240ggccaaaccg gttgcagtgg aggagaaggt gaaggagcag ctggaggccg ccaagcccg
300gcccgtcatc gaggaggtgg acctggccaa cctcgctcct cggaagcctg actgggacct
360caagagagat gtg

373

<210> 2787<211> 410<212> DNA<213> Homo sapien

ggcacgaggc taaacagaag agccatcgtc caggatcagg gatgtctgcc tggccttatt
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120ttggcagaat gccgtgcaaa cagagaaaag atgaaaagg aactgggtat gatgttgagc
180ttacaaaatg ttatacagaa aactacaact ccaggagaaa caaaacttct ggcctctgaa
240atctatgaca ttcttcagtc ctccaatatg gcagatggtg atagttttaa tgagatgaat
300tcacgtcgaa gaaaagctca attttttctg ggaactacaa aaaaacgtgc caaaacagtg
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410

<210> 2788<211> 407<212> DNA<213> Homo sapien

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120gcctgcattc tctgccctcc ctgagcctcc tggcctggct ggccacagct ggcattggag
180ccatcagcag gctccgtgca ggcggacggg ggcagcccc acagccaggg caccctggac
240ctcactcacc agcacccttt tggctctttc ctagcaaaat atgcaaagtg tgaccagtgt
300ggaaacccaa aggtgagtgg gttccggctg caagccacca aggttccagc tttgggggtg
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407

<210> 2789<211> 388<212> DNA<213> Homo sapien

ggcacgagtg aaaaccttat tagtgttgtg atagtagaga agcttttagt caaaagtcag
60tttattaaat gtttagaata cctaaacagg aagaaaattc tattgttttt tataacaaag

120tgggaagattt caagaaagga caactcactg tacacttgag aataatacct acagagggttc
180atactgaaga gtagtctcaa taatgtaaag aatttgacaa gcatgatgct attgaaatag
240ttctgtgaagg aagtgggtgtt ctttatacat caattattac aaaaagcagt gaattgtaag
300tgtgaggtgt gtttacttag atgtgaagag ttctccttac tgctgtgatg gaataacaag
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388

<210> 2790<211> 334<212> DNA<213> Homo sapien

tctacggttg cgagaagacg acagaaggga accagaacca tatagtgagt gggatctggg
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120gttctggtgg ttaccattat attaatacct ttatatggtt ttctaatttc cttctctttt
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240taaatgagta ttacattagt gtctttatcc gcggactgcc tcaattttca ttttatttct
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334

<210> 2791<211> 399<212> DNA<213> Homo sapien

ctccgttgct gacgggtgcca gggaaacgga ttcattctacc cacgaaggac gcgggagatg
60aggtgccagg gtaaacagcg ggacccgccca ctatgtcacc ctttctgccc gactgcccgg
120aggaactgca tgcagggcgg ccggctccgt ggcaggcaga ggcaggaaga ggcgcggagc
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240cgtggggcct gggccgcccc aggagggcct ctggctggat tcttagcaga tggagccgt
300gcaagggcag gaggcagggg cctgacgtgt ttggattgag gttgcaggag gggcccctgg
360ctgcttcagg gagaataatt tggaggcgag cggngagg

399

<210> 2792<211> 395<212> DNA<213> Homo sapien

ggcnnnntc tgcagcggcc tacggctgag agaagactac agaagggcac agaagggcggc
60tctatgagaa gagctctttt aatgtgggaa ttgatataca agaaggtact tagtccataa
120gatcaggatg tacaagataa cccagagggg cgtcagcca agcttagagc cactatcaaa
180ttataagtta ccatcatctt attcttcaaa tttttctgc aggttctcta gtctttactc
240atgggtatgtt cctgaatgtc ttgatatagg ttaagtatg ggacagtcta aaaattgata
300acatttagca ttttttttcc tcacaaagaa actgtggaaa atattagcat gacagagaaa
360gttccactca cggagtagca tctcaagacc ggaaa

395

<210> 2793<211> 372<212> DNA<213> Homo sapien

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60gacccaagct atattctgag tcagggttag ggcagctta gtgccaccac aaaggccttc
120cctcagcata tataacctca ctgtctccca ggagctatgg gggtaataca ggcattggga
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240atggcccaag gtcaatgtgg ggagtgtcaa ctggataaat gatattcagg gaagcccatc
300cctgttctgc tgcaagtctg gagagcatgc cacagggtgag cagcgcttgt gaaggtaaga
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372

<210> 2794<211> 372<212> DNA<213> Homo sapien

ggcacgagag agagagagag agctagtctc gagagcagct cttttttttt tttttttttg
60ggggggggga aaaaaccccc ctttttttgg gcttttaaaa aacaaccctt ttcagggaac
120tgggggactg gaaaataaaa ctccccggg gttgggtttt tgggaacctg aagcctttta
180gaaggagag ggtttttttt ccaaaacccc aggggagggg gggctttgca tttttggaac
240acaaaaaggg gccccctctg gggggggaaa aaggctaaac cttccccctt acctggggaa
300tgagcccccc cttttgtccc cttctggggg ggggggacgg ggcccttttt ttttttgacc
360cagggggcgg tt

372

<210> 2795<211> 393<212> DNA<213> Homo sapien

ggcacgaggt cccacctgaa gaaaatccat ggggtgcagc agcagtatgc ctataagcag
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120ctgtacctgc acgtgaacag tgcccatccg ggcagctcgt ttctcaaaaa gacatctaaa
180aaactggcag ccttctgca gggcaagctg acatccgcac accaggagaa taccagcctg
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300cgtatgtcta cgtggatttt tggttttcag cttccccac cccactggct cttcttaatt
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393

<210> 2796<211> 353<212> DNA<213> Homo sapien

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60ttgcctttta aatctggaag cgattcaagc caagctgacc aagaagccaa agaactggct
120aggcaaataa gctttaaggc agaagtcaat tcactctggaa agactatctc tgagtcagac
180ttaaaccact ctttttcact aactgattta caagatgata tacctacaac attccagggg
240gttacggcca gtacatcgta cggagtccag aattcctcag cagcatcctt tcatcaacct
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353

<210> 2797<211> 379<212> DNA<213> Homo sapien

ggcacgaggc aggaacagcc ctcaagcctg tgtcgggtggc ctgcacccag ctggcatttt
60ctggccctaa gctagcgcgc cggctcggcc cccgcccagt gcctcctcca cggcctgaga
120gcactgggac tgtgggcccc ggccaggccc agcagagact ggagcagacc agctcgtccc
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240ccagcgctc caccaagcac attctggatg acatcagcac catgttcgac gccctggctg
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360tccactgcct ttgccccag

379

<210> 2798<211> 380<212> DNA<213> Homo sapien

ggcacgagat tcttttgtct aaaacttacc gaaattgatg cttgtactct actggctccc
60tgatgatagt agaaaagcac tagtaatgta ccaaatgaaa ctgggtgtgt accagatgat
120tttgtttaact tcttaaatag cctagaaatc gtcagcaggt cacatacaac tgcagtgata
180atttcagaac atagcaaaat ggctgataat ttggatgaat ttattgaaga gcaaaaagcc
240agatggccg aagacaaagc agagttggaa agtgatccac cttacatgga aatgaaggga
300aagttgtcag cgaagcttcc tgaaaacagt aagatactga tctctatggc taaggaaaac
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380

<210> 2799<211> 340<212> DNA<213> Homo sapien

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60ctcatcctat gacgcgaaag taaccgagac tatcaggatc cggagacyga aatgtccgaa
120ggcagcagta cttgaccctg tattttggga gtcgaacgga gaatggaaac tgaaagtgga
180aatcaggaaa aggtaatgga agaagaaagc actgaaaaga aaaaagaagt tgaaaaaag
240aaacggctac gagttaaaca ggtgcttgca gatattgcta agcaagtgga cttctggtt
300ggggatgcaa atcttcacaa ggatagattt cttcgagaac

340

<210> 2800<211> 368<212> DNA<213> Homo sapien

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60caggaaaagg ggaagcgccct ggatggaaag gacgagtttg aggacctga gtgggtccgag
120gaggtccaga agctgcagga gcagcagctg cgcagcgacc tcctggacca gtaccgttcc
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240gaggcgctgc gcagaaagaa gggcctggag gccgctgagg tggctgaccg gggcgagag
300gccgaggccc ccgagaaaga gcaagcgtag ctgcgccatc tgggcatgct ggaggagctg
360aagaagcc

368

<210> 2801<211> 413<212> DNA<213> Homo sapien

cgacgaggca agatggaggc gactacggct ggtgtgggcc ggctagagga agaggcggtg
60cggcgaaaagg aacggctgaa ggccctacgg gagaaaaccg ggcgcaagga caaggaagat
120ggggagccaa agaccaagca tctcagagaa gaggaggaag aaggcgagaa gcacagggaa
180cttaggctgc ggaactatgt cccggaggat gaggacctga agaagaggag ggtgccccag
240gccaaaccgg ttgcagtgga ggagaagggtg aaggagcagc tggaggccgc caagccccag
300cccgtcatcg aggaggtgga cctggccaac ctgcctcctc ggaagcctga ctgggacctc
360aagagagatg tggccaagaa gctggagaaa ctaaaaaagc ggactcagag ggc

413

<210> 2802<211> 386<212> DNA<213> Homo sapien

cgttgctgtc ggcggctccg atttatgtct gtgggagtct cggagacgtg tctgggtgtg
60agggcgtggg tgcacgtccc cagggctctg ggctaggaag gcagcggcga ggtgcctccc
120cacgtacccc tcgcgggccc agccgagcaa cgtggggcga aggcggcggc gaagggcccg
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240gcgggtccag gagctggagc gggaaactgc ccaggagagg agtctgcagg tcccaggagg
300cggcgacgga gggggcggcc gggtcgcgcat cgagaagatg agctcagagg tgggtggattc
360gaatccctac agccgcttga tggcat

386

<210> 2803<211> 344<212> DNA<213> Homo sapien

tacggctgcg agaagacgac agaagggttt tcaaactgga gaaagtgatg gatgatttca
60gaacttcagc tcttgagcca agaggtcctc ccaaccctaa tgcgaatat attcccttgg
120atgaaatgaa ggaaagaata ctgaaaattg tcaactggatt taatggtatc ccttttacta
180ttcagcgact atgtgaattg ttaacagatc caaggagaaa ctatacagga acagacaaat
240ttctcagagg agtagaaaag aatgtgatgg ntgttagctg tgtttatcct tcttcagaga
300aaaacaattc caatagttta aatcgaatga atgggtgatg tttc

344

<210> 2804<211> 437<212> DNA<213> Homo sapien

tagtgcttct gagattccat ggagagcttg ctgtatcttn ngccccgcgc ggcttacggc
60tgctacaaga ccacagaaag ggattacagg tgtggggccac cacgcccagc cctcttgtgt
120aatttttgat aaataacaca ttactattg ttggtttaat gaaaacagct caattctgag
180gtattgctaa aatactgata ttaacctta agtttcttac ttaggtcaga aactcacagg
240ctattaaaaa ggttaacagg aaatagcttt aaatgatgac tatcacagtt ttcataaata
300acctatgtaa actatcagca ttactcatgt taatgtaatg gaataaatgc ttataaacia
360acttgatata taatttagaa tctaaagtta cattaaataa taaaactcat taactgggta
420gcttctaatt taaaaac

437

<210> 2805<211> 385<212> DNA<213> Homo sapien

gcctacggct gcgagaagac gacagaaggc catagaggag taattgggta attcctgtgt
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120ggctcctagt atccttctgg tggccaaagc ctccacagtg aaaatagata ggaagagcca
180cctcgcttgg ccgcatatct gtttttaaaa ggcctgggcat ggcttatgcc tgtaatggta
240gcacttcggg aggccgaagt agggagatca cttgagacaa ggagtttgag actagactgt
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385

<210> 2806<211> 401<212> DNA<213> Homo sapien

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120ctcagagatc tagacagatg gactctttac tatcttatga tgttgctgtc tcaacacaca
180gcttctagag ttctgtgtgt gggataaggt gtaaaaaact taaactttct cttaaagtct
240ttggccctgg ctagcatcag tcttatgaat ctctctcagt gctagggagt tgggatgtgc
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401

<210> 2807<211> 401<212> DNA<213> Homo sapien

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120ccatccctac tctactctg ccttgtggaa ttctccctc aaagggttta agcgtcttaa
180gtgcttctca cattccaga taagccttgg tgctctacct gggatgcagt cggtgcccgt
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401

<210> 2808<211> 424<212> DNA<213> Homo sapien

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120agagagagag agagagagag agagagagag agagagagag agagacacac tctctctctc
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240gtagtgtttc tctgtcgcgc ggttattttt atctatctct ctctctctct ctcatatata
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420accc

424

<210> 2809<211> 407<212> DNA<213> Homo sapien

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120tataacaata atattttatg gggcgcttat aatgtttata atattgtaaa ccactgtgta
180ctctattcat ttaatgctaa atgacttgac cattcttggt ggataagaga tcattaaaaa
240aatgctaggg ccgggcacca tggctcacgc ctgtaatccc aggactttag gaggccaggg
300caggtgatg acttgagctc aggagtttga gaccagcctg ggcaacatga tgaaaactcc
360gtctctacca aaaatcaaaa aaattatcc aggtgtgatg ttgtgtg

407

<210> 2810<211> 411<212> DNA<213> Homo sapien

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120ttcaggtctc ataaccagtc tatagtcagt gtcactttgg ggacagtatt ccttgagttt
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300ttttcttccc ctgacagaca tatgctggtt ttccttatat gcccaaagga tttttcctt
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411

<210> 2811<211> 381<212> DNA<213> Homo sapien

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60tāaatataaaa agtacaacaa tactacatac tctgaaggag gggtagataa atcatgctat
120aaaggcatga tcaaaataaa aagtttggat ctgcacagag aggtcagagg tttctctgtg
180gaagtaataa gagaattaag aactgaagga aaagaagggg ttaactatag aacgacaaa
240aatcacattc taaggaaagc aaataacaag cactaagatc ctgtgggttg agagaatatg
300ttatttcagta gagccacaag atggtacctg tggctagaat gctagagaga gtagaaca
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381

<210> 2812<211> 394<212> DNA<213> Homo sapien

ggcacgaggt gacctcaggc ctacataacc tttctgtacc tcaacttcct catccagaaa
60acagggatga tgctgtctac ctacttggt ggttgtgcag gatcaaagat tcagtcattc
120agcaaacctt taccgagtac ctactgtaca ttcattgagt ctaggcagcc agccttcag
180gtgctcaggt acatctgtga acacaactgg ctattggagg aagcaaatc agtaacatga
240cctgctctct ttgatctgtg ctacagaaaa aaaggaaagt ggagaggcat caggaggtca
300ggagtgtg ggaggggctg gtaacagtca tggattaaa gaggagggca ggcaggcctt
360actgtgaagg tggatttga gatgaagtag ttgg

394

<210> 2813<211> 386<212> DNA<213> Homo sapien

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60ctgtagtttt tcataagcag taggagcatg atcatgagac ttaggaggag caaactttgt
120cccagtatag tttaagaaat ctcatatctt tatacaaaat atgtttgcag ctgaacttta
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240tcccaggaat atgaaaattg tatagattcc tagttgctgg ctagagaagt gagagttgaa
300atgtttctaag atataaggaa atgcagggtt tgccttagtt atatataaag ttgtcatcat
360agagcctagt gctgaagagc aaagga

386

<210> 2814<211> 385<212> DNA<213> Homo sapien

cgttgtgtc gatttttaat tgagcaata ttgtatagat ggttcatttg gtcacccatt
60ttgaataata tatggaaagt taaaaaatgc ttctcagata caaaggaata aagctaagat
120gaagcttaac gtgagggatt acttactgtg gaattgcatt tcaaactggg ctgaggtggg

180atggtggtg tagataagag gccagctaga gtaaacataa gctttgtagt tttattat
240taagagtcag agtcttggtc tgctggccag gctggagtgc agtgggtctga taatgggtca
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385

<210> 2815<211> 392<212> DNA<213> Homo sapien

cggtgctgct gaaaaaaaaat tagctgggcg tgggtggcaca ttcctgtaat cccagctact
60tgggaagctg aggcaagaga attgcttcaa ccttggaggc ggaggttgca gtgagctgag
120attgcgcat gtacttcagc ctgggcaaca agagtgaat gccgtcttaa aaaaaaaaaat
180tcaaactgc agcaaagggtg aaagaatact acagtgaaca cccatagcc ttctgtttg
240attcgactgt taaccaacat ttaaccattt tgctttaact etatatectc cctttcttga
300atgatttgaa attaaattgc agatatactg cttttccctg taataacctca ggatgcatgt
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392

<210> 2816<211> 406<212> DNA<213> Homo sapien

cggtgctgct ggcgcggggg gcgcagctta tgagggcgcc ggacctggga agccgattcc
60aatcagttgt cagacccggg aagcccgcag ttcgctctc ccgagtcctt ctgtgggggtg
120aggaatgggt cttgtgaaat tctgagcaaa aacaaaggca aactctatct ccgaaagggg
180cggttggtc acatttctc tctggggcg gactccaaag ttctcaaat gagaaggcag
240aaatgaaac acttcaactt tttttttt ttttcccg ggcggtgtc ttgaaccct
300cttctccccg cccctctggc tccgttctc tccctctc caccgtctc ccggactcgg
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406

<210> 2817<211> 405<212> DNA<213> Homo sapien

ccatcgattc gaattccgtt gctgtcgaaa attttaagt tccattttct agccttacc
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120taaaacatgt ccatagttgc agcacgctcc attggacagc atgcttagga caggagtgtg
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240aagcctcgcc ccttctttc ctacacccca gctctgctc tcaactgtga gggccttga
300tgtgcctgga gcagaggcca ggcaggcctt ggaagcagtc ttgggtgta tggatggggg
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405

<210> 2818<211> 386<212> DNA<213> Homo sapien

ggcagaggc aacatggcaa aatcccatct ctacaaaaca tcaaaaaaaaa aaaaaattaa
60ccgggcctgg gggggccacc cctgaatccc cattttgtca ggaggctaaa ggggaagaat
120ccccctggcc caggggggca agggatccag ggaccaatgg tttaaccatt gctttttacc
180tgggggaaaa aaaggaaacc cgttttaaaa aaaaaaaaaa aagaaaaaat tctaaaaacc
240cttattttta taaaacttaa aaagggcggg aaaaaatagg ttttattatc ttattttaac
300aaagggaaaa ttgggggcta aaaaaataaa agtttattgc taagggcctt gggcttaaaa
360tttggaac ccttgtttaa aatccg

386

<210> 2819<211> 386<212> DNA<213> Homo sapien

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60attgattccg tcagccttga ggcagaacct agatccgaaa taccctgca agaacagaat
120tatctggctg tggattcccc tccaagtga ggaggatggg caggctgggg atcctggggc
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240aaagcaggag cactctacg gattcatggt gtaaattctg gatcttctga aggagcccaa
300ccaaatactg aaacggagt cctgaaata acagatgcag ccacagatca gggccctgca
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386

<210> 2820<211> 380<212> DNA<213> Homo sapien

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60tcagccacag ttgcacagg ggcgtggac ctggacctgc tgaggagggt tctcagggtc
120cggagctggc cttagggtgt caccatagt agatcctgaa ggcttcgaag aggccacaag
180aagtacagga atatagccca gtcttagcgg aggccatgca gcagatgggg cctgggggag
240ggattccgga gcacctggc ccatgctggg gctcagcatc gctgtctgct caggatgag

300catgcaaagg ccacatcctg ctgggtctaa gctctggatc ctgttgagga cagaactcag
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380

<210> 2821<211> 396<212> DNA<213> Homo sapien

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60ccaagaacac gtgatggctg ttactgcacc cgcgaaatca ctgacacgaa agttcacgc
120tggtgcctat cctacagaag aggggtgcat cttcttgaa gtgaaagacc agctgtgtgt
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240ggacatgatg cagttttgag actgggtggag attcgcacgg ttttgaaaa gcttcgtccc
300ttggacaaaa agctgaagta tcaaattgac aagctgatca agactgcagt gacaggcagc
360cttagtgaga atgaccact tcgtttaag cctcag

396

<210> 2822<211> 382<212> DNA<213> Homo sapien

cctggcaaac cttgttggtc tggcagaaaa tataaccag gaacgtgaca gtcttatgtg
60tttgcaaaa tgtttagaaa gtgagaagga tggagtgtt aataaagtca taaaaagcaa
120cattcgcctg ggaaagttag agaaaaagt caagggtac aagaagcagg cagcactgaa
180gctgggggac atcagtcacc gtctgtgga gcagcaggag gacttcgccc gcaagacagc
240ccagtaccgg caggagatgc ggcacctgca ccagggtgtg aaggacaagc aggggtgtc
300ggaccaggcg ctgcagcaga acagaagaaat ggaagtgaa cttgaagtta tttgggaatc
360taccttcagg gaaaaccgaa ga

382

<210> 2823<211> 382<212> DNA<213> Homo sapien

tacggctgcg agaagacgac agaagggaca taccagggtg atactctgca aaaagaacta
60ggggtgccta tcttaattat taggaaaaac tggacttcca gaacaaaaag caacattaca
120gatgagtttt caatttacca gggatacata attttaatt tgtatacccc taacagcata
180actttgaaat atattttaaa aaattactgg aactacggaa tattcaaaat cacaagggga
240cattttcaca catctcacag agggacattt tcacacatct ctctcaaaat tgatgggtca
300aatagacaat aatcagtaa ggagttaaaa ggtttgaaga acacaattaa gaagcttgat
360ctaattgact tacacagagc an

382

<210> 2824<211> 405<212> DNA<213> Homo sapien

cgttgtgtgc ggcgcagtc tgtagtccca gctactggg aagctgaggc aggagaatct
60cttgaaaccg ggaagcggag gttgcagtga gctgatatca caccactgca ctccagcctg
120ggaggttgca gtgagctgag atcgtgcccc tgcactccag cctgggcgac agagtgagac
180ttcgtctcaa aaaaaaaaaa ttaaaaaaag agcagcttct actgcagcct cctcttacct
240tattgccttc tcttgctctg gtctccactc aaagcatgca gccttctggg tgattttgca
300gatgggtcaa aacagcatac tcaatgttgc ctcccaaata aaaaaacctc ccgaccattg
360tacttctttc tttgtggtag gtactgcaac ttgcagcaac ttgtt

405

<210> 2825<211> 418<212> DNA<213> Homo sapien

ctgttctnn nngcccatcc catcgattcg aattcggcac gagtggaagc ctggcaggcc
60actcgagttt tctctaggag gtaggtctgg actgcggctc cagtcatttg ctgagccctg
120ttcagctgga gctggatgaa caaaagcttc catgacaggg ttggagttca ggatcctctg
180ttctatcttc tctgcaatct tgtggctctc ccaagatgca ggtgaggtgg ccaccacagc
240atagaacttc attaggcagc gagacgtcca tgtctttcca gcaccactct ctccactgac
300aacaatagac tgggtgactg gttcaatcag gctcttgaca ttctgtagg tctgttcacc
360cacagtgaac acatggggct tcagtttctg gggctgaggc gcagcatggt actctctc

418

<210> 2826<211> 404<212> DNA<213> Homo sapien

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60gaggattttt tgaagatgca tctcagtagc atgaaaacct ctgttccag gacatgaacc
120tttcccgccc tcttctgaag gccattacag ccatgggctt caagcagccc accccgatcc
180agaaggcgtg catacctgtg ggtctatttg ggaaggacat ctgtgcctgt gcagccactg
240ggacaggtaa aactgccgcc tttgccctgc ctgttttggg gcgtctgatt tataaacccc
300gccagggtcc agtccccgc gtgctgggtgc tagtgcacac ccgagagctg ggcattccagg
360tgcactctgt caccagacag ctggcccagt tctgcaacat cacc

404

<210> 2827<211> 357<212> DNA<213> Homo sapien

tacggctgcg agaagacgac agaaggggata tttcttcaat tcacatgaaa acagcagaaa
60gggagccctt atgaagttag aaaagctact ctgaaccatg cttctttcta caagtttagg
120aaaaacatttc acgtaaaaat gaacaacaga ttgtggtgat ggttacacaa ctctgaatat
180aaaacactga actgttggtc cacacctgta atcccagcac tttgggaggc ggatcacaag
240gtcaggagtt tgagaccagc ctggtcaaga tgggtgaaacc cgtctctac taacaatata
300aaaaaaaaag aaaaattagc cgggcatggt ggtacgtgcc tgtagtccca gctactg
357

<210> 2828<211> 361<212> DNA<213> Homo sapien

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120agtgcagctc catctcttaa aaaaaaaaaa gtttattctt tcctgtgggg taagcagagc
180tgaagtttta aaaagacagg gggggatctt cattaggga ctgggcaatg ggcttctcat
240gttaacaatg ttgacaacaa cagccaaaag gaaaaatgta aaaacaaaa aaaaagctgg
300cgaggggct cagcctgta gactggcact ttggatggct gaggcgggga ttgcttgagg
360c

361

<210> 2829<211> 375<212> DNA<213> Homo sapien

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120attaggatta aattatggtt tgacttttcc tagcagcgtg atcatgggca agtggctttt
180tttttttttt gaaaaaaagt ttattttttt tccccagggtg gaagggcagg ggcacaattt
240gggttacttg aaactccggc ccccgggcca aggggatttt cgggtggaat tttttaaaga
300agtgggaacc cccccccccc cgggttaatt ttggattttt aggaaccaac aagttttccc
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375

<210> 2930<211> 378<212> DNA<213> Homo sapien

cgttgctgtc ggattccagg tgcattgtac cagccccagc taattttgta tttttagtag
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120ccacttcagc ctcccaaagt cctgggatta taggcatgag ccagtatgcc cagctgttac
180ttttttttta gccattggga aaagtgtttt aagttacatc ttgtttgctg atatataaac
240tacaagtttt ctgttatgac ttgaattca caatctttct aaacttaatt aattctaatt
300tatctatttc tatctacata atatctgtga atgagttttc ttttagaatc ttacagcttt
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378

<210> 2831<211> 371<212> DNA<213> Homo sapien

tacggctgcg agaagacgac agaagggggg acgttatgtg aatcttaagt cttaccagtc
60cttgacattag tacattaaat ttggatggtt tggagcaaa ttcatacgat cgtgagtgat
120ttctccaaag aaaaaagcct tgtccagcct gaccaacatg gtgaaacccc atctctacta
180aaaatacaaa aattaactgg gtgcagtggg gcgcagtcct gtagtcccag ctacttggga
240ggctgaggca ggagaattgc ttgaaccctg ggaggcagag gttgcagtga gtcgagatcg
300cgccactgca ctccagcctc ggtgacagag caagactcca tctcaaaaca aacaaacaaa
360caaaaaaaaa c

371

<210> 2832<211> 375<212> DNA<213> Homo sapien

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60cagggtggcaa ggatgactac agggagtcac ctaagcaaac tgaaagcagg attcagaaac
120atagtttaac catagctcgg ttactaaac tataaaacat tctgtccttt tacttgaaa
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240ttattttaaat tttaaaaaat ggtaataaag cacataactt atgtgacatg gaagcaaatt
300taaaacattt atgagtaatt atatttttaa agtattagat accttagctc aacaatagca
360tagaaagtta ggctt

375

<210> 2833<211> 348<212> DNA<213> Homo sapien

tacggctgcg agaagacgac agaaggggtt ctaagatttc caaaatacta taaaatattc

60tcatgttctc aaaggcagaa ccagcctttt aaaatttaaat ttaatcagca ctttaaaaaat
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180ataacagaat taaatctttt tagctattgc tatgtgtctt gcctgtgcat ctaatggaaa
240ttgtatacat ccttgcccca ctgatttagg gcttgataat atgacataat ttgaccaatg
300ggatgcaagt acaataaatt tagctccatc ctggcagaag cttcagcg

348

<210> 2834<211> 348<212> DNA<213> Homo sapien

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60agtaacaagg gaaatcaaca cggaattgta ggcctaaacc actggcttat aaccagatta
120tggggccctt taagaatctg ataagaagtt cgcattttct ttatccccag aatagacata
180cataaaaaata atgcatacta agtatctggc attcatagac ttccctaaa tacattaatc
240acacattatc agtcctgct gttaaagata ctacaggctc ttgaaaaatt ccctcttagt
300tctgggtgta agtactaaca gtgggttaat tttcaacca ttgattat

348

<210> 2835<211> 379<212> DNA<213> Homo sapien

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120aaatgctgga gaaggaataa aaaaggaata atccaacaag gatcaagaga acaggaaagg
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240taattgactt aacagagaaa gctacaacct cactgattac agaggggaac acggaaagga
300ggcaagccta tttaccccca cagaatcctg gaaaaattca gcaattggaa gtacaaagtg
360taggtgaggc aatgagcaa

379

<210> 2836<211> 374<212> DNA<213> Homo sapien

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180caacctgtag cagatgtttc ctgtgctttt caaacatacc aaaagtctgc tcatctttaa
240gtcaattcca ccacaacaaa gaggttgatt acaaagatcg tcaaagagct cacatgaaaa
300tagtgtttct ctgtccattt aaaaattact cagctgatgc acttacaagc ttctaattcta
360caataatgac gatt

374

<210> 2837<211> 372<212> DNA<213> Homo sapien

tacggctgcg agaagacgac agagggggct ccaaaagcat gaaacattta atgttcattt
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120tacttaaatg gagacatata tcatgttcat tgaacagatg actcatcaag ataccaatta
180tccacaaact gatcaacgga ttcaacgtaa ttccattctt agtctgttta tgctgctatg
240acaaaatacc tgagactggg taattcataa aaaacaaatg tattttgta ggtttgggtg
300tctgggttagg gctatatgct cccgagggga gaaacaccat gtccgcatgt ggcagaaggc
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372

<210> 2838<211> 378<212> DNA<213> Homo sapien

tacggctgcg agaagacgac agaagggagt tgtaaatgtc caaagctaac aagtaaccaa
60caaaaagtgt gttaaacatt cttctagaca ttgcctgtag tagttaattt ggggaacaga
120tatctttttt gcatttgagt gtaagaaaag gaaaaagaca gtttgatgat ggaagttctg
180ttgtgttctc tctcctctc ctcctcaaag atgagtcatt taaagttgat tcagggtcca
240gacaatgaaa aagaggggtg caatgtctgc catatgaatt gaaatgtttt gatgagaggg
300catctgcagg agaattatct ggggggtggtc tatctttctt tctctggctc tttttctctc
360ctggatgctc agcttctt

378

<210> 2839<211> 344<212> DNA<213> Homo sapien

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60ctaagagcaa cagaagatca ctgacagtgt tttaaataga tagactagtt tattagattt
120gcagttttaga agttcccttt ttttgtaatt attggacagt gtagagaccg gatgggtgaga
180gatgagtttag gaagttgtga cagctctcta tacctaccgc taatgtagag gattatttat
240tttcatttca ttaccattcg tgtaaggtgt gtgtgtgtgt gtgtgtgtgt gtgtgtgtgt

300gtgtatatct agtttctcta tagaacatat atgggagaga gaga
344

<210> 2840<211> 347<212> DNA<213> Homo sapien
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60aggctgaggg aggagaatgg catgaacccg ggaggcagag cttgcagtgc gctgaggtcg
120cgccactgca ctccagcctg ggtgacagag caagactctg tctcataaaa aaaaaaaaaa
180aaaaacattg ccttgggggg ccggccgcgg gggtagaatg tccaacccgg aaacctttgg
240gggtgctgggg gtgctgttcc ccaagccaag gtttctccc cccccggccc cccccgggga
300aaccccttc tttataaaa atccaaaata acctgggggt gggggac
347

<210> 2841<211> 347<212> DNA<213> Homo sapien
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60aatctgatg gttactttta ggactaagac aaatattgtc agttcaggtc cttgggacct
120atacctcaag aacctggcct atgcctatag ctgacctct gtccagtact tccaaatgac
180tagaatttct ggatcaaaaa caaaagcagg cagatcacta agatttggc agacacaaga
240aaataatgga tccaagaaag caagtttct atggttaaga ggttaagtaa caattgtaac
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347

<210> 2842<211> 346<212> DNA<213> Homo sapien
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60aatctgatg gttactttta ggactaagac aaatattgtc agttcaggtc cttgggacct
120atacctcaag aacctggcct atgcctatag ctgacctct gtccagtact tccaaatgac
180tagaatttct ggatcaaaaa caaaagcagg cagatcacta agatttggc agacacaaga
240aaataatgga tccaagaaag caagtttct atggttaaga ggttaagtaa caattgtaac
300aggaagagaa aaagacatgt aatctacaca aggagggtag gggcagg
346

<210> 2843<211> 346<212> DNA<213> Homo sapien
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60catatgcact aacacatgtt tgaggtagag aattgaagct gatttttctg ctaaagatga
120atttctatta acaatcccat ttttatattg tattattaaa aaaaaatac ctctctttgc
180tagagagtat atgtatgact tatattatta actatgggtt gcatttaaca catggccgat
240tgccctgtaa tctgcttatt ttaacaacat acggtgctgg gcacagtggc tcacgcctgt
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346

<210> 2844<211> 373<212> DNA<213> Homo sapien
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60atgagattca catatgggtt cattaaagca cataggaaag tgctcagtca atatttaatt
120agtttaatta gataagggaa aggagaaatc cttaaattga tggattcttt tatactgtga
180atatatttcc atcagtgttg gtaagatc aaatgactat cagttgatcc cagtcacag
240tgacttattt gcatatttaa gccctattca caagagacca taatcatttt aatcttatat
300tttccctcag gaaatttagg gactctgaag cccctatttt attctcttgg agtaaactgt
360tgagtgtagt tac
373

<210> 2845<211> 345<212> DNA<213> Homo sapien
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120ttaagtcact gaaagtgtgt actacaaaag acttccatcc actattagct gatcacag
180tgtgtatcac cttaaaatgc ttagggaggg cagatagctg tgctctctac ctttatctgg
240agttattgag tctgatccct tcgggcgagg cctcattccc actttcatgg ctggtttggg
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345

<210> 2846<211> 374<212> DNA<213> Homo sapien
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60aaagaaaaaa agtaccttaa atgaggacat tcccatgtat gattaaaaaa acattctgga
120tgtaaacatt aaaaacggat ttctgtgtgt catcctaaag attttgagat tcatgtatta
180atttgttttc agaaattaaa gggattacaa ttgctagtaa aattgaactt cgtaataata

240tttttctctgg tattagattc agaaagccag cgattagaag agatgctaac tgtgttttgg
300ggtagcttct ttatgaatag gtaaaattgt attttcaaaa atttgtatca taaacaatat
360gtagtttccc tgta

374

<210> 2847<211> 351<212> DNA<213> Homo sapien

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60tagctggtat agcagacagg gaaaagttag cacattccca tctttaagag cactgcttct
120aaattctgtc actctttttg ataggaaatt accctaacag cctcattttt tccatcttag
180ccttcacaaac aaataataaa taaagaagga gtgatatagt catactgtat tatacctact
240tactatactt attcgtagt atactgtatg agagtactgg tcaggggatt gggatttgaa
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351

<210> 2848<211> 345<212> DNA<213> Homo sapien

tacggctgcg agaagacgac agaaggggtc ccatgggggtg cacagaatgt ctgtgagact
60atggagtgga agaagccat ccccgagcct ctccagctac tcgaggcatt ctgtagaaca
120taagccata gattgtgtgt gtgtgtgtgt gtgtgtgtgc atgcgcgcgc gtgcgcactg
180gaggaacctt agaaactatg tggcgcactt tctcttattt tagagctccc agagtgtagc
240tccagaatcg taaaggata tgctcagtct cacagccagc cgtgggatct cagtcccaac
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345

<210> 2849<211> 368<212> DNA<213> Homo sapien

aattccgttg ctgtcggcgc cgggggcgca gcttatgagg gcgccggacc tgggaagccg
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120gggtgaggaa tgggtcttgt gaaattctga gcaaaaacaa aggcgaactc tatctccgaa
180agggacgttt gggtcacatt tctctcttgg gggcggactc caaagtcttc aaaatgagaa
240ggcagaaatg aaaacacttc aacttttttt ttcttttctt cccggggcgg gtgtcttgaa
300ccccctctt ccccgccct ctggctcctg tctctctccc tctccaccc gtctcccgga
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368

<210> 2850<211> 347<212> DNA<213> Homo sapien

tacggctgcg agaagacgac agaagggcac tagctgccag ggcagttggc tgggcactga
60gaggctygtg gagccttata tcttactta cttctggcct ttccaatttg ctctatactc
120ctatccatga aaaccaacca caaatccatc tgtactacct acccgtcac tctctataaa
180gcaaacaaaa caccacacac acaacactat actgtcttaa aaagtctttg caaatgcata
240cctctgtgga ttgaaagccc tctcccagtc ttcttatctc aaaggccaaa ctcaaatct
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347

<210> 2851<211> 343<212> DNA<213> Homo sapien

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60aaagctgtga tacagatact tacacatcta aaacagaagc tgatgacaag aacgatgaaa
120aatgcatgaa agttgactta gtatcttttc catcttcacc tattatgggt gataatgata
180gctctggtac aagtataag gatcatagt aaatacttga tggattagt aacataaaac
240tgaattcaga ggaagtaaca cagagccaat tagattcctg tacaagtcac gatggctcgc
300aacagctaag tgaagttagt agcacaagag agtgccctgc ttn

343

<210> 2852<211> 374<212> DNA<213> Homo sapien

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60caggagagac gcggatgctg gcgcaggaag gctctgagga aggctgcaca cacaggatgg
120ccctctccag ctccacgtcc tcagggttac agatacagcc ggggctgggt gtcacagcaa
180gcaccctcca tctctgtctc tgctcctaag ggcccttctt ggtgtccagc ctggggcctt
240tgctaggtca gagccaagg gatccgtggg aagcatgtga tggggcaggg cagagggctg
300gggcgagggt ggagttcagc acaggagggtg tgccacagtt ggggcgtagt tgtaagtgt
360ggcctcatgt gtgt

374

<210> 2853<211> 377<212> DNA<213> Homo sapien

tacggctgcg agaagacgac agaagggaac tcaggattca gactccataa aaaagcctga

60agaaatcaaa caatgtaatg atgcacctgt ttctgttctt caggaagata ttgttggaag
120tcttaaatct acaccagaaa accatcctga gacacctaaa aaaaagcttg atcctgagct
180ttcaaagagt gaaatgaaac aaagtgaag tagattagca gaatctaaac caaatgaaaa
240ccgattggtg gagacaaaat caagtgaata taagttagaa actaaagttg agaccctaac
300agaagaactt aaacagaatg agagcagaac aactgaatgc aaacaaaacg agagcaccat
360agttgagcct aaacaaa

377

<210> 2854<211> 371<212> DNA<213> Homo sapien

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60ccaagtgaga ctgcgtcttt taaaaaaaaa aaaaaaaaaa aaaagggggg cggaaatttg
120gggggggggg cccaaatttt ggatttttaa aaaatttggg gccggggggg ggggcctaac
180ccctaaacc ccaccttttt ggaaggcaag ggggggggaa aaactggggg ggggggttca
240aaaaccaccc gacccaacgg ggaaaaaccc cgtttttat aaaaaaaaaa aattaacccg
300ggattggggg ggtggccctg aatccccact ttcccggggg gtgggggagg gaaaactgtt
360taacctgggg g

371

<210> 2855<211> 347<212> DNA<213> Homo sapien

tacggctgcg agaagacgac agaaggggtg ggaaaggcag agaatgtctg aattcttggg
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120ttctgcaatc tcaatctgtg tggggtaggc tggatatctg agggccttgg caattccttc
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240cttgacaggg ggagagcttt ccacagccag gcctaccatc aggggaacaa ctggaggggtc
300ttaaacatgc ccaggactca aatccccgct ctctacttt tgggatg

347

<210> 2856<211> 329<212> DNA<213> Homo sapien

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60cccgtaggca gcgctgccag gaggcagcag tgaaggtccc ctggctctc tggccccagc
120ctccctccct gtccacctt ctgcagttcg aggcactcgc ttggcctca ggacacacct
180gccttgctcc ctctgcaggc cataacatcc ccttcctctg acctcttcta aaatctctc
240tttcacgtgg ttcttcata ctatggccca ctggactact gagcctaate atccaaaaat
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329

<210> 2857<211> 325<212> DNA<213> Homo sapien

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60taaaacttca gaaattagat gaccaaattc tacaacttct aatgaaaact tctaattcaa
120tagataacgt tcttgagaaa gacccagac caaaaagaga cacagatata acttctgaaa
180gtgactatgg aaacagaaaa gaatgcaata gaaaagttcc tcgaagatca aaaatccctt
240atgatgccaa aaccattcaa actattaagc accacaataa aaactacaac tcttttgtaa
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325

<210> 2858<211> 380<212> DNA<213> Homo sapien

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120tgtctgatca attagtagtg gctgcctaga actgcactgg ccaatatgtg aaccattggc
180cacatgttgc tacttaaagt gagaaattca ttgcttcagt cacactagcc atattacaag
240tgctctatgc ccggacactg aacatttgca tcatcacaga aatttctatt ggccagcgct
300gacttagaac gtcagtgttg gaagagaagt gaggccgtgt ctaggaagca tgagagatca
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380

<210> 2859<211> 463<212> DNA<213> Homo sapien

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60agacaggata aacatctggg aagcacaggt atatgaggca cagaaacaca aggcactgtg
120gatgcctctt ctgtctggac agaaaactgg agtcaggaga cctctctgag tccccagaga
180cagaatcatc actactgtgt gtccttggaa cttaaagtag taaaaaaaaa aaaaaccggg
240ccgaaagtcc acagcttgca ccttgaaaaa ggacctcac aaaaaccctc ccatgctggt
300acctgatttg ggacttccaa acttccaaaa ctgtgagaaa aaaaatatgg ttgtgggtta

360taagccaccc acactatggt attttattat accaccccaa ccaaacgggt agggtaaagg
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463

<210> 2860<211> 422<212> DNA<213> Homo sapien

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120gagagagaga gagagagaga gagagagaga gagagagaga gagagagaga gagagcgcgc
180ctctctctct ttttttcgtg cgctcttgcg atagatatct tttttctct ctcgcgcgtg
240ttttctcaca cacacacaaa aaagcgctct cccctacac gccccccct ctctgtggag
300tgtagaatat gtgtgcgcgt gctttcttct tctctctctg tgaggggggt tccccccct
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420

422

<210> 2861<211> 380<212> DNA<213> Homo sapien

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60aattttctc catcagatct ttcatttctt catgattatg aaaatcctaa ataaaacaac
120agaaagtgtt agctagtact caataaaata acatatcatg attacctctg aagttaaaga
180ataacctgca catccatgca ctaaaaaggt tactgtaagt ggatatccaa ctggagaaaa
240agttgaagca aaattttgaa ccttatagag cataaattcc aaaaagttca gaaatttatt
300taaagtcaat gaatttataa aagtaaacac gcacacacac atgcacacca gagagttttt
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380

<210> 2862<211> 450<212> DNA<213> Homo sapien

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180cttttggcac cattgaaacc agttctggcc catttgtttg aatagctaac atacacatca
240gctctatag cttcatatac cacctgatag aaccctgaa taatgctctt gaaagtgtaa
300cactcatgct tcttaccaca agcaattaac ataaagctta tacgccagct gtacgacgcc
360cattgtttac ataactctc tacttttaat tcaaccatct tttgcacccc tcgattcgat
420cagctccacc tctagtctct acgtatcgtc

450

<210> 2863<211> 398<212> DNA<213> Homo sapien

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120ctcaaatatt caaattattt tcatcataat ttaaactctc aaatatatag tgttttattt
180tcagatatga tatatactgg aaacaggggc aagtattctt tatcaatatg atacttttag
240aaaataattg ttttcatttt tgtgaaattt atttcagaca gtctcaaccg ccagtgaact
300acagaaacca atttactgga ttgtagctgg taaagccctt gattatgaac agatgctgct
360tctcatggct aatgtgaaat gggatgtaga aaaaaata

398

<210> 2864<211> 408<212> DNA<213> Homo sapien

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120cagacagaca cacctgggtt tgctctcccc cctctctggt tgctcccaga gctacgtttt
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240tttttctctc tcgcccgcct tttttttttt ttctgcacac actgcccggg gtgaaactcg
300ttcccccccc cccgtctttt ctttttttat gtcacgtcc cagaggagg cgtggctgag
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408

<210> 2865<211> 399<212> DNA<213> Homo sapien

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120agaagggtca ggccacacag ggctggataa agggctctga cttcattctt ggtgtgatgg
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240agatggattg ggataagggt gggagttagc tggaagggtg atctacaaa ctccatcctg
300ctatgaccgc tgcccttaac tatttaagg accctggctc gaaggggtga ggaggacatt

360ttatcggaga cagagccctg agggacctga ccccatggg

399

<210> 2866<211> 388<212> DNA<213> Homo sapien

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120taatcctgga agtggttaagt ggcaataatg atcaaagtgt gtaaagggga ttgttactac
180agctaataatg aaatgggagg ctggactaaa tctaaccctt ctacccttga tttcaattct
240aaaaggacac gtactaccat tgcagaaaga aaagacagtt ccaaatgata aatttttagag
300ttgttttgct aggatgcaag agaaattgga taagtggacc actcatacgt tgctggtgag
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388

<210> 2867<211> 409<212> DNA<213> Homo sapien

ctggagtga gtggcaccat cttggctcac tgtaacctct gcctctgggg ttcaagcaat
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120cgaagtgcgtg ggattgcagg tgtgagccac tgcgtccagt ctggcgcca agtttaagaa
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240tgaagcgact taaaacagta agtccttggt catcatcatg tgggagtatg gatgtgggca
300gggctcatct ctgttactg tgctggccac gtagcaagg gcaattaaca gttggcaggt
360aggtggctt gtgcttcca ttgcccctcac ccacatgggc ttccagccc

409

<210> 2868<211> 413<212> DNA<213> Homo sapien

ggcacgagga agtaaccacc attcccacct ttcactgcct aggtccaag tctgaatata
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120acttgcccta tgagcagaca gcatgccaag aatggaatta ggctcaggat ccagcctggg
180ctcaccctgt gtggctcatt cccaccaggg aaactgaaga taaaagattt gggaaaacac
240accaagaaaa aggggcagtt ttctttgccc aagcatttgg tgctagttag aggtgtttca
300ctctctcctg ctctctctcg gtagtagaat aaaggctgtg acacaaggaa gccagtgggg
360tgggagggag gcaccataat cctccctat aaccacaga agactaacct gat

413

<210> 2869<211> 401<212> DNA<213> Homo sapien

ggcacgaggg aggcattccac ccaccagtg ggaatcggga tcgttactg attcagcata
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120ggtcgggtggc cctgaagaag ccccccaccc agcagggagg caggtatcca gttagcagga
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300agaggcagcc tgcaagagtg ccagatgggc cccagtgggt tgtgtgtgca gaagtgcgct
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401

<210> 2870<211> 414<212> DNA<213> Homo sapien

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120cccggggtgg gcccggtat gtggatgtct gggcctctt cctgctgcag atggcaacca
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240ctcgggaggg gcctggggcg gccgaggggc ggctgcgggc actgctgagc caactgagga
300tccgggctga ggtgcangag gtggtgtggg gcgagggggc cggggctggg gaaccgagg
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414

<210> 2871<211> 398<212> DNA<213> Homo sapien

ggcacgaggg ggaacgcaca aaaaatgttt tctccaaaga agcattcgg tagcacaagt
60gatagaaacc aggaggagag acagtgcatt aagacttcat cactgtttaa aaacaacctt
120gacattccag aactccacag acctgtggtg aagcaggtgc aagaaaaagt gtttacttca
180gtgctttt atgagctggg cctccacca catttaattt ccacaataaa tacggtctta
240aaaatgtcta gtatgaccag tgttcagaag caaagtattc ctgtgttgct ggaaggcaga
300gatgctctcg tgagatcca gacgggctca ggtaaaactc ttgcctattg catccctgtg
360gtccagtcct ttcaagcaat ggagtcaaaa atacaggt

398

<210> 2872<211> 402<212> DNA<213> Homo sapien

cacgcgagcc gagccaagat gtccaaccga gcggtttgtc gatatttttag ccacgccggg
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120ggacaggcta caattagacc tgctagagcc attattgccc cccggagaat tatcatcctt
180gggccttctc atcatgtgcc cctctctcga tgtgcacttt acagtgtgga tatatatagg
240acacctctgt atgaccttcg tategacctt aagattttacg gagaactgtg gaagacagga
300atgttttgaa gcattgtctt gccacagat gaagatgaac acagtattga aatgcatttg
360cctttatacag cttaaagccat ggaaagccat attgatgagt tt
402

<210> 2873<211> 391<212> DNA<213> Homo sapien

ggcacgagag gacgtggagc gctgccttcg ggacacgggt gtgcagggcg tcatgagcgc
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120ggccgaggag tatctggaca tctgtcggga gcacctctgc cccctgtcct acgtccgggc
180ccacctcttc aagctgtggc accacacgct gcaggtgcac caggagctgc gagaggagct
240ggccaagggtg aagaccctgg agggcatcgc tgctgtgagc caggagctga agctgcggtg
300tcaggaggag atatccaggc agggaggagc gaagcccacc ggcgacttgc ccttccactg
360gatctgccag ccctacatcc ggccggggcc c
391

<210> 2874<211> 382<212> DNA<213> Homo sapien

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60gtacacagcc tcaggaccgc agctgaatgc acagctagaa gggttgcttt cacaagtaca
120gtctacaaaa agacctgcta gagccattat tgcccccccg agaattttca tccttggggc
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300tgaacgcattg tctctgcaga cagatgaaga tgaacacagt attgaaatgc atttgcctta
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382

<210> 2875<211> 386<212> DNA<213> Homo sapien

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120ccttgccagac atcgtggtcc ccagagggag cggcaacacg gtggccatcg acctgattgt
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240ggcacaccag tgccaccgc tgccccggag gctgagcgtc ctgaagagca cgccgcaggt
300acggggcatg cacaccatca tcaggggacaa ggagaccagt cgcgacgagt tcattcttca
360ctccaagaga ctgatgcggc tgctca
386

<210> 2876<211> 367<212> DNA<213> Homo sapien

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120attgacataa ttttaactta gtgcttctca agggagattg ggggtggagtc aggatgtttg
180gaattacctt ttggattgta acagactatt ggccaggcaa gctaaaagt ttgcagtact
240gatgagctgt agggggaaga attgcttcag ccaaatgcc actagctccc cttttgaaaa
300cagtacaagt ttaacttaaa ctaaatctta atgacagtga aagttaattc ccagttatta
360tctttga
367

<210> 2877<211> 357<212> DNA<213> Homo sapien

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60agatatatga gtgaagaaat tatccagaat gtatcacaga gaaggaaatg ggcaaaaaga
120aagagggtaa gatatatatt tataaacaca cacatacaca tattacataa aatgagaaaag
180tgacatgtct ttcatagatt ttccaagagc agaagggaaa aataatggga aaggaataga
240caatatttga tgagataata gttgagaatg tttcagagct gataaaaagc accatgacaa
300atttgagaag ctgagagaaac tgcaagcaga ataacgtaaa gaaaatatgc ttctaag
357

<210> 2878<211> 376<212> DNA<213> Homo sapien

ggcacgaggg gctaccaatt tgagaccatt ggtctggtag atacactttc attaatatac
60ttactccatc actcttttcta tatttttagaa gttactagta gaaatgtatg caggagtcac

120tggagacctt attaaaatgc agcttctgat tcagtgaagt ggggtggggc ctgagagtct
180gcatttctcc caggctccct ggtgctgccg gtggtgctgc tctgagtaac aagggggtgg
240ggaatgatat ggagccgtcc attattatcc catctgacaa atgagtcaca gagcccttag
300gtaattgagg tgggacagt ctgattctgt aagctgtgtt ttcagccaca acatttactg
360caaacttggg gtaggg

376

<210> 2879<211> 367<212> DNA<213> Homo sapien

tacggctgcg agaagacgac agaagggctg gtaaagatta tttaggttcc cctgattttt
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120aacttcatgt tctgagcagg atagtgaatt cctattgtac ttgacaggat gaagtatctg
180caagatgtgc cttcaggcag ttaaataact tgacctgctg ttagaaatct tttttatttt
240ttattttatt ttatttttgg ttattttttt atttttttga gacggagcct cactttgttt
300cccaggctgg aatgcattgg tacgatctcc gttcacacgc tctgcctcct gggttcacgc
360cattctc

367

<210> 2880<211> 364<212> DNA<213> Homo sapien

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60tttggtactct tactcctctg gtttggattt acaggatcca aaccaaggat ccaagccttt
120agttgggttaa cagttagttg attagttggc actcattttg tcacatgatt caggatgact
180gggggaaaaac aggatattgg ggtatatctt taactttttc acttctaaga taatctacag
240tttccctacc tctcgctcat accttcccta tccaagatca gaacttcaga ccgtcccat
300gggaatatga gggctgggta gaaggagag gaactagtta caggtatttc tgaatttcag
360tttg

364

<210> 2881<211> 369<212> DNA<213> Homo sapien

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60agtccccatc cgcacagagc tgacattcta gaacagaaga tagacaataa acaaggtaca
120caggcaaaat acatggatgt tggatgaaga agaattccat ggagaaaaaa ataaaaacaa
180gaaggagagt tgctatgaca gtgaggccaa gataattgca ggaaagtagc cctgatacca
240aggagacaat aaaccactac ttcaggactt ctagtatttt aagacaaata aactggtttt
300ggttaagtct ctgttaattt gtttttcttt acttacagct gaatgaattc ctgagaccgt
360gtgtaggaa

369

<210> 2882<211> 334<212> DNA<213> Homo sapien

tacggttgcg agaagacgac agaaggggtcc aggtacaac cctgcacata tatcccagaa
60tctaaaaataa aaatggaaat tataaaaaaa aaagaaatta aattgtgaag aagacaaagt
120atcaaaagac cttttctgtt agagtctaac aatgttcaaa tttagcttct tggaaataac
180tttttaaatag ctaagagcgt caacagaaaa ctgtggacta caggaaaaga actgcttcat
240atttcccgaa tcttctcaaa cttggtatct gcataatcaat gacttttagat tttattttta
300tggtgctgtt acttttgcta aggaagtatt atgg

334

<210> 2883<211> 341<212> DNA<213> Homo sapien

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60gaaatagaca atagaatgag gcagaggttg cagtgaagt agatcacaca ttgcactcca
120gcctgggtta gaagatctca aaaaaagaaa gtgtcatcat ctactagatt ggaaatatca
180gatattcttg agtctttctt ctccctcata tacaggtagt catccagttc ttcaaaatct
240cgttgaaatg tggcttcccc tccagccagt ctactgcta tcagtactta cctgtctgtg
300cattagcccc caccgacctc tatccacca gcattgcct g

341

<210> 2884<211> 352<212> DNA<213> Homo sapien

tactactgct gcgcgaagac aacagaaggg acacagaata agttctatag atctaattga
60cagcatggag actacagtta ataatactgt attgtatatt taaaatttgc aaagagtaga
120tcttaagtgc tctcaccacc aaagaaagggt aactgtgaaa agagatgtaa actctatctg
180gactagagta acctcagttc actaagggtca ttatgaatat gtatatcaga acatcatgct
240atacacctca gatacacaca atttcaatta aaaaatttta aaaagaagaa atcagctgtg
300gtcacattcc agtgatcttt gtttcataca ttgctttggc tgaaggaagg gg

352

<210> 2885<211> 344<212> DNA<213> Homo sapien
tctacggctg cgagaagacg acagaagggg ggaggatttt tgatttttct actttttggt
60gaaaaaagga atttgtaact tgtgcattgg atggacttgt ttggtacttg ggattttcct
120ctcttaaccg tcaacatcag tgttgaaaat ttgctaaact gattcacttt tagcagcaga
180ctttgaactg cagtcctgcc aacgttgagc actgaggacg cccgacagag cttgtgcacc
240taagctgcag accaagcctt tgcccagaat ttaaggattc caatggacga cctatttgca
300cagaactgca tgctgattat cactgccttt actccttttt tttt

344

<210> 2886<211> 335<212> DNA<213> Homo sapien
tacggctgcg agaagacgac agaaggggtt aaaaaagaac catggagacg gatgcattaa
60ctaagcccag gggtcctttt tcaatcctca tctcacttga cctgttggtt ccatttaacc
120agatctcttc cttgaaacgt ttttattttt tttttacttt gcttccaggg ttttgttaca
180tgtttctggt acatgttaaa cttctttctg ttggagtgcc ccatggttca gtccttccac
240ttctcttttc tgtccacact ctgggtccaa tttcattcag attcattcat gatgtaatat
300accacctata agctgatttc gacacttaag atcag

335

<210> 2887<211> 334<212> DNA<213> Homo sapien
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60aacagctggc attcacagta caggtattta gtactggagg gagcacagca gaacttatct
120ttaataaatt gcattttttt tttgttttg acctgtatgt tggctcccaa aaggaaggga
180tcaaggggtt tgcttttatt tctcctaatt caaaacatac cagggttttc aacattctat
240caaaaacttt taaaggcaaa tgtaaaaatc actccatctc actcaaagga tagcatttag
300gagaaacaat agaccaatca ataagcttg gagg

334

<210> 2888<211> 338<212> DNA<213> Homo sapien
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60atctgcagtt tgcaagtgca gcgaatcttg taggttagatt taccttgagt ttttttgaaa
120cggtagaatt aatatattaa aacatatggt ttttagttaa aataggatgt taaaggaata
180gagcgcacga aaaaaaaaaac tttccacttg aacccatggt gtttcactct acagtgggta
240tggtgtccct ggcaggatag ggcttccacc tcctgtgtgt gccggtagga cagggaagag
300gtggggaaca ctgtgtctcc atctcccaag catcttaa

338

<210> 2889<211> 347<212> DNA<213> Homo sapien
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60gccgactgag cctctaaagc gacttcagct ctgccccacc aacaccaccg cgcgcccggg
120aacagccgct ccggaagaa acctgagggg actgcggggg gcacgagga cagctgaggg
180aaggaggagc gcgagagaaa cagcgcgagc acgctgaggg ccggggggtg ccaggagag
240ggcccgcgga cccgcatagc ggaggaaggt ccgggagaaa aggggcggga cggaggagaa
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347

<210> 2890<211> 378<212> DNA<213> Homo sapien
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60ggteccatca cctggctgct catgtctgag gtctgcccc tgcgtgcccg tggcgtggcc
120tcagggtctt gcgtgctggc cagctggttc accgccttcg tctcaccaa gtccttctg
180ccagtgggtga gcaccttcgg cctccaggtg cttttcttct tcttcgccc catctgcttg
240gtgagcctgg tgttcacagg ctgctgtgtg cccgagacca agggacggtc cctggagcag
300atcgagtcct tcttcgcac ggggagaagg tccttcttgc gctaggtcaa ggtccccgcc
360tgaggggggc caaacccc

378

<210> 2891<211> 432<212> DNA<213> Homo sapien
cgttgctgtc ggtctttcag taggagattg gttaataaaa ttatggtaca tttccttcaa
60tgactgtgca gtcctcagaa gagattaggc tgatctttac caattgacgt gaaaagatga
120tgatattaag tgaaaaaaaa acaggttgct ggctgggcat ggtggcttat gcctataatc
180ctaacacttt gggaggccaa ggtaggagga tcgcttgagc ctaggagttt gaggctatcc
240tgggtaacaa agtgagaccc atctctacaa aaaaaatcaa gaaattatct ggatgtggtg

300gcacatggtc ccagctacac tggaggctga ggcgggagaa tcacttgagc ccaggagggtg
360gagtcctccag tgattcatgt ttgtgttatt gcactccagc ctgagcaaca cagttagacc
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432

<210> 2892<211> 434<212> DNA<213> Homo sapien

annncaattc ggcacgagga gagaactagt ctcgagagca gnnnnnttttt tttttttttt
60tttttttttac aaaatgcccc ctggggccca agggggcaaaa atttaccttt gcttaggggt
120tttttttttt taaaaaacca accggtttta ataccctcc tttaccctt ggaaccattg
180gggggaaaaa aacccttttg gaaaaacca ttttcaaaag gaagggttcc ccgggggggt
240tttaataaaa atattgttg gaaaaaac aaaaagccct ttgatttaa aaagggataa
300agggaggggc cctgaaaaac ccccccttt ttttttttt tttggggggg ataaaacct
360aaaagaaaaa ggggttttcg ccttaaaaa agaaaaattt gcccccaaa aataaccccc
420cttaaaaaaa tttt

434

<210> 2893<211> 425<212> DNA<213> Homo sapien

ggcacgagga gagaactagt ctcgagagca gttttgttca tctctcttt ttgtccttta
60tctctctgcc actgttctca cctcctcta aaacctggc aggagggtt gaaacctatc
120agaactaaag gtaatatct catctcctc aggtttttt catttaaaaa aaaatgggt
180atattagtta aattaaaaa ctgtgtgaa aattattgtc aaagggaag ggaaatacat
240ctaggggaaa catcatgtct ttaggcct ttatgtcact gaatgactta aggtcgaca
300aatgatattc ttggaaagt taatcttgag gttttcaaat ctttttttt aatggctccc
360atgtttctca ttgtctgatt gattcattag ttgtcttaa gaagatttcg cagttggaaa
420taatg

425

<210> 2894<211> 403<212> DNA<213> Homo sapien

ggcacgagac cattcttgcc tcagcctcaa tccccattct tgcttcagcc ctatcatcaa
60cttcagctcc aacgccagcc ccagcagcct cttcccagc tgccccagtc atcacagcac
120caactatccc agcctcagcc ccaactgcct cagtccact tgccccagtc ctatcatcaa
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300caaaaacaacc accaccatca attaggtgc cttcagctca aacacctaat ggcacagatt
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403

<210> 2895<211> 387<212> DNA<213> Homo sapien

ggcacgagag aggaagcagc ggcagggcga ggacctggcc catgtccagc acccgacagg
60cgctgggct cagccccagg aggaagacag ccaggaggaa gaagaggagg atgaggaggc
120tgctcaagg tactatgttc ccagctacga ggaagtgatg aacacaaact actcagaagc
180aaggggagag gagcagaacc cgaggttgag catctctctc cgtcctatg agtcaactgac
240ggggctcgac gagaccacc ccacatccac cagggtgac gtggaggcca gccctgggaa
300ccccctgac aggcagaact ctaagtggc caaacgactg aaaccactga aagttcgaag
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387

<210> 2896<211> 405<212> DNA<213> Homo sapien

cgttgctgtc gctcgtaa atgtcataaaat tttttaacat ttgcatcag gactcaataa
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300catcaggaag cacataatgt ccaattggct atttagtggg attagcagct acttatacat
360aatagatcca gtaaatcatg agagactggc tgngtatggg agctn

405

<210> 2897<211> 419<212> DNA<213> Homo sapien

ggcacgaggc aataatcaac agttctaagc ctaataaaga gagctcttaa tcagctcagt
60gggtgggttaa accagctatc ttttaagaa gagaaaaaac aaaacacagc aatgccctgt
120ctcttcagaa aattgtttta aaaagttagc caggcatagt tagtggccca cgcctgtagt
180ccgagctgtt tgggaggttg aggtgggaag attggttgag cccaagattt tgaggctgca

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360ttctatttat ttttctaagt cattcttaat cattatttg tgtttcagtg tttgaattt
419

<210> 2898<211> 387<212> DNA<213> Homo sapien

tctacggctg cgagaagacg acagaagggg aaaaatctct ggtcatctcc gagaattaac
60ttgcaactgt tttctatagt gctgtcgtct tgggcaatgg gcaattacat gactttgtgt
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387

<210> 2899<211> 411<212> DNA<213> Homo sapien

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60ggtcagatgc caaacgcaaa aaaaagcctt ctctctaaa gacacggaaa tgcaccgagt
120ccggctctga ctcaccccca aatccttacg gtccccaac tcggcagcca aaatcgaaaa
180ctactctcgt ctacagcgccc ccgctgttga ttacctgcca ttcgcacgg gcgcctgcgc
240cccgccgggt gtcgccgact tcggaaggca tcccgagact acccttctca aggccgtatg
300accagtcga gctgccatga tagactctcc gaagccggtc gtgacctccc ggaccagccc
360tgcagcaccg acctcctctg gtcggggccc gagcccggt ccggtctctt n
411

<210> 2900<211> 407<212> DNA<213> Homo sapien

ggcagagaa ggccgtgggg ctggagcatg tgggtgcctg ctggggagcc tgggtcaggg
60acaggggtcat ggagttagg ggaactggacc acccagggca tgcgagtggc tgagccaggt
120tgcgggcaga ggggtggccag gggcccatgg gagcatttgc aggtgagctc cctggggagg
180gttactgtgg gcgtggacga ggctgcctgg gcgtgtggct cagggccggg cctgggtagg
240tggtgctgctc aggggtggctg atgacagaca ggtcttgggg aggaggaccc gggactcggg
300atgagcctgc gtctggctgg gtggtgcctg ctcttgttt tgtggtggga gactgaaggg
360gagctgaggc tttggcggca acgggccttg tccagtgggg cattttt
407

<210> 2901<211> 401<212> DNA<213> Homo sapien

ggcagagca cagtgcctt ggaggtgttc agcttatccc aggtgctga cctggctaac
60aagggcccga agtgggagaa gagcatgcc gaaattgcag aacaggccaa gcatgaggcc
120gagatcgaga ctcggattgc tgagctgcgg aaggagggtt tctggtcact gaagaggtg
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240cagtggctct ctgctgactt tgctcaggag cgcggttga aacgggtgt ggcccggaag
300gtggtgcga tgggtatccg gcaccagag gagcagcggc agaaagagga acgggcccgg
360agggaggagc agccaagct gcgtcgaatt gcttcacca t
401

<210> 2902<211> 375<212> DNA<213> Homo sapien

tacggctgcg agaagacgac agaaggcaga catacgggca cgcaccacca tgcccagcta
60atttttaaat ttttagtaga tctgcgtct cactatgttg cccaggttg tcacaaactc
120ctggcctcaa gtgattctcc ttccttggcc tcccaaggca ctgggattcc aggcagagc
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240tgagaagtc aggccaat taaatttcat tttgtcttt tatcagtga aaagtagcat
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375

<210> 2903<211> 350<212> DNA<213> Homo sapien

tacggctgcg agaagacgac agaaggggat ctgtcttttg aaacacataa acatgtacat
60acataaacat acaaatgtct ttcaacggtt tatggaatat cttatagcaa attaaagatg
120agtatgtttg tcattcaatt atgaaagatg ttgatataaa taaatttatt catatatttc
180aaaaagtatg tagggcttcc agtcaaggta aagaaacaga gaccacattt actgtcttcc
240ctataataga aaaaaccag aaaatttatg aaatgactgt ttttttagac attggacaac
300aaagaacagt gacctctgag acacaggata caagatgagc cctaaaagtg

350

<210> 2904<211> 369<212> DNA<213> Homo sapien
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60atttttaaat ttttagtaga tctgcggtct cactatgttg cccaggctgg tcacaaactc
120ctggcctcaa gtgattctcc ttccttggcc tcccaaggca ctgggattcc aggcattgagc
180caccatgcmc agtctcattt ctgttttctc tagaacatgt tttcatcaca ctgacttttt
240tgagaagtcc aggccaat taaatttcat tttgtctttt tatcagtggg aaagtagcat
300atttatgttg cagcacaag atgaatcaaa taggaagaaa atgtaaaaca ctttggggc
360cgggcacag

369

<210> 2905<211> 372<212> DNA<213> Homo sapien
tacggctgcg agaagacgac agaagggtag cacactgaat tatgggggtgt gtgtttgtgt
60gtgtgtgtgt gtgtgagaat tctaagctac cttgtgattc tcataattag ctaggttttg
120aaactcttgt gtgatgtgt ttttattttg tttttttgc tttatgtaaa acgtcaatgg
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372

<210> 2906<211> 363<212> DNA<213> Homo sapien
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120tgagtcaata atgtcaccaa gaaatgtgtg tgtgtgctg tgtgtgtgtg tgtgtgtgta
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240gactcatgct cacatgatgg gtggcaacaa ttacagagnt aatgtttttc tcatatacat
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360ccg

363

<210> 2907<211> 375<212> DNA<213> Homo sapien
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120ggctgggggt atgctgtttt atataaggtg gatcaaggaa gggctctctg ataagagaat
180gtttaagcag agatggaatg aagtggggc cagaatcttg ctcatatctg gggaaagcat
240ctctgggcac aggaagagcc agtgtaagg ccctgagcca ggaacatgct tggctccttg
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375

<210> 2908<211> 374<212> DNA<213> Homo sapien
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180ccccgagttg ctgattatat aattattgaa aaataaaaata taaagatgca gcaatacat
240tgcaatattt atatttctat tatcataatt ccagagtgg ttttttagac ctatctctaa
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374

<210> 2909<211> 352<212> DNA<213> Homo sapien
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352

<210> 2910<211> 340<212> DNA<213> Homo sapien
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120tcttttctgc gtcttttgag atgagtatca gggttttttt ttttctttt atcatcggag
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340

<210> 2911<211> 339<212> DNA<213> Homo sapien

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120gttgattgag tgctctctat gtctggggc ctgttctaag aactttgatg catccttatt
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339

<210> 2912<211> 334<212> DNA<213> Homo sapien

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120gaaccctggg cagtaatctt cagcgaggac agtattattg cttttcatgt aaaacctcaa
180ttattaatag ttttaaatga caatttttct ttagtatatc taaaaatatt ttgttcaa
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334

<210> 2913<211> 344<212> DNA<213> Homo sapien

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240actgttccac cgcaccgcag acagacctca agtactacag ccttccagca gccttcccag
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344

<210> 2914<211> 337<212> DNA<213> Homo sapien

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337

<210> 2915<211> 342<212> DNA<213> Homo sapien

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120atcgctctca gcgctgggg agtgatcatg ttgtaatcca cccaccgcca cttcaagaag
180aaatgatatg aagaagtgcc ggtctccct cccctcttcc gcaactgtcc gtgatgatga
240cgctccaga gaggacgata atctgggttc ctgggagaga tggcttggtc actattccca
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342

<210> 2916<211> 390<212> DNA<213> Homo sapien

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60ccagagattt agtcaaatat gatactggga gtttcagtga gaatgtttct aaatgagatt
120gacattggaa ttggtagact ggggaaagca gatggccctc cctaatatgg ggggtggggg
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390

<210> 2917<211> 367<212> DNA<213> Homo sapien

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367
<210> 2918<211> 412<212> DNA<213> Homo sapien
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120tccggctctg cctcaccccc aaatccttcc ggtcccccaa ctggcagcc aaaatcgaaa
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412
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120cagtttctga atcaacaaat atatctgtga ttcttttata ctactacata aaagaacagg
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394
<210> 2920<211> 448<212> DNA<213> Homo sapien
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120gatttgtttt tgttgtaata ggattttaa aaatgtaata tattgcagga ttataacca
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300aaaaggggac aaaaatctgc tgtggaatt tttattttt ccgggttaaa ttgaaaagg
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448
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347
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402
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371

<210> 2924<211> 350<212> DNA<213> Homo sapien

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120cccacaaccg gctgatgtga aggagtccca cttagggatc caggaacagt gggaatagca
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240gatgagggag cctccccctg tgtcaggaga gccctggggg cccccacaca cagtgagggg
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350

<210> 2925<211> 347<212> DNA<213> Homo sapien

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240aaagactgtg ctgagagaga acttggtggc gttatatgtc cttattgtga gaagaatttt
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347

<210> 2926<211> 345<212> DNA<213> Homo sapien

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120gcctgggttaa gaagatctca aaaaaagaaa gtgtcatcat ctactagatt ggaaatatca
180gataattcttg agtctttctt ctccctcata tacagttagt catccagttc ttcaaaatct
240cgttgaaatg tggcttcccc tccagccagt ctactgcta tcagtactta cctgtctgtg
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345

<210> 2927<211> 346<212> DNA<213> Homo sapien

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120tagccaactt ttgggagcgc ttctgtttgc aaagcgctgg ggatgtgctt gtctctgtgt
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240tcaaggctga tctttaaaac cctgccttg ctgacaagt ctttaaaggc agtctgcac
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346

<210> 2928<211> 341<212> DNA<213> Homo sapien

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300tgagacaagg gtacaaattg gaactaaaaa ttgacattgt g

341

<210> 2929<211> 343<212> DNA<213> Homo sapien

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120gccaaacttt gggagcgctt atgcttgcaa agcgctgggg atgagcctag ctctgtgtga
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343

<210> 2930<211> 342<212> DNA<213> Homo sapien

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342

<210> 2931<211> 400<212> DNA<213> Homo sapien
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400

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417

<210> 2933<211> 404<212> DNA<213> Homo sapien
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404

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389

<210> 2935<211> 399<212> DNA<213> Homo sapien
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399

<210> 2936<211> 403<212> DNA<213> Homo sapien
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300aagacaattt cagcacttct ggcattgaga caacatgtgc atcaaatatg ctgaaagggt
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403

<210> 2937<211> 379<212> DNA<213> Homo sapien

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379

<210> 2938<211> 388<212> DNA<213> Homo sapien

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300aaaatctgaa tgaggaaaga caattaacac taagatgaca aaaatgttg aattattgca
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388

<210> 2939<211> 374<212> DNA<213> Homo sapien

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180atgctcgtct tccagggggg ttcagtctaa ggtaatctct accaggaaga aaagctagat
240gaccttagac atgtgcattg gtttgacct tctaattagt tgaattttta cttattttga
300catgagagat tacatagaat ctctatgttg cccaggttg tctccaaatc tgctcaaaca
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374

<210> 2940<211> 378<212> DNA<213> Homo sapien

ggcacgagga ccacacaggc cgaatccggg tgcattggtat tggcgggggc cacaagcaac
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120aggagaagg tttccaagtc cgctatgatc cctgtaggtc agcagacata gctctgggtg
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240tcttgaactc taaccacata ggccgaatgg cagttgctgc tcgggaaggg gatgcgcac
300ctcttggggc tctgcctgtg gggaccctca tcaacaacgt ggaaagttag ccaggccggg
360gtgccaata tatccgag

378

<210> 2941<211> 387<212> DNA<213> Homo sapien

ggcacgaggc atcaactatg gtggacatgt tacagatgac tgggaccggc gcctgctgac
60cacctacatc aatgattatt tctgtgacca gtctctatca actcccttcc accggttgct
120agcactggag acttatttca tccccaggga tggcagcctc gcttcttaca aggaatacat
180cagcttattg cctggcatgg acccccctga ggcctttggc cagcaccaca atgctgatgt
240ggcctctcag atcactgagg cacaaccct ctttgatact ttgctttcct tgcaacctca
300gattacaccc accagggctg gaggccagac ccgggaagag aaggtccttg agttggccgc
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387

<210> 2942<211> 465<212> DNA<213> Homo sapien

cgttgctgtc gggcatggtg gcagggtgtc gttatcccag ttaggaggct gaggcaagag
60aatctcttga acctgagagg cggaggttgc agtgagccaa gatcgccca ttgactcca
120gcctggggga caagagttag acttagtctc aaaaaaaaaa aagaaaaaaa aattcggggga
180tttgggtcaat atcccatttt tttgttaacc ccaaggccct taaaaataac ccggaactta
240agggactggg aattttgggt taaaggggcc ctccggggaa ggggggggaa cactgacttt
300ttgaccctct ttgaaaagat aaaaggaccg gggccctggg gggaaacct tgtgaaaagg

360ctcgggaatt cagaatggcc taaaaaacct cccccacac cggcaaaaaa naaaaaaaaa
420aaaaaaaaa aaaaaaaaaa annnaaaaaa aagggccgtt gttgc

465

<210> 2943<211> 442<212> DNA<213> Homo sapien

caccggcttg ctcgtttggc cgatgcccgc tacgggtgtg agaatacgac agaaggggga
60cacaaatgtt aaaattagca aagacattaa gatagcttta tgactgtatt ctatagttt
120taataagtca aatagagcca tagaagaaat ttaaaagact caaactaatt cctagagatg
180gaaactacaa tgtctgctgt gaaaaatata ctggatggga ctagtggtag attcgccatg
240ataggagaag tagattagt aacttcatga cacagcaata aaaacatcat gatggagcag
300aaaaaaaaatc caaacctttg aaaagagctt cattgagctg tgggacaatg tcaactagca
360taaaaaaaat tttgagaaat aatagctaga aatatctgaa ttgatgaaac tataaaaccg
420agatcaaagn gtgaaacaag cg

442

<210> 2944<211> 468<212> DNA<213> Homo sapien

ccttaaggcc ctggccccgc ctgcgtccgc atcactctgc atcagcactg cgggccagt
60gacaccgagt tccaccccat cggcttccat atcttccagg tcccagaggg tggaaggagc
120caggacgcac cccactgct gctgcaggag ccgctgtga gctgcgtgcc acatcgctac
180gcccaggagg tgagccggct ctgcctcctg cctgcaggca cctacaagggt tgtgccctcc
240acctacctgc cggacacaga gggggccttc acagtacca tcgcaaccag gattgacagg
300ccatccattc acagccagga gatgctgggc cagttcctcc aagaggcttc cgtcatggca
360gtgatgaaaa cctaacaggg tggccccctg tgccagctca ngtgactgga gcccagggc
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468

<210> 2945<211> 406<212> DNA<213> Homo sapien

ggcacgagaa gttgggggca ggggaggcgg ttcatgaagg cgggctctac atgacttaac
60ccttgcttgg catggcctta agcctgttt acaatttgg atcttattgc cacagtgtct
120gttctgtcca tctcatgac cctattttgt tcatctatgc tcggcagctg cgtctaaacc
180ataaagggat ggggtataac aagttgcatc tgacctcca acccatcacg gccaggaatt
240gttttaagtt tttctgaga ttccctcggc cagaggtgg catctgtca atcgttggg
300ttttatgatt tttagcttac ataactgatt tgataatcca gggcatttgt taccgcgtat
360ccaggcgaga ttatgactca actatttagc acctccatct caacag

406

<210> 2946<211> 407<212> DNA<213> Homo sapien

tttgccaggg gaaaacattc tgcttttagg tagtttcaaa attcagggga gggagcctga
60aatttttgcc atgattgggt tgtagaaaag agcaggcatc agactacttc tgataaaatt
120gtttggaagg tcacgacctc gcaaaaactt ttcaagagca acaaggaaga attctgctgt
180gaagaacaca gtgtacggat cctccgcata ttatctcaac agaggacagt agctcaggag
240gcagcttcaa acggtgacct gtggcctggg ccatctcttc gtcattgtct tcaactttcc
300ctgtttccct gtgaactggc ttccatgggt ctgtagggtg gtgaagtcgg gttgtggctg
360cagcagagca agagatgctt gcccagtggt gagcaacca ccccgct

407

<210> 2947<211> 380<212> DNA<213> Homo sapien

ggcacgagat aacacttgcc acaacttggg aaattccatg ggtctatgcc acattgctcc
60cagagtaatg aggcaaaata gtgctctgtt atagaattgc ttgtttcaca atacatcatg
120acagataacc atacaacatg gaatgacaca aacataatat gccacactcc agaatatgta
180atgctcgtct tccaaggggg ttcatgtctaa ggtaattctt accaggaaga aatgctagat
240gacttttagac atgtgcattg gtttgacct tctaattagt tgaattttta cttattttga
300catgagagat tacatagaat ctctatgttg cccagggttg tctccaaac tgctcaaaca
360atcctccgc ctcagtttct

380

<210> 2948<211> 374<212> DNA<213> Homo sapien

tacggctgcg agaagacgac agaaggggaa cacatTTTTG atcatgcata ttttgatttt
60taaatattat tggtagaaa tttgaacaaa gtcaccata catTTTctaa cttccagaac
120tctacttatt atatatcttt tgctttatag cctgaaataa ctctatagcg aagtaattta
180caagaaatgg tctattatga aaagcaggct ttaaagcata aaaatttttt ttataggaaa
240tatgcatgat tataaaacaa cctgattttt attttattgt tcataaaaga gactaatatt

300gggtgcatgtg ctgctgtaat ttgttggtga ttatgtgtgt aggaaaactg cccagcttgt
360agccagcttc ctca

374

<210> 2949<211> 407<212> DNA<213> Homo sapien

ggcacgagaa ttgctgtgcg tggggcacgg acggacagcg aggtatagag agtggagaga
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120gggactcaga ggtgtcaggg caagcatgca ggcaggcttg tgacaaactc cttggccagg
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240ctgtgtgaca gctcaggcca gggggtcggg actcccccca tctcctccgc acacacatac
300ccctgcacac ataccagcc acgtacagct ggggtggctgt acgcaagtca tttttctact
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407

<210> 2950<211> 387<212> DNA<213> Homo sapien

ggcacgagga gagagagaga gagagagagt ttgagagtga gagagagaga gagagagaga
60gagagagaga gagagagaga gagagagaga gagagagaga gagagagaga gagagagaga
120gtgtgggcgc cctctctct tgtgtgctc cccccccc cgctctctca ctcttatgtg
180ggggggcgcg cgctctctct tttttttgtg ggggtgtgtg gcgctctccc acacggggct
240ctctctctga gagtgagcg tctgtgtgtc tgtgtatata ggggggggtg tgtgtctctc
300tgtgcgcccc ctgtccctag gcagagagag agtctctctg tgtgcgcgcg ctcttttgtg
360tgtgcatatg tttctctctc ccctctc

387

<210> 2951<211> 400<212> DNA<213> Homo sapien

ggcacgagac actaagatgg ctgccgttg catgacaccc aacctgtgc agacccttca
60ggaggaggcg gtgtgcgcca tctgcctcga ttacttcacg gaccccggtg ccatcggctg
120cgggcacaaac ttctgatgca gattttagct gagggatttg gaagccattt ggggaggcag
180gctgggccaag agggtagagc tgggtaataa atgtctatc tctggggag gagggattct
240aaactttctc tccgtcctca atttctacct ccatagaccg gccagaattt agcttcactt
300gagagagacc tggaaatggc gccatgattg aaaccacgca ccattacatc atcattacat
360taattacatc aacataaatt atttcttccc ctttccctn

400

<210> 2952<211> 395<212> DNA<213> Homo sapien

ctttaagatc atcctgggaa tttccttcac tttttctttt gggagacctc ttatttctg
60atcccaggctc ttcattcttc ttggtttact tctttattg gtggactaca tctccacat
120gggaggtaaa ttgttgaaac cttgcatgac tgaaaacttt attttaatct caccctcaag
180ggatgatttg gctaggtatg gaattctagt ttggaaataa ttgctctca gaattttaaa
240cacattctcc attgcctcat agttttggcg taaatgttga gaaatacaat gccactttta
300atttctgatg ctttgcattg gatctatttt tctctcaagt agcttttata atctccttat
360ccttgatatt ctgaaaattc atgatgctgt gcctg

395

<210> 2953<211> 418<212> DNA<213> Homo sapien

accgatgctg ccggaataga gaaaacatta tctgtatgag ctcttctcga tttacatgta
60attggcaaaa ttcaaagagc tgattcttca acaaataaat tacttaaaaa cggatggaca
120gggaacctcg taaagccttt atcaactgca atgtatggac ttctatactg aaatgtttac
180agatgaaatt atatgatgac tgggatttaa aagaaatcct acgatagcca ggtgtggtgg
240tgcattgccag ctactcaaga cgctggcgga gaattgcttg aaccaagag gtggaggctg
300cagttagcca agaccacacc actgcactac agcctgggca acgagagact ctgtctcaca
360aaatataaat gaaaaactaa aagttattct atgagtggcg gaaagaacag attacaca

418

<210> 2954<211> 394<212> DNA<213> Homo sapien

cgttgctgtc gagctcagga ggctgaggtt gcagtgaccc gtgatcgac cactgcactc
60caacctgggt gacagagcca ctgcaaagca ctctgtttag tcatggtttc ttttatgtat
120tcttttcatgt attgacctta aaaaagaatg tttctgaata tgcctttaat ctgacaaacc
180accaccttaa tttctttta aatcagttt ggcctacag ccatgccact gtgaatgtgt
240ctgatctcat gtgatcatgg aagctaaagt gagtttgata tgataaatat atgcaacgta
300acttttaata taacttttaa aaatatgttt ttaaggccag atatgggtggc tcacgcctgt
360aatcccagca ctttngagg ccaagggtggg agga

394

<210> 2955<211> 407<212> DNA<213> Homo sapien
ggcagcgagca gctactcggg aggctgagac aagagaatca cttgaaccca gaaggcagag
60attgcagtga gctgagatca tgccactgca ctccagcctg ggtgacagag tgagactcca
120tctcaaaaaa ataaaatatt gtggtattgg cacaggagtg gacaactagg tcaatctagg
180aacagacctt ttggaacttg atatacatga aatgactcaa ccaatcagtg aagacagggg
240ggatgttcac tgaatattgg agaaaactga actcccccat acaaaagaaa acagatttcc
300acttttacaca cactcaaat taaatttcag attaaatact aggatatttt taatgattta
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407

<210> 2956<211> 412<212> DNA<213> Homo sapien
cgttgctgtc gggcaggccc ctgtaatccc agctaattgg gaggctgaag caggagaatt
60gctcaaacct gggaggcgaa gattgcagtg agctgaaatc acaccactac actccagcca
120aagcaacaag agcaaaaact tcgtctcaaa aacaaaacaa aaaaagagta ttcattgtga
180ggacaaacaa tacaataacg aagaggggtg tagtaccttt acttgatca cagatacttt
240tgtaccatt ttgcactaga ggaaaacat gaagcagttg ctcaaagtgt gttcaacacc
300agaaaattta tattggagaa aagcactgta aatgtaatgc atttgtgaaa acatttttta
360aaaaactaca gcttagaaaa taccagaggc ctcatactaa aatatatttt gg

412

<210> 2957<211> 407<212> DNA<213> Homo sapien
ccgtgacctg cctgggcgcg gggaactgaa agccggaagg ggcaagacgg gttcagttcg
60tcatggggct gtttgaaaag acccaggaga agccgccccaa agaactgggtc aatgagtgg
120cattgaagat aagaaaggaa atgagagttg ttgacaggca aataagggga tccattggag
180tcttttggtg aatactaagc tgtgcatgct tagagtgaag tttcaagaga ctgggcaaa
240aacaattact aggaacagaa caactaccag gaagctgtaa gctgaataat tcttagagct
300aataaaggat tgagaagtgg ttgagctctg atcagacaca gaaaagagac tttgttgaac
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407

<210> 2958<211> 328<212> DNA<213> Homo sapien
tacggctgcg agaagacgac agaagggact ctgcattaaa caggagcttt tctaatatgg
60ctggaaactg ttgggggtgg attagagatt ttaaggatc ttatggcaag ctttggtcgg
120tagagtacaa gaatctagtg gtgtctttta ttgggggttt ggggtgctg ggaactatga
180cattacaaag agccactaat tgtaactga aggaaaaaat actggtcaat gaagggaac
240ttaactataa aatcaactta gtagaataa accattaagt ggtactaata tgggcaggca
300cagtggtcga cagctgtaat tccagcac

328

<210> 2959<211> 344<212> DNA<213> Homo sapien
tacgggtgcg agaagacgac agaagggtct gtgtggcaca cagagatgag acctactcaa
60tctgacttag taaaaccatg ctgtagaatt tttgtcttaa aaagaccaca taccagcac
120ccatgaaata aaagattcat ctgtaattgg gattcaaagt gattaaattc ctttgttcat
180actcataaat agcactaaag tgttataaca ttttcattta cctattttta gttccttcat
240tttaacttaa taaaaatctt ggattgatat tctttttttt tttttttttt ttttttggga
300aaaaaatttt ttttttcccc ccgggggggg aaagggggtt tttt

344

<210> 2960<211> 340<212> DNA<213> Homo sapien
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60gaacagtgtg taaaggattt agaactgata tgtactcgtg agtcaggagc agtctttgag
120gttggtggtt tgaatttgtt gttaccttc attcgtgaca gtggacatct agttcataaa
180gacaccttgc actctgctat ggctgtggta tcaagactct gtggcaaat ggagcctcaa
240gattcttctt tagaaatttg ttagaatct ctgtctagtt tattaaagca tgaagatcat
300caggtttcag atggagctct gcgatgcttt gcactactgg

340

<210> 2961<211> 388<212> DNA<213> Homo sapien
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60tgggggttaca ggcttgagcc actgtacca gcccatcaat aatttttgcc tgaacaatt
120tttattgcca tctttgtgtt gagagtcctc catggatctg ttgtgtgctt acatgtcttg

180ctgggtgtgc caagaatgca aggcccaaga atgctcttta tttgggcctt ttctcaggg
240tggttacaca gctggaatc ttcagagaca agttaatgtt tcctcttgga caaagagcag
300gcttgccac tgcttggtat aaaaacaata gatttcagcc gggcgtggtg gctcatgtct
360ataatccag cactttgatt tttttttt
388

<210> 2962<211> 403<212> DNA<213> Homo sapien

ggcacgagag aggagctcag agaggaacgg agaggcagac agagggaaac aacgcagaaa
60gaaacagagc caaagccaga gtgtgggggg agccggagga agaaacaaaa acacacacat
120gtggagtcgg aacgacacag gcagagaggc acagagtcgc agcaatccag acagaaagag
180acacgcagaa agaaacagac agtgacagag aagatggtag cctctctgcc ctcccaaac
240accttgcccc actggctctg gctggcggca ggggactcac aggccttga cctatgcca
300gtaggggaag agacaggact tttcctcaga ggccttcaat gagaccccat tcccaaaaag
360gttgggtctg acacacagca gccatggtgt ccacggcccc cat
403

<210> 2963<211> 393<212> DNA<213> Homo sapien

tcagatgca gctgcagccg cgcaggcagg agccaggac aagtgggagc cctgcctctt
60ccaagtggc ggggtgggag ctccaggtg cagctgtggc tgcccccca ggcacaggac
120gagggcatct ctgcagcctg caccatcggc catccagga aggacagccc ccttcacct
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240ctgctctgat cttggagggg agtcggagcc aagacctgca gccatgaatg gcagcaggag
300gaaagggggg gggnnccan naaggcccca cctcangcc agggaggggc tgaattctgg
360gggctgggt gccagtcct ctgaccagag agg
393

<210> 2964<211> 423<212> DNA<213> Homo sapien

ggcacgaggt tcaataagg tgtaattgaa aagtgtcct ctcttcagag atgtcaaaaa
60caaacaaatc caagtctgga tctcgtctt ctctcagc atctgcatca agatctcgtt
120ctcgttcatt ttcgaagtct cggccccgaa gccgatctct ctctcgttca aggaagcgca
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240acccaagagt atatcagaat cgggatttcc gaggtcacia cagaggctat agaaggcct
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360atggaaacta tcgctcanat tggcagaatt accggcaagc atacagtct ctctcaggcc
420gtc
423

<210> 2965<211> 385<212> DNA<213> Homo sapien

cggtgctgtc gggttattgt aacagtaatt aaatgctgcc ttaattgaag gggtttgggt
60ggattttttt ttctcaaat agctgtagg gactatttta acagcttaa caggagctct
120caagatgcac ttctgtattg agaggaatat gggcttgatc ctcttctat cttaattgggt
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240aggttgctca cagcctaacc tggcgtgttg tttagggtg atggagacc atgtgagcct
300ttgctttcct ctggccccag cccaccctg aacacagctc atacgcagaa tcaggaccag
360catgtgcaga gctggccacc agcac
385

<210> 2966<211> 376<212> DNA<213> Homo sapien

cggtgctgtc gtggggacag atttgtgatg ctgattcac ccttgaagta atgtagacag
60aagttctcaa atttgcatat tacatcaact ggaaccagca gtgaatctta atgttcactt
120aaatcagaac ttgcataaga aagagaatgg gagtctgggt aaataaagat gactatatca
180gagacttgaa aaggatcatt ctctgttttc tgatagtgt tatggccatt ttagtgggca
240cagatcagga tttttacagt ttacttgag tgtccaaaac tccaagcagt agagaaataa
300gacaagcttt caagaaattg gcattgaagt tacatcctga taaaaccgg aataacccaa
360atgcacatgg cgattg
376

<210> 2967<211> 384<212> DNA<213> Homo sapien

gaaggaatga agattgacct catcgatggc aaaggcagg gtgtgattgc caccaagcag
60ttctcccggg gtgactttgt ggtggaatac cagggggacc tcctcgagat caccgacgcc
120aagaaacggg aggtctgtga cgcacaggac ccttcacgg gctgctacat gtactatttt
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240ctgatcaatc acagcaaattg tgggaactgc caaaccaaac tgcacgacat cgacggcgta
300cctcacctca tcttcacgc ctcccagac atcgcggctg gggaggagct cctgatatgac
360tatggggacc gcagcaaggc ttcc

384

<210> 2968<211> 225<212> DNA<213> Homo sapien

tcacactgcc ttccaccgc tagcgagccc aattgcatgc aatatatgcc tgatgatcca
60ggggaggaga gagagtgatg cagagctggt gcagaagggc agcgagctgg tggctctgcg
120gggtggcgctg cgggaggccc gtgctacgct gcgggtcagt gaggggcctg cgcggggtct
180acaggaggcc gccccgactc gggagctgga gctggaagcc tgttc

225

<210> 2969<211> 413<212> DNA<213> Homo sapien

ggtgctggcg attctgtgtt attaattata ttcatactat tgtgcaacca ccggcaccat
60ccgtctacag aactcttgat ctcccaaac tgaaattatg tattcattaa acaataacca
120cccattacct cctctctcct cagcctttgg taaccagcat tcagtctcta tgaattgact
180actctggata tctaaaagga atcattctta ttccatttac cataaagact tcaaagtcca
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300gtaaataccg tagtttgtgt atcaggctcat ccattactgg aactgggtt gcttctgctt
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413

<210> 2970<211> 405<212> DNA<213> Homo sapien

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60taaaaattta cccggggggg gggaggccc cctgtatttc cacttcctca ggaggggggg
120gcagaagaat cttttgacc caaaattcaa aaatggcaag gacttataat attgttattg
180ccctccacct taggcaacaa aggaacacct tgtttttaa aaaaaaaaaa taagccaggc
240ttataatagg ttatcccaa gggagtaagg aggttttata gggccaaacc ctcttataa
300aaaagaaatt agccaactta tgggtgttta agggtaatag gaaaggctta tatggagaac
360ctttattctt aaaaaaagg gaaattttt ttcggtacc catgt

405

<210> 2971<211> 381<212> DNA<213> Homo sapien

gcctacggct gcgagaagac gacagaaggc ccattcacta atagattgggt cagcaaacaa
60tccaagctgt gagccaaagt cagccacta tgaggccaac tctgtttgca cccattcttt
120atagcttttg cactacagtg gcaaagttaa gtatgtgcaa cagagactgt ataacctgta
180aagccaaaaa cctcactgtc tggacttta tagttccaga ctctcact agttgaatac
240tttgaaaatc ttcaggttct ttctgggaag ttggtgaaga ctatctctaa gcagtattag
300ataattggaa tcttaccatt tagcacactt tcatacaaaa agtgacaggt aatggttggg
360atcagaacag aacaacataa n

381

<210> 2972<211> 437<212> DNA<213> Homo sapien

aggatccctc gattcaattc ggcacgagga cagagccgac tccatctttt agaaaaata
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120ggtcgggtgt gggttctgca aaccagggtg ggattctgtg taggttctgc agggccaggg
180taaaggctca cacctgtaat cccagtactt tgagacgctg aggggggagg atcacttgag
240cccaggagtt caaaaccagc ctgggcaata tagggagacc gtatcactac aaaaaagttt
300tttttagttca ccgagcatgg ggcacatgc ctgtagtccc acctactga gaagctgaaa
360tagggtcacc tgaccctggt aggtgaggc tgcagtgagc caaatcgca ctactgcact
420ccagcctggg tgacaan

437

<210> 2973<211> 399<212> DNA<213> Homo sapien

ggcacgagat tacatttccc agtacttctt gtccctctt cctgctttct cttttttttt
60tttttttgaa ttaaaaacgg agtttggtt tgccccggg tggggggcca ggggaaaaat
120tttgcttaat tgaacccca ccttgggggg ttaagaatt ttgcctgcct aacctccgg
180agaaagggtg ataaaggggc ctgccccccc cccaaccta tttttggttt ttaagaaaa
240aaggggggtt aacctgggtg gccgggtgt tccaaacttt tggccctggg gggatcccc
300cccctgagcc ccaaaaaagg tgggaataac gggggggacc aaccatgcca aaaattgggt
360ttaatttttt taaacctttt aaccaaccta accaaaaat

399

<210> 2974<211> 346<212> DNA<213> Homo sapien

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120acctgaatat atgcatccaa gtatgtcaac aaattccaag taagatgaac tcaaagagac
180cacacagata ccaacatttc acaagccaaa gccagagaat tttgaaagca tcaagggaga
240agcaacttgc tacatacaaa ggatcctcag taacaggtcc ccaagccctg ggccacagac
300tgtaacagt ctgttatgtt ccagaccaca cagcaagagg tgagtg
346

<210> 2975<211> 341<212> DNA<213> Homo sapien

tacggctgcg agaagacgac agaaggggca cttatgacaa cattaacaca gaatgccagt
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120cagcagtcac catcttcttc ctctcttctt tcttatcat cgtgttcttc atcatcaact
180gttggtacaag aaatctctca acaacaact gtatgtccag aatctgattc aaatagtcag
240gttgattgga cttacgatcc aaatgaacct cgatactgca tttgtaatca ggtatcttat
300ggtgagatgg tgggatgtga taaccaagat tgccctatag a
341

<210> 2976<211> 427<212> DNA<213> Homo sapien

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120aggaggagac cgcagcagcg cccccagtgg aggaggggga ggagcacaag cccccgcgg
180ctgaggagct ggcagtggac acagggagg cagaggagcc cgtcaagagc gagtgcacgg
240aggaagccga ggagggggccg gccaagggca aggacgcgta ggccgctgag gccacggccg
300agggggcgct caaggcagag aaaaaggagg gcgggagcgg cagggccacc actgccaga
360gctcggggcg cccccaggac agcgactcca gtgctacctg cagtgcagac gaggtggatg
420aggccga
427

427

<210> 2977<211> 427<212> DNA<213> Homo sapien

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60gagagagaga gagagagaga gagagagaga gagagagaga gagagagaga gagagagaga
120gagagagaga gagagagaga gccccccctc tctctctttt ttttggggcg ctctctttt
180tctctctctc tctatatctc tctctcgtc tctctgtgtg tgtggctatg cccccgggg
240ccccccccc cccacacaag agagtgtctc tctctgtgtg tctccactc tctctctctc
300tctccccccc cccccctctc tctctttttg ttttgtgaga gtgtgtgtct cctcccca
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420acacgct
427

427

<210> 2978<211> 339<212> DNA<213> Homo sapien

cgtttttttg ttgcgagaag acgacagaag ggtacggctc cataaacacg acagaagggt
60aataacaagc tgtatatatt tcaaagggtt tttaaacttt ggacactctt tcttttgta
120accacttaaa ggaataaaaag agctggaaaa aaaattggac cttcaactca ggtgttcca
180tatacaaac gtattctttg ctgttacgta agattttcga ttcacagagt ccatccatgt
240acatcactta cacttaaatt gccaaaataa ttagtctgac catctgactt taaaagactg
300ttgctacaca tacatcatgt ttaggagaat gtgggatat
339

339

<210> 2979<211> 394<212> DNA<213> Homo sapien

cgttgctgtc ggtagcattt gatcagcttt gccacagatg aaaagcagaa ctggacatgg
60aagagaagtg aagtaaggac aagctggaat ctataggcat ctctgcatct atctttcact
120gcatctagcc atgacaaact tcatagtata atgactacag ctttatctcc aactttttt
180tttttttaag aagaaacttc cggacgaga tcccagaggg gtatttttagc atcctagaga
240cctcctccta gagggccaag gaagatacct gcctcaagtt ctgggagaag aggaaatata
300gggcatgggc cactatacac gggaagtgtt tttttttaa acaaaaaag gctttgacca
360cttagaaaag gctgagtttc gacacatccg ctgc
394

394

<210> 2980<211> 399<212> DNA<213> Homo sapien

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60ccataatgga aaatatctat ctatctgttc tcaaatcctg tttttctcat agtgtaact

120cacatttgat gtgtttttat gaaggaaagt aaccaagaaa cctctaggaa ttagtgaaaa
180aagaactttt ttgaggtgtg ttactatact gctgtaagtt atttattata taaagtattg
240taaatagaat agtgttgaag atatgaaata tggctatttt taatggtgac aattatgact
300tttagtcact attaaattgg gggtacctat atcagtacaa tttgtagttg tttccaggtt
360tggctaataa tcattcctta acctagaatt cagatgatg
399

<210> 2981<211> 399<212> DNA<213> Homo sapien

tatagtggaa acagtatttc tagatgtag atttagcaga caaagacttc aaagcagcta
60ttgtaaatca gtttaaagca gcaaagtaag ctaagaatga aaataaagtg tgacaaatag
120agatgttcaa aaaggagata gaaatgattt taaaaataac aaaatgaaaa ttctgagatt
180gaagaatata gtaactgatg tgaaaaattt actagagggg cttaccagag gtttgacatg
240acagaagaaa gaagcagtga atttcaaagg tagatgatct aatctgaaga tcagagagga
300aagattaaag agaaatcagt agagccacag agatctgtgg gtcagcatca agttaccta
360tgtatgtgtg atgggaatct cagaatgaat agagaaagc
399

<210> 2982<211> 397<212> DNA<213> Homo sapien

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60aaaaatgtaa aaaaaaaaaa aaaaaaaaaa aaccctcgcc ccttaaaaaat .tttggggggg
120ggtttaccgg aaacccaaac ttgaaaaaaa ccttgggtggg gtgggaacaa cccccaataa
180aagggcgagg aaaaaagggt ttttttgtaa aaattgggaa ggctttgggt tttttgaaac
240cctttatagg cggaaaaaaa aaggtaaaca ccacaagggg cttttttttt tttttcaggg
300ttagggggggg ggggggggga gttttccna acaccaatat acagggtata cctctaacta
360cagcttgcac aatggcttaa aattgccatg gggaaag
397

<210> 2983<211> 372<212> DNA<213> Homo sapien

tactgttggt agaagacgac agaagggtct acaagcacat gctgcctgag ggcttggaga
60ctggcctgtt catccattg cagcaaccca atatgaaagc aaactgctca ggaaccagag
120ggttgtcccg ccattgtcac tgtcattgcc catgccacac tagctgccc gaggcctaag
180aacctgccc cttgctggaa ccaaggcttc aacacctggg taagtcacct ggaggcccaa
240gtattggccc acctagacgt gccaacatca gtggtaggtt tgggtgtgctt gttcctyggc
300cccaaatact gaactatttg gtatccaaat ccccataaaa actccagcac aacctccact
360aataactaca cc
372

<210> 2984<211> 410<212> DNA<213> Homo sapien

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120gcctgcggcc cactggcttg cctcactgta gttggtggtg gcagtgcag agactgcagc
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300cagggctgca ctgcccacag cagggagggt ggggttatggg tgctttctgg ggctgcaatg
360cccatggagg aggacagggt agggcatatc ggggtatatgc tactggcgga
410

<210> 2985<211> 407<212> DNA<213> Homo sapien

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60ctgcagtcag tgcctgccc ctgagctgta cctctccta tgataatcac tcttaagaag
120ggcaaccctt ggtgttttcc ccttaaggct acccaggctg gaatgcagt gtgtggtcat
180ggctccctgt accctggaac tcaggcttgg gtgacctct ctcctttgcc tccgaagtag
240ccaggactac aggtgtgcac ccaccaccac actcagataa ttgctttggt gtttttaaag
300cttgtaatga tcagttaggt gaggtgggca aatcataagg tcaagagttt ttagatggg
360gtgagcacag accaattcct gttttattta ctgatttaaa attttga
407

<210> 2986<211> 453<212> DNA<213> Homo sapien

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60tctattgggtg tgtgtttgtt tatttagaga tgggtgtcact ctgcgttgcc cagtctggcc
120ttgaactcct ggagtatcct tttgcctcag cctcccgagt agctgggact gcagggtgat
180accacctccc caacttggat ttactagtag tagcaagtgt agacaagagt ctctatttg

240gaatgtaaat tgttggttg aatgtacgtt ggcacaactt ggggaaagt tggcaatgta
300tatcaaaagc attaaaattg tgtatatctt gtggcctggc aatactcctt ttatgaattt
360attataaaaa aaagtacatt ttttataaaa cttagctggc tgggtgtggt ggctcattcc
420tgaatccca gcactttggg aggctgaggt ggg

453

<210> 2987<211> 407<212> DNA<213> Homo sapien

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60attggggaat tgatttcaca gtctgttacc ttagtaggga acggttaaggt tattcttttt
120tttttttttt ttgggattaa aaacctgggg gcctaaattt aaccaaaaag gggccaaaag
180gtggaatgaa actaactttt gggcaaaatt aaaccatccc ccaaagggc gaaaataatc
240caccgcccc cccggttttt tgggtgggta aatttggttt agattaaaaa caggcttttg
300ccccccagcc gggagggcag gggggtaatt agaactttt cccccggga tgaaagcaat
360atcctgcctt ccccccca gaaatctaaa ataacgggcc cccctt

407

<210> 2988<211> 339<212> DNA<213> Homo sapien

tacggctgag agaagacgac agaaggggta agctattaag tgcattgttc cctcaggccc
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120aaagcaccct cttttttttt tttttttttt ttttaaaaag ggaattttgt ttttgtgccc
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240aatttttccg gccttgcccc ccaagggggg gggaataaag gggccttgcc ccctcccccg
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339

<210> 2989<211> 399<212> DNA<213> Homo sapien

ggcagcaggg aagatgagct cgccaagaag cgggcggcct tcctcctgaa gcagcagcgc
60aaggccgagg aggcccgct gcgcaagcag cagctggaag cgaggtgga gctcaagcgt
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240gggctcggca agcccaagtc aaagccgaag aagccgcggc gaagtcggt gcaccgggaa
300gagtcgtgca gcgactccgg caccaagtgc tcctccacc ctgataactt gagccggact
360cagtcaggct ccagcctgtc cttggcctct gcggcgaca

399

<210> 2990<211> 326<212> DNA<213> Homo sapien

tctacggctg cgagaagacg acagaaggga tggtaaaatg ataataacg aatactataa
60tcaaccctat gtccacaatt tgataactgc aatgaacca tcctttgaaa gacacaattt
120gtcaaaactc acataagaaa tagaccatct gagggggcct aaacctttta aagaattgaa
180ttaataatgt taaccttcca aaacagaaag cagggaccca gatgggttca ctagtgaatt
240ctactaaaca tttaaaggaa aaactaataa atgagatatt ccatgtttat ggatcagaag
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326

<210> 2991<211> 380<212> DNA<213> Homo sapien

tacggctgag agaagacgac agaagggcgc ggcctcagcc tccagtggcg cgatctcagc
60tactgcaag ctctgcctcc cagttcacgc cattctctg cctcagcctc ccgaggagct
120gggactatag gcgcccgcga tcacacctgg cttttttttt ttttttttg ggaaaaaacg
180gggttcccc atgtaacca ggagggccta aatctccgga cctaaggacc cccccctg
240ggccttttaa agggctagaa taacggggg gacccccgc ccagggcctg ggaagcacac
300agtttttacc ttgttacc ccttgggga aaagggtttc ggcacggggg ttcttttaa
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380

<210> 2992<211> 378<212> DNA<213> Homo sapien

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120ccactgaaaa taaatcactc caacaatgca atagtaaac cccctgagat gacacctcag
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240tcagcagcta ttgaaccaga gtctggaaa agcaatgaaa gaaaaggcgg ncgatctcgt
300tcccatactc gtcataaac caggtctagc tcaaaatccc attctagaag gaaaagatca
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378

<210> 2993<211> 450<212> DNA<213> Homo sapien

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120aggggtcccgt tgcaaaagcc ccctcacagg ctttggttca gaatataggt cagccaaccc
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450

<210> 2994<211> 405<212> DNA<213> Homo sapien

nncaccanna aacttcagcc aaccgggtca ttgtggacac cattgttatg gccaatctgg
60gtacttttca gctgaaagcc aaccaggag cttggatcct cagacttagg aaggagcgt
120ctgaagatat ttatagaatt tacagccacg atggcaccga ttctccccct gatgtgatg
180aggtgggttat cgtcctcaac aacttcaaaa gcaaaattat taaagtgaag gttcagaaga
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300tttgggattc cttcaaattg ggctttacag gacagaacac tgagggaagtg aagcaagata
360aagatgacat aattaatatt ttctccgttg catctggtca tctct

405

<210> 2995<211> 400<212> DNA<213> Homo sapien

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60gcgactgccc acgagaccca aaaaagggtg tccgaaatc tcaccgtgag gcgcgggtca
120tcagactgaa acttgctcac agacttcacg ttatttat ttgggtctgaa ggatatcaac
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240agagttttat atatttatag tcacagacgg cagaggaaga ggctctcagt cccacctgt
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400

<210> 2996<211> 336<212> DNA<213> Homo sapien

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60ttattaggaa atgcatgtat acggaaaaag aagaaggaat ctttaccaat ggactacagg
120aagtgaaagc aaacggtttc cctacctgaa agtttccttg tgtgagactg gaatatatag
180ttttacctct gtacaccatt tttgctctag cctatatgga ctacctacac tcataatgag
240aataatgac aaatgaagga gttcgggttt gttttgttct tttctttctt ttttttttct
300tgagacaat ctactccgt caccagggt ggggtg

336

<210> 2997<211> 375<212> DNA<213> Homo sapien

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60agcctagggt tgtagtaggc tgtaccatct aggtttgtgt taaattcact ctttgatgtt
120tgctcagggg cgaaattgcc taaaaactca tttcttagaa tgtatccctg tcgttaaggg
180actcgtgacc gtattactat cttacagatg aagaaagtga agttctgaaa ggtaagtgt
240cttggccaaa gacacacagc cagtataatg ggagcaaaac acaactgcct gaagaaaaac
300tttgggtgat taaagtaaag taaaaacaga tctgaaaaga tctaccaatt caaatccttc
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375

<210> 2998<211> 373<212> DNA<213> Homo sapien

catgcgacgc catggaacat taagaggaaa aagttttgaa aaaattaaag ccattttacaa
60cctgggtttc aacgctagcc ctttctggat tgccatacgc cctgccaaga tactgcaggc
120ccattcaggc ctgtgctatc tgcatacagc gagggctttc caggaaactg actgtctttc
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240ataagggcgg ggtgtggtgg ctcatgcctg gaatcccagc actttgggag gccgaggcgg
300gcgcatcacc tgaggccagg agttggagac cagccaggcc accatgggga aacctgtct
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373

<210> 2999<211> 399<212> DNA<213> Homo sapien

gggaagaaga aggaggagt gtaaaggctc caccaaccca accagttctg cctcctcaaa
60ctataatcca gcagcctcag ccattaattc aaccaccacc attggtgcaa agccaactgc
120ctcaacagca gcctcaacca ccacaaccac agcagcaaca aggacctcag ccacaggccc
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240acagggggagc aggtttcaac cagaacaatg gagcgggcag tgaaaacttt ggtttaggtg
300ttgtacctgt cagtgttca ctttctagt tagaagtga tcccgtgctg gaaaagctaa
360aggccataaa caactataat cccaaagact ttgattgga

399

<210> 3000<211> 428<212> DNA<213> Homo sapien

ctttactagt ttgaaaaaa gtagaacaaa ataaccaaag tgacttttgt acttttttat
60tgggtgtgtgt ttgtttatatt agagatggtg tcaactctgcg ttgccagtc tggccttgaa
120ctcctggagt atccttttgc ctcagcctcc cgagtagctg ggactgcagg tgtataccac
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240taaattgttg gttggaatgt acgttggcac aacttgggga aagtttggca atgtatatca
300aaagcattaa aattgtgtat atcttgtggc ctggcaatac tctttttatg aatttattat
360aaaaaaaaagt acatttattt aaaaacttag ctggctgggt gtggtggctc attcctgtaa
420tcccagcn

428

<210> 3001<211> 390<212> DNA<213> Homo sapien

ggcacgaggc tactcttacg cactcacgtt cattaactgc gttctgatgg cagaaggtag
60acagcaactg gacaaagggt aatttacgga gaagtacgtg gtcccgaga caaggctggc
120attcaagttc atcacactct accggcgat acgggagcat ggcttctacg tcaactgactg
180tccccagcag caggcacaac cccctgaggg cggcggtttg tgctgagagc tatgtaagcg
240cagcctgtac gctggagggt agggaggatg ctacctttaa tcaactat ggatctctaa
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390

<210> 3002<211> 405<212> DNA<213> Homo sapien

gtccgttget gtgggaagt ccttacctt gtaggtatct cctcaatgaa tactgtgtgt
60aaggctgaaa tagttcatta tgtaataac cttctttatg ttctcagga aatgcttagg
120tgggtgtcaca aaatgtgcct tttcttttct tttctttttt ttttttggg gcaaagtctc
180ctttttttcc ccaggttgaa ggccagggg ccaacttggg ttaattgaag cctccccctc
240cggggttaac ctttttttct ggcttagacc ttcaaggaat tgggaattaa agcttcccc
300cccccccccg ggatattttt ttggattttt aataaaacac gggttcattt ttgttatcca
360gggggggttca tatctccggc cccaataatc cccccgctt tgcct

405

<210> 3003<211> 433<212> DNA<213> Homo sapien

nnccggcacg agagttggac cagaactccc tcttgacac atcccaattc aagtgatecg
60caaagaggtg gattctaaac ctgtttccca gaagccccc cctccctctg agaaggtaga
120ggtgaaagt cccctgtctc cagttccttg tctcctccc agccctggc cttctgctgt
180ccccctctcc cccaagagtg tggctacaga agagaggga gccccagca ctgcccctgc
240agaagctaca cctccaaaac caggagaagc caaggctccc caaaacatc caggagtgt
300gaaagtggaa gccatcctgg agaagtgca ggggctggag caggctgtag acaactttga
360aggcaagaag actgacaaaa agtacctgat gatcgaagag tatttgacca aagagctgct
420ggccctggat tcn

433

<210> 3004<211> 335<212> DNA<213> Homo sapien

tacggctgcg agaagacgac agaagggtac agacagagag gtgagttggg tttagaagag
60gttggttaagg tgggtcaca caaaaaggc ccagtggacc ctacactatg gaatgaattg
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335

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405
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408
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422
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403
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387

<210> 3012<211> 380<212> DNA<213> Homo sapien

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380

<210> 3013<211> 391<212> DNA<213> Homo sapien

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391

<210> 3014<211> 385<212> DNA<213> Homo sapien

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385

<210> 3015<211> 372<212> DNA<213> Homo sapien

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372

<210> 3016<211> 381<212> DNA<213> Homo sapien

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381

<210> 3017<211> 442<212> DNA<213> Homo sapien

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442

<210> 3018<211> 427<212> DNA<213> Homo sapien

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427

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418

<210> 3020<211> 375<212> DNA<213> Homo sapien

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375

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384

<210> 3022<211> 401<212> DNA<213> Homo sapien

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300ggcttggttag tccttcttca aagggggatc cagatggcat gtcacagtgt ctacctgaaa
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401

<210> 3023<211> 406<212> DNA<213> Homo sapien

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406

<210> 3024<211> 399<212> DNA<213> Homo sapien

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120caccctctct cctcaacaca agcccaaact gctaccgcg aggtgcaagt aagcggcacc
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399

<210> 3025<211> 399<212> DNA<213> Homo sapien

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399

<210> 3026<211> 407<212> DNA<213> Homo sapien

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407

<210> 3027<211> 353<212> DNA<213> Homo sapien

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353

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180ctactcctaa cctggtcatt ttaacctcct gtgccctcag tttcttcac tgtataatgg
240acataggcct ggtgtggttg caagaagcag ctaaaaatca ggaaaaagaa catcatgtat
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340

<210> 3029<211> 417<212> DNA<213> Homo sapien

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417

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407

<210> 3031<211> 423<212> DNA<213> Homo sapien

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120gtggtccaca tgtgccagga gatgtgggaa tggctacccc tgaagtcata tggagaaatg
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423

<210> 3032<211> 410<212> DNA<213> Homo sapien

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120gaacttttct ggatttcagt tctttcatcc ggggcctgcc ggtgccgtaa acggccattg
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300cgctggtgc ggccgcggcc gggagggact ggattatgtc ggccccgttt gaagagcgga
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410

<210> 3033<211> 416<212> DNA<213> Homo sapien

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416

<210> 3034<211> 431<212> DNA<213> Homo sapien

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431

<210> 3035<211> 335<212> DNA<213> Homo sapien

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335

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300atgcttgcca acaactgcat tgttgctggt ggctgttctt agtcttccac tctgccttct
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408

<210> 3037<211> 353<212> DNA<213> Homo sapien

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240ctcaaaatca tgggtggaagg ctaaaggata tcttacatgg tagcagacaa gagagaatca
300ggaccaagca aaaagagttt ccccttgtaa agctatcaga tcttgtaga ctt
353

<210> 3038<211> 352<212> DNA<213> Homo sapien

tactgctgcg agaagacgac agaaggggtac ggctgcgaga agacgacaga aggggtgtaga
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120gaataacact tcgacctgcc taaaaatctt caacagttta ttccagctat tacctccttt
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240ctttcaatat tatctgtgca cctctggctc tagccactac caatttaaaa gctttttgta
300tgttatctat ttctcagtct gcttaaaaca aagaatacat aatgaacgg cg
352

<210> 3039<211> 346<212> DNA<213> Homo sapien

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120ggagaggggtg ccttgcttga atgggggcac cgcaggggtt ttctgacct gtgcttcac
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240tttgcttccc cacactgact atattagagt cctcatttgc agagcagcac tgcaagctaa
300gtattttgtag cacagattaa agagactgag gagggctctg gggagg
346

<210> 3040<211> 335<212> DNA<213> Homo sapien

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120tgaaaagtat gtatgactgt gatagaagat gtgaaaatac acattgattt tagagtacag
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335

<210> 3041<211> 375<212> DNA<213> Homo sapien

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60tccaatttca tctgctgttg caggcgtagc aataggattg gtcacaaaaa ccgacctga
120gaaggggtgaa atagaagatt atcgtttgct gacagatatt ttgggaattg aagattacaa
180tggtgacatg gacttcaaaa tagctggcac taataaagga ataactgcat tacaggctga
240tattaaatta cctggaatac caataaaaat tgtgatggag gctattcaac aagcttcagt
300ggcaaaaaag gagatattac agatcatgaa caaaactatt tcaaaacctc gagcatctag
360aaaagaaaat ggacg
375

<210> 3042<211> 389<212> DNA<213> Homo sapien

ctgcctcag cgtttctggt tcaataggtt ttgggggaga ccaagaacgt taacatttct
60agcaagtttc caggtgatgc tgttggtgct ggtctagaga ctattttgag aaccactgtc
120caggagcgtg gtttctgat tgtgatctga ggttctgccc caactgcaca gcagttgggc
180tgcttggttaa aaatgcaggt gcagatcttg gtggtagtag caaatattca aacgagaact
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300aaaaccgctc tttatgtgcc tggaaatccc cctgctcagg tggctagggg ggatggatgc
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389

<210> 3043<211> 387<212> DNA<213> Homo sapien

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60gcattcccaa ggacagatga attgaaaaac gaccttttaa agaaatataa cgtagaatac
120caagaatatt tgcaaagcaa aaacaaatat aaagctgaaa ttctcaaaaa attggagcat
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240tcggagcagt ttctgttttt cgaagatcaa ctcaagaagc aagagttagc ccgaggtcaa
300atgcgaagtc agcaaacctc agggctgtca gagcagattg atgggagcgc ttgtctctgc
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387

<210> 3044<211> 373<212> DNA<213> Homo sapien

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120taaatcatat atcagtgaag aaatgtgatg ttgcaacat cttctctggg gatgctaacc
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240gtgagaaatt ccaccataat ctacacacca taatatcatc aatgtgtcta gaagtcagat
300cctctatgtg tgaaccaaga caatgcctgg caaacaagac agctgggctc tcaggtctct
360gcaccatggg gag

373

<210> 3045<211> 379<212> DNA<213> Homo sapien

tacggctgcg agaagacgac agaagggtac ggctgcgaga agacgacaga agggctcaca
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120ggccggccttg ggaacagtg aaatcctgtt tctacacaaa ataaaaaaaa ttagtttgct
180gtgggtggtat gcatctgtag tcccagctac ttgggaggct gaggtgagag aatcacttga
240accagaagt tcaagactgc agtgaactat gatcgaacca ctgaacttca gcctgggcga
300cagtgaagac ccttctcaaa aaaaaaaaaa aaaaaaaaaa aaaaaggggg cccttttttc
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379

<210> 3046<211> 410<212> DNA<213> Homo sapien

ctgcgctagt cctaaagagg aaatgtctct actctgcgtg gatgcagccc gcaccctggg
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120taaaaaaaaaag gaactcctac agaatggacc agaccttcaa gattttgtat ctggtgatct
180tgacagacagg agcacctggg atgaatataa aggaacctta aaacgccaga aaggagaaa
240gttaagacta cctccatggc taaagacaga gattcccatg gggaaaaatt acaataaact
300gaaaaatact ttgcggaatt taaatctcca tacagtatgt gaggaagctc gatgtcccaa
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410

<210> 3047<211> 396<212> DNA<213> Homo sapien

caaccgagat gaagggtgaag atgctgagcc ggaatccgga caattatgtc cgcgaaacca
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120cacgagaata tataagagct ttaaagtcta ccaaactgga acgagtattt gcaaaacat
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240agctggctac tgccttttct ggggcgtgtg atggagaggt tagaatttgg aatctaactc
300agcgggaattg tatccgtaca atacaagcac atgaaggctt tgtacgagga atatgtactc
360gcttttgtgg gacttctttt ttcactgggtg gtgatg

396

<210> 3048<211> 358<212> DNA<213> Homo sapien

gcctacggct gtgagaagac gacagaaggg tacggctgcg agaagacgac agaagggtt
60ctcaattttc cctttgacgc aaaanttact cactcagttt ctaaagaaat attttttaa
120aagggttca gtatacgta gttctctcat ctgacctgg ttgctcta atcggtgacatg
180aaatgcaggc tttttaccat cgtaagcagc actaatatga acttggaat atttttaaca
240cgcgaaaggc taacaagatg actcagcaat accaaagaca ggcctgaatg tccgttacta
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358

<210> 3049<211> 413<212> DNA<213> Homo sapien

cgcacgagga agaaaaatgt ttgtaatcta ttcatttgat aaaagaccaa tattcaggat

60attcaagaaa cccaaacaat tcaacagtaa acaaataagc ccatgaaaaa gtaggcacac
120tttttctatt tacctccata aatagacaat tgtcaaagag agacttacaa atggccaaca
180cgaatatgaa aaaataactca atgttcccaa tcatcaggga aatgcaaatt ataaccacag
240tgaaatataa tctcatccca gtttgaatgg ctattataaa aaagacaaaa aataaccaat
300gctgatgagg aggtagagaa aaaggaactc ttgtgactg gttggtggaa atgtaaacca
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413

<210> 3050<211> 398<212> DNA<213> Homo sapien

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60taggctgtta aatccaacat ttaaaataaa aattaagcta tttcttttgg gtttcccaca
120ccacttttac ctgtactgat tttttttctt cttttttttt tttaaaaaaa caggggttttg
180ttttgtcact cccaacctgg agggcaggga cccaataata tttccttaca gcctcaaatt
240cctgacctca agggatctcc ttcccaaagg gttgcaattg cagggggaac cactgcccc
300tggttggtga aaaatttttg cctacaggga gggaaactac taaagtctct ggggaaccaa
360agtaaaattt cttaaaaaca aaagggaggg agaggaga

398

<210> 3051<211> 340<212> DNA<213> Homo sapien

tacggctgcg agaagacgac agaagggggc cctcagtggg catgttccgg tctcccaggt
60gacaccaacg ggtcccacag agaccagcct catctccgtc ctggctgatg ccacggccac
120gtactacaac agctacagtg tgtcatagag ctggaggcgc cccgtccggt cagccctcgc
180gccctctcct tctgtgcct tgagtggcag aggagccgtc cagccacacc agctttcctc
240ccaccgtca gggcaggagg gtctgaactg cggccccaga gcctttggcc taagtggag
300tctcttacc cgagtgcgc ctctatcccc ttccccacgt

340

<210> 3052<211> 383<212> DNA<213> Homo sapien

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60cttttttatt atattcatct gtaatgtgaa gtgtttatct cattgtgggt ttgatttaca
120tttccctgat ggttgatgat tttcaacatc tttcatata cttattagt attatgtatc
180ttctttggag aatgtctgtt cagatcctt acctacttta taattgggtt atctttttaa
240tattgaactg taatagtttt taaaaaatat atcctaaata caagtctctt atcagataat
300atgatttga gatattttct gtcattctat gtactgtctt ttcacattct tgatgataga
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383

<210> 3053<211> 415<212> DNA<213> Homo sapien

ctcaggctga tctaaactcc tggcctgaag caattctcct gtctcatctt ccgaaagtgg
60tgggattaca agtgtgagcc actgcgctag cctatgcttt acttattcca aaaaaataac
120atgaatggaa agaggaaaaa taacctgaa agcaagtga gatacattaa tccagctgta
180tttttaaatga gtaacataac cacaccgacg gggattggtg aaggaggat ggaaaatcta
240atccaagtga tttatcgaca catcaaagt gttgactgt atactgtcag ttgtggtggg
300ggatgggact gcaagaaaaa tcttgaggcc aggcgctggt ggctcatgcc tgtaatctta
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415

<210> 3054<211> 421<212> DNA<213> Homo sapien

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120ggggaaaagga ctctgtcccc ttggggctca tcaccttcc acatctctct cctcgttgcc
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240cttgaaagcc aggggcccga tctgggttaa tggaaaactt tgctccgga ataaaagcaa
300tactccggcc tcaccttta aagtaccggg aataacgggg cccctcccc cccccgggt
360tattttttgt ttttaaggga aaacggggtt tacccttgc gcccgaatgg gtttaaaact

420g

421

<210> 3055<211> 162<212> DNA<213> Homo sapien

acctatnatg gaattcta atgtcattat tttaattggaatc aatcgaaata tgctctatag
60agaatatatc ttttatatat tgctgcagtt tcttatgtt aatcttttaa cactaaagga
120acatgacata atcataccat agaagggaac acaggttacc at

162

<210> 3056<211> 381<212> DNA<213> Homo sapien

cgttgctgtc gggctgtgag gcgctgggga atctcaaaaa acttcagccg gggacaatca
60aaaaatctgaa gcaggacaat tggggagaga gagatcactc ttcttgaaga gatcatcatg
120cagttgtaga tccttttgtt ctagaaaggc cacaagaagc tgagaggaag tctgattcct
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240tgacaagata gggggtgggt cagtgtgggg caggggttga gagtgcgggc cctgggtcag
300cctgcttatg tatcagtcct gcctctgccca cttactatgc aacctggagc aagtgaacac
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381

<210> 3057<211> 400<212> DNA<213> Homo sapien

nnnaccgagat gaagtgtttg atgtgtacaa agccccactg cagggcgacc acaatcatct
60ttttataaga caaggtactg gtctacaggg acaagcagtc tttaaaacga aactcacctt
120cagacctcac tctacggaca gtgccacaca tagaaagatg actctgtcac ttgcagatag
180gtgttcaaag acacagaaga ttagaatctt gccaatggct ggtcgtgac ctgaatgccca
240acgcacagaa atgattaaga aagaagaaga acgtttgagg gcttccatac gtagggaatc
300tcagcagcgc cgaatgagag agaaacagca ccagcggggg ctgagcgcca gttacctgga
360acctgatcga tacgatgagg aggaggaagg cgaggagtcn

400

<210> 3058<211> 335<212> DNA<213> Homo sapien

tacggctgcg agaagacgac agaagggcta ctatgttcct gataacctga tactgtccg
60ttaatcctcg tgggttgata ctgaaagat atattaatcc tcatggagca ggtacagatt
120accaggaaca taggagtgga ttctgttcca aaccaaattg cattcctttg gatttttaaa
180tttaacttaa ttggctattc taaagagtcc cctcaccaca atgtttgatc attggagccc
240ttaagatgca caatgaaatt gtgttttgca ttttttggtta acaggactaa aggaaggacc
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335

<210> 3059<211> 387<212> DNA<213> Homo sapien

ggcacgagca ttgctttgct tgtgcatttt gtccaattct tggttcaaaa tgccaaaaac
60ctggacaact ttagtcaag gccctccact ggcaacatgt atatgtgttt ttgagggtgt
120aggtagctga gattgaagat gagtggattt atgaattgaa taacaataaa taccctactt
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240atctgttgga cagattggag ctggcagggt agggcctgta ttgttgaagt tgccatggct
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387

<210> 3060<211> 395<212> DNA<213> Homo sapien

ggcacgaggg tgtggagagg gcagtggccc tcatttatca ctctgacctt cacagggaca
60gatctgattt atttattttg gttaaaaaaa aaaaggggaac aaaaccaact ttgcattgca
120tgggctggac ccataaacta agttatatcc gggaaaaaaa aaaaaaaaaa aaacccctt
180aaaaataatg gggggggttt tcccgaacc ccaacctgaa aaaaaccctt ggggggttg
240ggccaccccc ccctaaaagg ccgggaaaaa aaggcttttt ttggaaaatt gggggggtt
300tggttttttt tggaccctt taaacccgga aaaaacaagt taacccccac aatgggtttt
360ttttttttt ccagggcccg gggggggggg ggggg

395

<210> 3061<211> 399<212> DNA<213> Homo sapien

ctggtgtag ggtactttgt ttttgagggt tggcagagat gtgtttaaga gctgaggctc
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300catatggcat gtccaacatt caggggtgtc atagcccgat tggaaatggg tctgatgaa
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399

<210> 3062<211> 399<212> DNA<213> Homo sapien

tgacccttgg actctcagac accttgaggt tcagcagagg aaaaaggtac cacaaaagaa

60tttgaacaga gggcctgatg aaacagtgag gtttcacata acccaagcaa agaacatttt
120tcaagagaaa aagaaaggac agttccatct attgatgttt gagaaatcaa atgagattag
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360gatagagaag ctttaagaaat gtgtgtgctg ttgggggtgn
399

<210> 3063<211> 385<212> DNA<213> Homo sapien

cgatgctgtc ggcagaacac tgatgagctt cccagcacag ggacaggaaa ggtggcttgc
60gggtctggaa gaagggtcag gtggcattta cacagtggga gagggctgat cggagacagg
120cattccatgc agggcatttg gaagcaaaat gtggaggtca ggccatgctg ggctattcag
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240gaagccaagc tgatggcatc tctctggcac ttggcagcga tggccttcac tacttacgtg
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385

<210> 3064<211> 334<212> DNA<213> Homo sapien

tacggctgcg agaagaccac agaaggggtac ggctgcgaga agaccacaga aggggtacggc
60tgctagaaga ccacagaagg ggaaaaataaa aaaaataaaac attttttttg gcccctttttt
120tgcaagttc caactttatc aaaatctttt tataatttgg gccaaccccc aattaaagt
180ttgggaaaaa actttttttt tgggaaattt tggaaccttt tgcttttttt ggaccccttt
240aaacttggca taaaccagtt aacccccccc atttcctttt tttttttttt taagtacacg
300ggggggggggg gggaggggtta gcttctgttg aaac
334

<210> 3065<211> 422<212> DNA<213> Homo sapien

cgttgctgtc gccaggcccc actcacacca ctacaggctc tacctatagt gccattacca
60ctaccacag tgctccaagc cccctcactc acactactac aggtccacc cacaagccca
120taatctctac ccttactact acaggcccta cctcaatat cataggccca gtccagacta
180ccacaagccc caccacact atgccaaagg ctaccatac cacagcaatc cccgcgatac
240ttcaacgct tctgacttcc aggtgatgac tgggccccca ataaatcccg tctttgggtc
300nnnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn
360nnnnnnnnnnn aaaaaccccc cgcggcgcct tttgttagaa aaaaacaaaa aaaaaaaaaa
420aa

422

<210> 3066<211> 421<212> DNA<213> Homo sapien

ggcacgaggg gctggggcgc ccccaacttg catctcagag accccggaat gcaaggcctc
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120gccctgcccc cagcgcttgg gcgggaagctg ctgtcacacc cagcaggtgc gggccgagca
180ggaccaaca gagggctcag gagggcaagg cccaaccggg agccacgtgg aacccagagg
240aagccgcccc acccagcttg gccacagcca tcttccctcc tgccggacag ggtgggcccg
300ccaccgagca gaccagtgc cccgccttgg tcccgggtca gcagccccag ggtccocttg
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420n

421

<210> 3067<211> 398<212> DNA<213> Homo sapien

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300gtgacttgcc aggacttatc ctacatctg aacattgtaa tgaagggtga cagctttctc
360tgtcatctct gttccaggat agcaaaactg tgtatatt
398

<210> 3068<211> 421<212> DNA<213> Homo sapien

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120gtgactgagg agatgctatg ggagtgaag cagcttgggg ctcactcccc ctccaccttg
180ctgaccaccc tcatgttctt taataccaag tacttcttat tgaagacagt ggaccagcac
240atgaagctgg ctttctccaa ggtcttgca cagacaaaga agaaccctc taatcccaag
300gataaaagca cgagtatccg gtacttgaag gcccttggaa tacaccacac tggccagaaa
360gttacagatg acatgtatgc agaacagacg gaaaatccag agaatccatt gagatgtccc
420t

421

<210> 3069<211> 386<212> DNA<213> Homo sapien

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120ggagatggaa taggaaaaat acttgaagac ataatggcca aagattttct gaataata
180aaaactaagt ccacagatcc aagatgtca acaaacctg agtatgagaa atatgaagaa
240aaatatgcca aggtcatca taacttctg gaaaccagt ttaaaaagaa aatcttaaat
300gcaaccaggg gagaggatag ttacttgca tggaacaaag acgaagtga cattacactt
360ctcattggaa acaatgccag taagca

386

<210> 3070<211> 415<212> DNA<213> Homo sapien

cgttgctgtc ggaggaacaa ataaacactt atgacatata gaaaacaaaa agttagaatg
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415

<210> 3071<211> 411<212> DNA<213> Homo sapien

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120gatgatggat ggcccagtgc ctggaggaca gtagcacttt gtccttaata gggattttag
180caataaagcc agcatgaaat ttatttttca tgccttaga tttgaaaatt tatgacttag
240aatgtgtgta cttcttaggt taacctgccc ttcgtcacct catgaaaagt aagacagact
300taggtggctg actttggagg gttttttttg ttatatttgc tttcattata gatcagcaac
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411

<210> 3072<211> 406<212> DNA<213> Homo sapien

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60agctacagct aggactcgtt tgggtggggg tttttagttt gtctttctaa agtcatgtgg
120accttaattt aattacaaaa gtctaccctg gtggtcatga aataggcagg cctatgaaga
180aaggcctttt actcttccag catgcaagct cagaaccaac acattactct ctgtgcctaa
240tgttctcaa tgtggttgat tttttttttt aatttataga gcatttcggg ggaggtgtgg
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406

<210> 3073<211> 409<212> DNA<213> Homo sapien

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300cctgttcggg ggctggagga tggcttccca gaggacctgg gacactcacc tagctcgttc
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409

<210> 3074<211> 406<212> DNA<213> Homo sapien

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180agaagcagcg ccaggacctg gccaacctac agaagcagca ggcccagtac ctcgaggaga
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300tcctggccca gcgcgaggag gaggtgcagc aggggcagca ggacctggaa aaggagcggg
360aggagctcca gcagaagaag ggcacatacc agtatgacct ggagcg

406

<210> 3075<211> 399<212> DNA<213> Homo sapien

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240cttcaatggc agttggcaac actcattttg ggaggaggag gctataacct tgccaacacg
300gctcgatgct ggacatactt gaccggggtc atcctaggga aaacactatc ctctgagatc
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399

<210> 3076<211> 425<212> DNA<213> Homo sapien

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120tcagcaaaac acactaaaga ttgggcagtc actggggaga acactcagcc cgctgcacc
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300ccctgttgc gccctcactc cgtgaggaga tccacctatg atctcaggtc ctccagacaa
360ccagcccaag gaacatcttg ccaatttcaa atcggatagg agtgtcaggc ctctgagtc
420aagct

425

<210> 3077<211> 404<212> DNA<213> Homo sapien

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240agatctgtgt tgggggtgat ggggagagaa aatgtgggct ccagttgagt ttaaggcagg
300agtgtccaat cttttgttt ccgtgggcca cattgggaga tttgtcttgg gccatacata
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404

<210> 3078<211> 376<212> DNA<213> Homo sapien

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60cgccggctac gccgctgtt atccgtgggt cccttctgc actactggta cttgtcgctg
120gaccgcctat tccctgcgtc tggcctccga ggcttcccaa atgtcctcaa gaaggtcctc
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240ctggaggggc agacagtggg tgagagctgc caggagctgc gggagaagtt ctgggaattc
300tacaaggcag actggtgcgt gtggcctgct gcgcagttcg tgaacttctt ctctgtgcc
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376

<210> 3079<211> 326<212> DNA<213> Homo sapien

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60tactccctta aactagaaga ggcgactgtt ccaccagatg cacagatata aacataaaga
120cccaagaaac acaaagaagc aaaaacaaaa cgaaacaaaa aacacacaaa caaatgaaac
180gaaacacaac acttccaaat gaacataata attctcctgt tacagaccct aaagaaaaga
240aaatctatga aatactacga agaacttgaa aataatgac ttaaggagac tcagtaagat
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326

<210> 3080<211> 393<212> DNA<213> Homo sapien

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120caaagcacag ggcaacagcg atctctaagt gaagcgagcg cgttaccgtc tcatgcggga
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360taatgagaac tttctgctgg cagcgctat ggg

393

<210> 3081<211> 390<212> DNA<213> Homo sapien

ggcacgagcc acaagaagca aaccagatgc ctctccatt tcccaagaag agcctcaagg
60agaagccaca cctgtgggca acagagaatc cccgggacaa gctgggatga attcaattca
120ttccccaggc cctgagagcc cagtcagtca cccggatggc caagaagcca aggcactgcc
180gccctttgca tgtgacgtgt gcgagaagag gtttacgtgt aattccaagc tagtcatcca
240caagagatca cacacaggcg agagactctt tcaatgtaat ctctgtggga agcgcttcat
300gcagcttatt agcctccaat ttcaccagcg aaccacact ggcgagaggc cctacacgtg
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390

<210> 3082<211> 349<212> DNA<213> Homo sapien

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60aaggcaacga aagataagct ctatttagca acttcgtgat gctatctggt ttattgggaa
120ccattataaa ctgcaataaa ctggctagct acgacaattg catatcttgt atgttacaag
180attaagggga ggagcgtgga ggcttagctt anagtcacaa aaggagaact tgaaaaacaa
240atgcaagaaa aatctgacca gctatagatg catcatgcca aaataaagga actagaagat
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349

<210> 3083<211> 410<212> DNA<213> Homo sapien

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120tcctctgtcc acagtcccgt tgttccttca cagccttaca ggttatccca gcaaccagac
180tgagccctgg ggaagggttcg aataacctca ggcaggccag agcacaactc ctgccatcct
240tctcttagct tagggaagct tgcccctaga gcagcatctt catagtatgt tccccaaaac
300tagtcctatg cgatgctcat cagaaaaaaa tctgagcaa taactccttt ctctatcccc
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410

<210> 3084<211> 390<212> DNA<213> Homo sapien

ggcacgagac atcttctcct acttctacat ggtatacggc ggcagctcgg gcaagccctc
60cgagaagaac ctctacgccc acatcgacgc cgcgtggcag gcgctgcgca cccggtatgg
120cgtgagtcct gagaacatta tctctatagg tcagagcatt gggactgtcc ccacggtaga
180cttggcctcg aggtatgaat gcgcagcggg aattctccat tccccctga tgtctggttt
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390

<210> 3085<211> 424<212> DNA<213> Homo sapien

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120ttaggcgatg ggaggggggc gccgaccgc ctcagcgcg atgtgcatcg gaaacttttc
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240gccttcgcaa agtgtcagg gaagtgtagt gtgcaggga agtaggtcac tcctgctatc
300gcctggtccg gaggtgtttg aggactacaa tcccagagt gcagagcggg ccctcaccgc
360ccgctctctc gcctacgttt gggttgagtc gagttttcct ggctcctgag gaacatggag
420tgcn

424

<210> 3086<211> 395<212> DNA<213> Homo sapien

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60tgcgagaaga ccactgaagg ggacggctgc gagaagacga ctgaagggtg cggctgcgag
120aagacgactg aagggtagcg ctgcgacaag acgacttatg ggtatcggct gcgagagacg
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300tataggatgt ggagtttaac tttcttttcc cagcaaggta gtggccatct gagtcagctg
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395

<210> 3087<211> 423<212> DNA<213> Homo sapien

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120ggaaggtttt ttgaacttta aaaaattaaa aatatagctt attgaataac cgccataaaa
180aatataaatg cgaatatcat aaaactcata ctgctaaact aaattttttt tttttcttgt
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300agctacacct tccgaggtca ctccatcatc ctgcataaac cgtataagta gctggcacta
360caggtgacag ccaccatatac cagctaattt tttttgtgtt tttacaaaaa gagagagaaa
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423

<210> 3088<211> 409<212> DNA<213> Homo sapien

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120ggccgccaag gagtgccaac cttttgctcc ctctatctg ggagtgcagg atgggagagc
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240gcaggttggtc agtcgtcagc aagctggcaa tgagaaggct ccgaactgat gaatggaaac
300ctgctgagct ggagggcgct aggtgacct tgccgagcat ctctgacagc aatcggcaca
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409

<210> 3089<211> 417<212> DNA<213> Homo sapien

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120ggcaaaagacc cctctgaaac caaagagcaa gtatcacgc ctgacacata aacttcatga
180cctcgacatt gagacaaaat ctgcctgtgt gacctacaac accactcatt taactccacc
240aacttggggt caaataaagg tcttatccca tcaacagaaa aatcattaag agaaaaatga
300atccccaaaa cgacagtctg cagatccgc aaggaatccg aagacaagtc caaagtcaac
360gacaagcaat gatggcaatg gtgacctag ttaataaaaa gcggggagaa tgtgtgg
417

417

<210> 3090<211> 337<212> DNA<213> Homo sapien

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60tcccacctta gcctctccag tagctggaac tacaggcatg catcaccatg cccagctgat
120tttaattttg taaaggcagg accttctat ttccccagg ctgatctcta actttggcc
180tcaagcaatc ctctctctt ggctcccaa aatgttggga ttacagatgg gagccccat
240accaccaat cacaaggatc ttataagag aatgaggcag gagagtcaga attatagaac
300gtgatgcggt aatggaagaa catgtcaaag agggacg

337

<210> 3091<211> 375<212> DNA<213> Homo sapien

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120gatcccggtg acagttgctg tggaatttcc atgctgggca cacttgaggc ccaaagctcc
180gattcccaag aggcgccaca gcaaccatgc caggaaactg ggccaggctg agggtagcag
240gagagggaga caggaggagg cagggaaggc gcagggcctg tcagatggat ccctgacaac
300catccgtctc aagtcgagg taacctata tctttgctc agcagatagg atgactttgt
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375

<210> 3092<211> 428<212> DNA<213> Homo sapien

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120ctggacttga ctccctggga tccaggaag ggcacacct ttcctacca cccgagtga
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240agcgccatct cccgcccttg gtgtgcccc cgggcggtac ctgctctctc ccagcgccac
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428

<210> 3093<211> 384<212> DNA<213> Homo sapien
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120aaataactcaa atacctgagg ataatttgcg caggagtcaa agtgataaac tagtttaatg
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384

<210> 3094<211> 345<212> DNA<213> Homo sapien
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240attgggcctt tgaaaggact aatcagacac acacacacac acacacacac acacacacac
300actcgcatat tcatgcacat tttccttcat ttccagatcc tttag
345

<210> 3095<211> 425<212> DNA<213> Homo sapien
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120aaagtggctc aatagtcaaa gacaggttta ttttgaagaa taaacctgag aggggttctt
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425

<210> 3096<211> 402<212> DNA<213> Homo sapien
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120gcccctatcc tgcccaggg caggtccagg ccttgaccc cgcctagcgt aggctagtgt
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402

<210> 3097<211> 386<212> DNA<213> Homo sapien
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60tgccagaagt ggacttccct gtccccccag gcagaggcag gagtgtggag tctgtgcaga
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386

<210> 3098<211> 407<212> DNA<213> Homo sapien
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240cccccttccc aactaaattt tgttttttaa gaaaaaacgg ggttttctt ttggggcaag
300gggggtctta aactcttgac ctaaaggaat cggccacact gggcctccaa aagggcggga
360ataaagggcg gaacccttg ttccaaaagg aaattttttt ttaatag
407

<210> 3099<211> 426<212> DNA<213> Homo sapien
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360gatcaagagt ttgagactag cctaggggac acaggggagac cccatctcta cataaaatta
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426

<210> 3100<211> 375<212> DNA<213> Homo sapien

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120agaaacaaag atagttttct gaacattctg tgcctgcct gtctcctgtt gattcgaga
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375

<210> 3101<211> 388<212> DNA<213> Homo sapien

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120cccaagaaac acaaagaagc aaaaacaaaa cgaaacaaaa aacacacaaa caaatgaaac
180gaaacacac acttccaaat gaacataata attctcctgt tacagaccct aaagaaaaga
240aaatctatga aataactaaga agaacttgaa aataatgatc ttaaggaaac tcagtaagat
300ataagagaat acagaataac aattcaacaa aatcagaaaa acaatttcta aactgaaaga
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388

<210> 3102<211> 417<212> DNA<213> Homo sapien

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417

417

<210> 3103<211> 340<212> DNA<213> Homo sapien

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300tataattaag cgtactacac tttaatgctg gggttattcg
340

340

<210> 3104<211> 351<212> DNA<213> Homo sapien

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240tttactcatt ttgcctttta atcttttata cctttttggt gaaggtttcc ctttaggaaa
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351

351

<210> 3105<211> 342<212> DNA<213> Homo sapien

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342

<210> 3106<211> 395<212> DNA<213> Homo sapien

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120gtttcccggtt ttcaagggat tctccggcct cagcctccca agtagctggt tttataggag
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395

<210> 3107<211> 160<212> DNA<213> Homo sapien

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160

<210> 3108<211> 422<212> DNA<213> Homo sapien

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360tttgggatgt ggagacaggg aattgcattc acacgttaac agggcaccag tcgttaacaa
420gt

422

<210> 3109<211> 154<212> DNA<213> Homo sapien

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154

<210> 3110<211> 351<212> DNA<213> Homo sapien

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120tgccgcttcc gcatgaagggt ttcctggcct gttgcagcca tgggtgcattg cacctgcgtg
180ttgttcagaa agattcccaa atgctggaaa atcctctttg ctaagctgcg tgtcttatgc
240agaacctgct attgcccatt acgcatttac aacattacag cctgaacttg gaaagatcat
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351

<210> 3111<211> 391<212> DNA<213> Homo sapien

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120caagagaaaa agaaccgaca gttccattta ttgatgtttg agaaatcaga tgagattaag
180tgagagaaga aactattgag ggaactaat gatactaact tactaacaca aagaaggaaa
240caacacatac tgagggtctac ttgaagtgcg gggaggtggt gnaagtttat cacacacaa
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391

<210> 3112<211> 396<212> DNA<213> Homo sapien

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120cggagcttat gagaggtgtg aattcatgga cccatcctgg aatcagaatc agggccctact
180tctgcatcag aagccctggg tggcaccagc aagtgttttg caagcccttg agaagcagtg
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396

<210> 3113<211> 179<212> DNA<213> Homo sapien

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120cggggaatgg ccgcggtgtg gcagcaagtc ttagcagtgg acgcgaggta caacgcgta
179

<210> 3114<211> 352<212> DNA<213> Homo sapien

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180cgacagaagg gtacggctgc gacaagacca cttaagggta ccgctgcgag aagacgacag
240aagggtagcg ctgcggtaga ccacagaagg gctattgcat gccagcagct atctggggcc
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352

<210> 3115<211> 333<212> DNA<213> Homo sapien

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120aggaatccta attaaagcaa tcaggtaatt tcattctgct ctgtcagtga ctggccatga
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333

<210> 3116<211> 346<212> DNA<213> Homo sapien

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180ttttgttttt ttctaggaac actatgacca gccagccaat gctgtagggt tctgtgaatc
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346

<210> 3117<211> 343<212> DNA<213> Homo sapien

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180ttgaaaaaaaa ttttaaaaaa ctaacttggc ttgggggctc acccctgtag cccacctat
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300tatcacacca ctgttttcca cctgggtga caaaccaaaa tct
343

<210> 3118<211> 403<212> DNA<213> Homo sapien

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120gaaaaaaaaa ctaccaactg tcagccatgg gcctgacggc gctaagctct ggggctccgt
180gcactgacgt ggggccagcc acagggaggc ggggatcaag tagcggaggc caggattttg
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300tcatgcacct ggagtccttt tatgaaaaaa cctcctcctg ggcttatcaa ggaagatgac
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403

<210> 3119<211> 357<212> DNA<213> Homo sapien

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120gaagacgaca gaagggcctc tctacaccc cagggccttg tcatcagact cctcagctc
180cagacctccc tgtgcagtaa ctccccctc aaagaattca catccttga cagcagtgga
240cctttttaac tataagccc attctgtcc tacttttaga cgatcctacc aagtttagag
300aagaagggtat ctaggattga aagtaccca taagaagata ttccgaatac catagag
357

<210> 3120<211> 404<212> DNA<213> Homo sapien

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120ccatgtgagc ttcattcacag ctgccctgtt ccatggcaca gtgctgcgct acgtgggcac
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404

<210> 3121<211> 372<212> DNA<213> Homo sapien

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180gggagatcag tctcaaattc atgtccctga ctaactaaaa ttgaagggtt atatagcaga
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300tcaataggaa gcagggtggc ccttagtaaa ccaataatta cagcaggtaa agaaacaatc
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372

<210> 3122<211> 387<212> DNA<213> Homo sapien

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180ccccgcctct ataattttt ttttttttta aattatccaa gtggggcggc acaccccttt
240agtcctatct actctggaag ctgaccagga ggatggcttg accccaggag ggcaaggatc
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387

<210> 3123<211> 342<212> DNA<213> Homo sapien

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342

<210> 3124<211> 338<212> DNA<213> Homo sapien

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180aaggggcaaat aacattttga ggggggtattt aattaaaaat ccatgcaggg acagctgagt
240tcggggtttta tgttgggcta atacttcta aaattattta gaacaggact ggctagaaaa
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338

<210> 3125<211> 393<212> DNA<213> Homo sapien

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120tagacattgc gggcctaggc cactgtgact tcatgaacag accagcacca gaaagtttga
180tgcaggcatt ggaagactta gattatctgg cagcactgga taatgatgga aatctttctg
240aatttggaa catcatgtca gagtttcttc ttgatccaca actctcgaag tctatcttag
300cgtcctgtga atttgactgt gtagatgaag tgctaacaat cgcagccatg gtaacagctc
360caaattgctt ttcacatgtg ccacatggag ctg
393

<210> 3126<211> 325<212> DNA<213> Homo sapien

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120agaagacgac agaaggggac ccagaattat ctgggtcaat aaaaataatt ggcctattct

180tctataattg ttggggctaa aatgacaaa taaattagtt cacttcagta acctaaactc
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325

<210> 3127<211> 325<212> DNA<213> Homo sapien

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325

<210> 3128<211> 375<212> DNA<213> Homo sapien

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375

<210> 3129<211> 377<212> DNA<213> Homo sapien

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377

<210> 3130<211> 337<212> DNA<213> Homo sapien

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240aagggtacggc tgcgagaaga cgacagaagg gtacggctgc gagaagacga ctgaagggta
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337

<210> 3131<211> 336<212> DNA<213> Homo sapien

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180acagaagggt acggctgcga gaagacgaca gaaggggtacg gctgcgagaa gacgacagaa
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336

<210> 3132<211> 379<212> DNA<213> Homo sapien

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379

<210> 3133<211> 338<212> DNA<213> Homo sapien

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338

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334

<210> 3135<211> 344<212> DNA<213> Homo sapien

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240aaaaattcta taccatttta gagggtttct tcttttgctt tcaccatgat gttcttcccta
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344

<210> 3136<211> 353<212> DNA<213> Homo sapien

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353

<210> 3137<211> 384<212> DNA<213> Homo sapien

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384

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373

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421

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180ggctgggttt ttccaccgg cggtttaat tttaaaaaa tttaaaaaa caaaacaaag
240gggggttttt ctaatttggg gaggaacccc cccttggctc aaaagaaaaa ggcgttaaaa
300aagaattcca aaaggaaaac cttggggggg gcccaacggg ccccggtgcc aataaacttt
360tttctgggga acgggagggg gagaacctcc cccccctcc caaggcgc
408

<210> 3171<211> 405<212> DNA<213> Homo sapien

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120tcaagacatc ctctgcttc agcctccaga gagttgggac cataggtgca caccaccaca
180cctagctaatt ttttggggga ggtcttgcta tgttgcccag gctggctctg aactcctggg
240ctcatgcaat cctcctgcct tggcctccca aagcgctagg attagaggtg tgagccgctg
300caccctgccc cagtacaatc ttttttgaac tcaaattttt gctgacatct gagtgcacac
360accacagtgt aaattatgcc ttatcagaat ctaaataaaa atagg
405

<210> 3172<211> 400<212> DNA<213> Homo sapien

cggtgctgtc gacgacctgc ttctgggtct ggggttcgta cgtagcagag cagctccctc
60gctgcgatct attgaaagac agccctcgac acaagggttt ggacactttt aagaaacaaa
120gatagttttc tgaacattct gtgtcctgcc tgtctcctgt tgattcgag atgtaatatc
180gagtattcat caactggtct caatttcctg aacacattca ctgtatccct cattgtaacc
240gttatccccc tgcttcaaaa tgtgccagtt ccacttggtg ataacgttgg gaaaatgcag
300gtttatgaat gatgtggact ttttagaggat caaatcaata aattggattt tttatttttt
360gagggcagct gccctcactt gtttaaataa agaattctac
400

<210> 3173<211> 478<212> DNA<213> Homo sapien

gcaggaatcc ccatcgannt tcgaattccg ggcgctcgtc gagtccatta tatacantgt
60gacgtgccag cgtgatcata acttatgagt agcagacatt ggatagcagt attcttttcg
120tactagggtg tggacataac ccgactcta gtaatcgat cgccttataa ctgctcctat
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300attattaaca tgttagaggg ggtaagaaa gccaccttgt tacaaatttt ttaatttcca
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478

<210> 3174<211> 412<212> DNA<213> Homo sapien

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120ggctgaatat acacgctcca gcgacctgc ctggctgaat gaagagcttt gagattttga
180agaaacagga accatgaaat ttgctttgca actgtttgca accttaagg aagactgaaa
240aggcatctct gaagcatgtg ccttcagccg ctacaagagc agaagcagtg ggcattggat
300ggagctgagt acaggaccat acaggctaatt tgcaccggca caggaatcgg atataacatt
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412

<210> 3175<211> 171<212> DNA<213> Homo sapien

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120tcgcaacatg gacgccccct accccggcct tctgtcgggt caagggcttg a
171

<210> 3176<211> 384<212> DNA<213> Homo sapien

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120cctttttatgc tttgataatt agcagtttgt ctacttggtc actaggaatg aaactacatg
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384

<210> 3177<211> 393<212> DNA<213> Homo sapien

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120attccgaaaa gcaaatggga gatggacaca tctgaggcaa agctagacaa gttggatggc
180ttgaggactg gtactaaaag gaaacgtgac tgggaggcca ttgccagcag aatggaggat

240tatcttcagc tccccgatga ttatgatact cgtgcttctg agcctgggaa gaagaggggtc
300agatgggcag acctggaaga gaagaaggat gcagatagga aaagggccat aggttttgtg
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393

<210> 3178<211> 389<212> DNA<213> Homo sapien

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120cgatttatta accttcagcc ttcgacactg accgataagt ggtatggaga atctcagaaa
180ttgggtgctg ctgtcttctc ccttgccata aagctacaac catccatcat ctttatagat
240gaaatagact cttttctacg aaaccgttca agttctgacc atgaagctac agccatgatg
300aaagctcagt ttatgagtct ctgggatgga ttggatactg atcacagctg ccaggtcata
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389

<210> 3179<211> 426<212> DNA<213> Homo sapien

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120ggtataggaa tatatggggg ggggtctatt tcttttttta tataaccttc cccccgggat
180ttttgggttt aaaagtccg gttaccccca acccaaaatg ggttttttac ctttggagtt
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300aggagggggg gtttagccaa acccacccca gggcaaat tgggggggaa acctgaaagg
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426

<210> 3180<211> 383<212> DNA<213> Homo sapien

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300ctcacctacc cgacaggatc caggtgcctg ccagagggac tggggagcgg tcgaggattg
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383

<210> 3181<211> 372<212> DNA<213> Homo sapien

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120ttttgcacat taaaaattc agtattaatt aacattact tattctaccc tcttttttgg
180caaggaggac aaatacga aagttgga aacattact tattctaccc tcttttttgg
240tgtaaagata atttggtctt gaggggttaa acggttgata atgcctctac aacaacaaga
300aaaaagataa aatactagga tagaatcatg gtgggcacag tggcttctca ngaggctgag
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372

<210> 3182<211> 372<212> DNA<213> Homo sapien

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60aggggggggtg ggggggaccc ttttttttct agtggccttt agggaaaaaa aatttaactt
120tttttttggg tgggccc aaa tttttaagaa aaaatctcca attggtttcc cttttgaacc
180gggtaaaggc taatacttgc cacttttaaa ggagggggggg aaaacccccg ggtttttttt
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372

<210> 3183<211> 389<212> DNA<213> Homo sapien

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180ggcatctgcc tggccagaa ccttgggagt gacatcaagg cagtgaagc caactggagc
240aaatggaatg atgactatga aaaccactgt gttacgcca ccatttgca ggtcctgtcc

300acggtggggc ctcaacagaa ctctctgact ggggcccctg gcccggaccc acccagacga
360catgttttct ttggcctggg tggatatag
389

<210> 3184<211> 451<212> DNA<213> Homo sapien

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120gagtttcaaa acaagatgcc caggaactct ttaaaaatta taccatcttt gagaagaagt
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240aagaagtga ggcgaatcca cacaattatg atgcatgggt tgattacttg cgcttggtag
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360caccattca ggagaagagg cactggaagc gctacattta tctttggatc aactatgcac
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451

<210> 3185<211> 409<212> DNA<213> Homo sapien

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300ttcgtccacc ctgaatggag aagagcaggg attgcaactt tcatgatcta tcatctgatt
360cagacctgca tgggaagga cgtaaccctt cagtatgac caagcaacg
409

<210> 3186<211> 396<212> DNA<213> Homo sapien

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240gaatattaag ggaccaggcc cctataatta ggcctaatac tagcctgttg tttgaaaagg
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396

<210> 3187<211> 412<212> DNA<213> Homo sapien

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120cggggccctt tggcccaaaa atggccttaa cccctaaaaa tggaaaattt ttgtcctaaa
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300gcccttgtct tgtttggaag ggggggggtt atttccttgg gaaataaagg gtggtttctt
360tttttataaa aaaaacttgt tggaaaacaa acctttttat attaactttg an
412

<210> 3188<211> 404<212> DNA<213> Homo sapien

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60tggagagaga gagcccgaga gactgtgaga gagccagaga gtttgagcgt gcgcgagcga
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180cttacagaag gatgtttcct tcttgaggaa gcagcactat tagcactctg agtcaagatg
240agtgggaaac catctcaata aacacatttt ggataaaaaa aaaaaaaaaa aaaaccggct
300ctcggccctt taaaactatg gggggccttt ttccttttat ccgggggggg ggaaaccttt
360gttgggttg cccacccctt ttttaattgg cgggaaaaat agtt
404

<210> 3189<211> 334<212> DNA<213> Homo sapien

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60atgggtggcaa aactggggaa ccgggaggac cactcccccc aggactcctt tgaaggcgtg
120gacgaggacg agtgggacta gcctgcgcc cgtcacctc cacctcacct gtgctgccac
180ttcctagtgc acacctcacg gctcactctc aagctggaag atacctctct ggcctcggca
240catgtcacc ctgcactcct gccttccctg gggcacttcc acatcctctg ggcctcggc
300agttcccagg gactgttttc acctctgctg tctn

334

<210> 3190<211> 393<212> DNA<213> Homo sapien

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60cccagagatt gccgatctat tctacaaaga tgatcctgag gaacttttta ttggtttgca
120tgaaattgga catggaagtt ttggagcagt ttattttgct acaaatgctc acaccaatga
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240atattgctta ggctcagcct ctgatttatt agaagttcat aaaaaaccac ttcaggaagt
300ggagatcgct gccattactc atggagcctt gcatggacta gcctacctac attctcatgc
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393

<210> 3191<211> 385<212> DNA<213> Homo sapien

ggcacgagga aagctagcag attcttggct tagtattact aataggcagg attgtacaat
60gagcaactat cagattattc ctttcagtgg ttcttatggc atctaaatta ctgaataaat
120tattaatcca ttaatcagtg aatcaaatta tgattacaat tatcaaatga atgctcagca
180ttaattgaaa actgttttgt gaaacatgtc taccagaaa agtagcattc tataataact
240attaaacaac ttagctatat ttttttaag tattaaatta tatgtcaagc agctaaagtg
300aatttcagag taaaagtaag gcatgtttct gagcaacatt gataatttct taatttgcaa
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385

<210> 3192<211> 397<212> DNA<213> Homo sapien

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120caagcggaag gtcgagcgaa agaaggcagc cattgaggag attaagcagc ggctgaaaga
180ggagcagagg aagcttcggg aggagcgcca ccaggaatac ttgaagatgc tggcagagag
240agaagaggct ctggaggagg cagatgagct ggaccgggtg gtgacagcaa agacggagtc
300ggtgcagtat gaccaccca accacacagt caccgtgacc accatcagtg acctggacct
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397

<210> 3193<211> 395<212> DNA<213> Homo sapien

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120tgatggttgg gcacgcgcaa aaccattcat tagtgtttct tttctctcga ccacatgaaa
180cgatgcacac agaacataag ccgtatgaat gtaacgttta tgggaaaaca ttcagtttgc
240ccagtttatt tcatagacat gaaaggactc acactggagg aaaaacctat gaatgcgggc
300agtgtggcag atccttcaac tggtggagct gctttcgata tcatgggtggg actcacactg
360gagagaaacc ctatgaatgc aagcaatgtg gaaan

395

<210> 3194<211> 352<212> DNA<213> Homo sapien

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60ctatgctcac agtgtaaaca aaacagggaa gcttgaactt ggtagagccc actgcagctc
120agcaaggcct actgcctcta tagattccac ctctgggggc aaggcatatc tgaacaaaag
180gtagcagaca gcttctccag acttaaatgt ccctgcctga aagctctgaa gagagcagtg
240gttctccag cacagagttc aagctccaag agtggacaga ctgcctcctc aaatgggtcg
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352

<210> 3195<211> 394<212> DNA<213> Homo sapien

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120caggacaacc tgattgtggt ggcgggagtc ttcattgggca tcgccctcct ccagatcttt
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300acggcggggc ctcagcaaaa ctctctgact ggggcccctg gcccgcccc acccagccga
360catgttttct ttggcctggg ttggtttatac cctg

394

<210> 3196<211> 374<212> DNA<213> Homo sapien

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120tttgatacat taataaaact gcttgcataa gcagttctat ggaagacact ggtgtaatta
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300aagattcaag tgaacacatt tacacatatt aattccttaa agaaccctaa acgtttctc
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374

<210> 3197<211> 401<212> DNA<213> Homo sapien

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60gttgtagag ggaggagctt cccaccatct acaagtgtcc ttaccagggc tgcacggccg
120gtgaccgagg cgctgacggc atgaagaagc acatcaagga gcaccacgag gaggtccggg
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300ccttcaagca gcggaagcac ctctctgtcc accaaatgcg acattcggga gccaaagcctt
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401

<210> 3198<211> 392<212> DNA<213> Homo sapien

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120caaatacaaa caggacgtgg aaggcgctga gtcgcanctg gacgaggatg agcatggctt
180acatactaag tacattcatc gaatgatgca gattgagttc ataaaacaag gaagcatgaa
240tttcagattc atccctgtgc tcttcccaaa tgctaagaag gagcatgtgc ccacctggct
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392

<210> 3199<211> 134<212> DNA<213> Homo sapien

nncnnnnnnn cctnnccacc caccctgaa aaagcacanc aaaacccac gctgctggcg
60gagctgcggc tgctgaggca aaggaaggat gaactggagc agaggatgtc gggcctgcaa
120aagagcagyc gggc

134

<210> 3200<211> 393<212> DNA<213> Homo sapien

ggcacgagcc ggaacacgct gtctctgcgc ttccttcggg tggacatcga cgaatttgac
60gagaacaaat ttgtggacga gcaggaggag gcgccggcgg cggcggcga gccaggcccg
120gacccgagcg aggtggacgg gtcctgcgg caaggggaca tgcttcgggc attccatgca
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240gtggtgctga aagtgtcac aaacttcaag agcagtga ttagcaggc tgtgcagtca
300ctggacagaa acggcgttga cttgttaatg aagtacattt ataaaggctt tgagaagccc
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393

<210> 3201<211> 452<212> DNA<213> Homo sapien

cggtgctgtc ggatgttcac caatgtcagc aagaactcaa cctgaattta aaggtggcat
60tccatatact aacatcccc aggtcctctc aagtacttct gctgaaacaa atttatttgg
120ctaggcacta agttgttttc cagtgaatag taactaaaga agccctacc ttgtccatg
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240ttgtgcatgt ttctattgat ttcctctcc cggcttttgc ttctcttgaa actgttgccc
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452

<210> 3202<211> 403<212> DNA<213> Homo sapien

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120tgtaaaatt tttttttttt ttttaaaaat aactgcccgg gtactgactt tgctggcttg
180gaacatctct tttttttttt ttttttctg actaaggctt ttgatgattc tgaattagaa
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360gtccagcttt tctgctcaaa cgagatctcc agaatatggg ctg

403

<210> 3203<211> 404<212> DNA<213> Homo sapien

ggcacgagca tgggttccct cccctcagat tcttttgagc caaagaggaa acttccagct
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120gattctggtg cttacaactc attagattct gaccacaga tattctttgc cttggggtct
180tcaattgcta tgtttctcac tattcgagga gttgattgga tagatgagaa ttacagcctt
240cctacctgta aagggttctt cactatttat catccgcttg atccagtggc atatagatta
300gaacctatga ttgttccaga ttgggacctt taagctggtc tcattccaca tcacaaaggc
360agaaaaagac ttcatttaga attgaaagag agtctctctc gtat

404

<210> 3204<211> 378<212> DNA<213> Homo sapien

cgttgctgtc gcattgatga tcattgctga gatccacact ataattaggg gcggcagaac
60aggtgttttt ctaattctgc tatccctttg gcatttgta gttggaattc ttctataaaa
120acataggcgg ggtacagtgg ctacgcttg taatcctagc actttcggag gccaaaggcag
180gcagatcacg aggtcaagag atggagacta tcctggccaa catgggttaa ccccttctct
240actaaaagta caaaaattag ccaggcatgg tggcacacgc ctgtagtccc agctaccag
300gaagctgagg caggagaatc gcttgaaccc aggagacaga ggctgcagtg agccaagatc
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378

<210> 3205<211> 419<212> DNA<213> Homo sapien

ggcacgaggt ttaaggagaa gcctgaggcc cgcactgagc agctggatgt cgcgtgcggc
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120agtcgaacat cagttgtgga aatgagaagg aaccacagcat gtgtggctca gccccttctg
180tgttcccttc ctgcaagcga ttgaccttg agactatgaa aatgatgtta gacaaaaagc
240aaattcgagc aattttctta ttcgagttca aaatgggtcg taaagcagca gaaacaactc
300gcaacatcaa caatgcattt ggcccaggaa ctgctaacga acgtacagtg cagtgggtgt
360tcaagaagtt ttgcaaagga gatgagagcc ttgaagatga ggagcgtagt ggccggcca

419

<210> 3206<211> 409<212> DNA<213> Homo sapien

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60cttcatectg ggggatatct ttgatgaagg gaagtggagc acccctgagg cctgggcgga
120tgatgtggag cgttttcaga aaatgttcag acaccacagt catgtacagc tgaaggtagt
180tgctggaaac catgacattg gcttccatta tgagatgaac acatacaaaag tagaacgctt
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300caacagcgtg gcgctgaacg gggatggctg tggcatctgc tctgaaacag aagcagagct
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409

<210> 3207<211> 390<212> DNA<213> Homo sapien

ggcgcgacgt ctgctctgac acttttgatt tggaggaata tgacgacggc gagaagcccc
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120aattgcccct gagggcccgg gaccggctcc gtgtgattga tgcgtccaaa catgcccata
180agttttgtaa cacataagat gaggagacta tgatctgtg gagacctgaa cgcattgaac
240gacagtacag gaagaaatgt gcaacgtgtg gactgccgct cttctaccaa tcccagccaa
300agaatgctcc tgttaccttc attgaggatg gacagtaat caagtttggc cacggttttg
360ggaaaacgaa catatatact cagaaacaaa

390

<210> 3208<211> 350<212> DNA<213> Homo sapien

tacggctgcg agaagacgac agaaggagac aaaaagaaga aagataagaa gaaaaagaaa
60ggagaaaagg aagaaaaaga gaaagagaag aaaaagagg acctagcaaa gccactgtta
120aagctatgca agaagctctg gctaagctta aagaggaga agaaagacag aagagagaag
180aggaagaacg tataaaacgg cttgaagaat tagaagccaa gcgtaaagaa gaggaacgat
240tggaacaaga aaaaaagaga aaggaaaagg cccaaggaaa aagaaagaaa agaacgcttg
300aaaaaaagaa gggaaacttt taactaaatc ccagagagaa gccagagcca

350

<210> 3209<211> 341<212> DNA<213> Homo sapien

tactgctgcg agaagacgac agaagggaca atacaatgga aaaatgcata gaaaaacagg
60aaagattttg tcaactaaaa aaacaaagta tgttgcttca acagcaactg gatgatgctc
120gcaacaaagc tgacaatcaa gaaaaagcaa tacttaatat tcaagccaga tgtgatgcta
180gagtacaaaa ctttcaagct gagtgcagaa agcaccgtct tttagtagaa gaagacaata
240aaatgttggt caatgaactg aatcattcga aagaaaaaga atgccaatat gaaaaagaga
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341

<210> 3210<211> 380<212> DNA<213> Homo sapien

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60gatgaagatg atgatgaagg ggaggaagga gaggaggatg aaggagaaga tgactaaata
120gaacactgat ggattccaac ctctcttttt ttaaattttc tccagtcctt gggagcaagt
180tgacgtcttt ttttttttat tttttttccc ccctggggcc taaagccctt ggttttagggg
240gctttttttt ttaaccccg ggtccacaat gattgggggg gaaaaccctt gggccaaata
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360ggaccaaacg gtgggggaaa
380

<210> 3211<211> 406<212> DNA<213> Homo sapien

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60actgaactgt gggttctcta taagtggcat tttgggcttt cctctttttt tgtaaagcaa
120tgtctgccta gtttattgtc cagttaactt tagtgacctt taaaagtgtg gcattgtaaa
180taaaaact tgcaaaaaaa aaaaaaaaaa attggttttt gacctttaaa aatttagggg
240ggcggttttc ttaactcca accttaaaaa aaccctttga ggggttgggc caccaccaat
300ttaagggggg ggaaaaaatg ggtttttttg ggaaattgg ggggcttttg gttttttttg
360gacctttaa aaccggcaaa acaaagttaa caacacctat ttgttt
406

<210> 3212<211> 391<212> DNA<213> Homo sapien

ggcacgagag gaaaggcaat tgctctcagc atgaccgggc cttggagcgg ttctatgaac
60aggtggtcca ggtatccag cgccacatac actttgatgt tgtaaagtgc atctgggtg
120ccagcccagg atttgtgagg gagcagttct gcgactacat gtttcaacaa gcagtgaaga
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300acactaaagc tgctggggaa gtcaaagcct tggatgactt ctataaaatg ttacagcatg
360aaccggatcg agctttctat ggactcaagc n
391

<210> 3213<211> 388<212> DNA<213> Homo sapien

ccagtgcagg aattgttctg ccagttattt gtataggaac aaaagattgt taagagttac
60ctgggagagg agagatacac agttaggat actatggcat tgagtgttta ctgtgagcaa
120tgtctcacat tcctggttct tcaaaagaa tttttttata acttggctctg tttatttcta
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240tatgcacctg gatcccaaga aagctggaac atattttctca aatcaggcag taagaaatgt
300tgagcctata ttttcttgat tccagttgtg gtccatttgc tgtccagtat cacagctagc
360tacaggaggg tcctaggact gcatgcan
388

<210> 3214<211> 340<212> DNA<213> Homo sapien

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60cataaccaga ggagaagctg aggagccctt ctctactggt acatccttcc ctttacagcg
120gctggatctc tgctctggtg gtgccgaagg gcaacacagc agtatacgcg ctcatgctgc
180tgcccgccct gctcttact ggcattgctg tgctaggaat tgtcatgctg aaacgggtga
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340

<210> 3215<211> 369<212> DNA<213> Homo sapien

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60aaacgccgta caatcttgac aacttcaaac tcgtttcctt acgtgaagaa gaggattcct
120attaactgtg aacagcagat taatttaaaa ccaattgatg ttgccactga tgaaataaaa
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240caactttaat tgcagggtctg tgtttctgtg cagggtcaatg ctgggtccatt agcatatgca
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369

<210> 3216<211> 384<212> DNA<213> Homo sapien

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60acattaatctt cagactgaac agacttcaca gcaagaaaag ttattaggga tcaaagaaga
120gtattacaca atgataaaga ggtcagttct ccaaaaaaac atgtctttaa tgtgtatatt
180cttaacaata agcatcaaaa tatctgagga aaaaactgat acaactgcaa ggagaaatag
240atgaatccac tatttatagt tgaagtcttc agcactccta tcagtaatgg acagatgtag
300caggcaaaaa atcaccaagg atatagctga agtgaacagg atcattaatc aactaaatct
360aagtatcatt tatgtactac taca

384

<210> 3217<211> 387<212> DNA<213> Homo sapien

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60atcaaaggcg tgagccactg cgctcggctc catctgcata ctcttaccac ctccaaattg
120gacctagcag ttccccatct ctactccttc caggaagcca ggcccacaac tcactcctggg
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240ggttctgatt tcctcttaça gataggctca ccttatcttc caaggctcac cttatcttcc
300aaggccaagg agaggtcaag gactggatct ggctttgcc ggtggtgaa aggacccgaa
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387

<210> 3218<211> 383<212> DNA<213> Homo sapien

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60cttcgtcaga ttgggcagag gacgataagc actgcttccc gcaggcattt taaaaataaa
120gttccggaga agcaaaaact gttccagta ctgaagtatt ttataggaga tgttacttgt
180aattattaga ttacaaaaag gtaagagttg ggataaaca grtggtgtat aaattagatc
240atatgacaat ataaacatta caaaaaaagt caaggacatg taccatagt ctaatagtgg
300ttgtctcttg gggaaagacc tgggtggagca gagcaattta cctttataag tagtttgatt
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383

<210> 3219<211> 412<212> DNA<213> Homo sapien

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60tctaacacgc ccacctcata actggatgaa agattttatc ctcacagttt ctatagtaat
120tggtgttggg ggctgctggg ttgcttatac gcagaataag acatcaaaag aacatgttgc
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240agagaggctt gaaaaggcac aggaagaaaa cagaaatggt gctgtagaaa agcaaaattt
300agagcgcaaa atgatggatg aaatcaatta tgcaaaggag gaggcttgtc ggctgagaga
360gctaagggag ggagctgaat gtgaattgag tagacgtcag tatgcagaac ag

412

<210> 3220<211> 133<212> DNA<213> Homo sapien

antnnnnnnn cntgctgngg tggcggtcac tccctctgcc actatcccca gggagggaaa
60ggctccgcc tttgggaaag tggtttctac gtcactggac accggttctg agcaatagtt
120agagaactcg ttc

133

<210> 3221<211> 170<212> DNA<213> Homo sapien

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60tagtttagtt ttctctcttg ccttcccttc tgtgtgaccg accccttggc caaaaaaac
120caaaaggcaa aaaacaaaag cctaccctgt tctggttttt ttctctctt

170

<210> 3222<211> 417<212> DNA<213> Homo sapien

ctcggcacga gggacagtgg aggctgttat cttttgttga aagcactgca tgtaagagg
60gggcacagcc ctctcccaa gggaaagtgt ctttgcataa aatgtatttt ttacttttg
120gaggattctt ttgtataac ttcaataaag attgtaagca aagggttagg ctttgatggt
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300aacgcggagg tgatcaagtg tgggtgtagg ccctttgttt ccaatggtgc tatattctgg
360tttcaaacac ttcactgaac ccagctatct tgcaaacttt cagtgggtgct gccctg
417

<210> 3223<211> 396<212> DNA<213> Homo sapien

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60ttcctaggtg ggggccataa gaccagataa gccagtttac cagtctgggt gtctccagca
120ggtccttcag tatgcagggt ctgaaaaata cctcaaacac caatcttagg tttacaata
180gtaatgttat ctgtaggagc aagtggggga ggtagtgat attgtggcct ctggctacat
240gacttctgag ccataatttc taatctagt gctaatttgt tggttttaca aacgcagtct
300ggttcccaag caaggaggga gtttgtttca gggagagtct attaccgtct ttgtttggtt
360ttttgcgttg ctttggtttt tgagccaagg tctcgc
396

<210> 3224<211> 407<212> DNA<213> Homo sapien

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60aacccaggtt ggcgactgca acaggaactt ggagtggaga ggaaaagcat cagaaagagg
120cagaccatcc accaggcctt tgagaaaggg tagaattctg gctggtagag caggtgagat
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240tgaggaagaa tgggtgtggga gagggatgat gaagagagag agggcctgct ggagagcata
300gggtctggaa caccaggctg aggtcctgat cagcttcaag gagtatgcag ggagctgggc
360ttccagaaaa tgaacacagc agttctgcag aggacgggag gctggaa
407

<210> 3225<211> 382<212> DNA<213> Homo sapien

cgttgctgtc ggcaggaccc tgggtgggt gccttttctt gtcaggaggc ccggagagcc
60tggctggatc gtcattggaa ccttgatgaa gctgtggagg agtgtgtgag gaccaggcga
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360cgggcagagc tggcactgtc ag
382

<210> 3226<211> 427<212> DNA<213> Homo sapien

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180gattttcaaaa gaacaaggcc ttgaagttct accagaacat gatccaatac gtgaccaaag
240ttggtatgtg aacaaaaagc tccgtcaaag gctgcttgaa gaatatggag tcagaacctg
300tactcttatt cagttccttg gtgatgctat tgttttgcca gcgggagcac ttcattcaggt
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420agagtcn
427

<210> 3227<211> 398<212> DNA<213> Homo sapien

cccgcctgca ccaggtgaa ataaacagcc ttgttgctca cacaaagcct gtttgggtgg
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120aggagaccag tcccctgtcc tcacctcac tccgtgagga aatccaccta tgaccttggg
180tcttcagacc aaccagccca aggaacatct caccgatttt aaatcagatc tacttggctt
240agctgctgaa gactgatgct gactgatccc ctgagaagcc ccagaccat caccgacacc
300aagctttggg taactcttac agtggaggga aggcaggaat gtcaggcctc tgagcacagc
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398

<210> 3228<211> 422<212> DNA<213> Homo sapien

cacacatcct ttttgcttac aaatttccta gcttgtgacc attctccacc atctcccccc
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360tacaaaaaaa gtatagttaa aacatttggt ctacaaatta acctttataa atataattac
420tg

422

<210> 3229<211> 413<212> DNA<213> Homo sapien

ggcacgaggc agagtccatc acttcgccag gtggacatgc tgtgggtgga tgttcccggc
60gtgtgccggg cctgaatgga caggggccac ttcacagcat gtcagggaaa atcactgtca
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240atcccctggg gaatgaatga aattttgagc ttttccctta cgtaaaacta aatttatacc
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360atgctgtctt atgtccattt gtgcagccct gacctgctaa ggagcgaatc ttt

413

<210> 3230<211> 146<212> DNA<213> Homo sapien

gcatcatttc tatccaaata aagccttate ttgacctgat ctattaaaac ctgccacacc
60cgccctttcc tacctagatt taatgagccc aagtttttaa aatggaagaa atgactctgg
120ggcaaagacc cctaataaac tagggg

146

<210> 3231<211> 380<212> DNA<213> Homo sapien

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60ctctacaatg ctgcagaagt ttctacctgc ctggctggga ggtaggaggg tctggtttgg
120ggatgtggcc ctgaggagag gaccagtgtt tggcagtggc catgtattga tctcccagtt
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240tcgagctacc aatgaaggcc tcagtctgat gctcattggg cctgaggatg tgatcaactt
300taagaagatt taaaaacgc tcaagaaaga tgaggatata ccactgttcc ccgtgcagac
360aaaatacatg gatgtggtcg

380

<210> 3232<211> 182<212> DNA<213> Homo sapien

agaacaagtg cttatagggt tgccaccatt gtgacagcag ttggcttctc caagggcctc
60tggtatggaat gtgccacaca cagcacaggc atcacccagt gtgacatcta tagcaccctt
120ctgggcctgc ccgcttgcat ccaggctgcc caggccatga tggtagacac cagtgaatc
180tn

182

<210> 3233<211> 396<212> DNA<213> Homo sapien

ggcacgaggg ataaggcagc tgctgcatca tcggcactac aagccaaatc atatgagaag
60gcggcggttg caggcaagaa gcctgtgctc gtcccccgcg gagtggccag gctacggcgg
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240ccggaggttg gctatgtgac caggcaacat gctgagccgg ctacaggaac tgcgcaagga
300ggaggagacg ctgctgcggg tgaaggcagc cctgcacgac cagctgaacc gcctcaaggt
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396

<210> 3234<211> 342<212> DNA<213> Homo sapien

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120cactcttgcc tgaatgacag agcaagaccc tgtctaaaaa aaattttttt ttaagttggc
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240ttgaggtcag gaattcaaga ccagactggg ccgggcgcag tggctcacgc ctgtaatcct
300aacacttttg gaggccgagg caggcgaatc acgaggtcag gg

342

<210> 3235<211> 377<212> DNA<213> Homo sapien

ggcacgaggc caccaacacc atttgtcttt ataatggacc tcaaggccta cgaacaggtg
60atgcactacc ccggtacgg atcccccatg cctggcagga tggccatggg cccggtcacg
120aacaatcgg gcctggacgc ctgccccctg gacgcagata ctttctacta ccacggggtg
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240tttcaccccg gatcgaggac aagtgaagaa gcaagagggg gtcgagactt tggggagaca
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360cagaagactt attcacc

377

<210> 3236<211> 390<212> DNA<213> Homo sapien

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120gaggcctccc ccttctcct cgcctaccta ctctccctc ctcgtcatcc tcccccttcg
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300tgaggccct gcgcgcgtc acggcgctct tcaaagagca gcggaaccga gaaacagcac
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390

<210> 3237<211> 347<212> DNA<213> Homo sapien

tacggctgcg agaagacgac agaaggggat agaaaatcag taaagaaaca tgtcacttaa
60tctgcactat agagcaaag catctaacag atatttacag aacatttcat ccaacagctg
120caaaatacac attctttttc tcaacacatg gatcattctc cagggtagac catatattag
180atcacaaaac aagtctaaca acattcaata aattgaaata atatcaagca tcttctctga
240ccacaatgga ataaaactag aaatcaataa tgaggaattt tggaaactat acaaatacat
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347

<210> 3238<211> 139<212> DNA<213> Homo sapien

gtctgagtca gagatctgtg cacactttct aaacagcttg tgatgcaagt gtgagcctat
60tgtgttactt gaccttattt tggaagtttt gaattggcct aggaggaaac ctagaatga
120accaggggta tgtcatcac

139

<210> 3239<211> 399<212> DNA<213> Homo sapien

ggcacgagga tctggcacac tcaggctcat tggcaggtag aagaagggga ataaaggggc
60tgtgtgaagg cactgtctgg agccattaga acacagatac aagagaagcc aggaggtcta
120tgatggtagc gatttttaaa atcaggaaat aaaagatctt gactctaaaa gaaaaaaaaa
180aagaacgcgt cctagggtct gatggactaa tcagggtgaa tttctaaaat ccacttttg
240cagaccctct tgtcttgaat ctggcttttc acaacatgga gggggagaaa aagaagcttc
300tttctctgaa aagagggggg tttttgtttt tttagaaaac taggaggggg gggagcataa
360tggtcaaca gaagagtttt ttctttttat gttcctgtg

399

<210> 3240<211> 387<212> DNA<213> Homo sapien

gcaagaagcc ccctgacccc ttgttccaaa tatactcttt tgtcttctc tttattccca
60cgttcgccct ttgttcagtc caatacaggg ttgtggggcc cttaacagt ccatattaat
120tggtatcatt atttctgttg tttttgtttt tgtttttgtt tttgttttg agacagagtc
180tcaactctgt acccaggctg cagttcactg gtgtgatctc agctcactgc aacctctgcc
240tcccagggtc aagcattct cgtacctcag actcccgaat agctgggatt acagacaggc
300accaccacac ccagctaatt tttgtatttt ttgtagagac ggggtttcgc caagttagcc
360agcccagttt caaactcctg acctcag

387

<210> 3241<211> 160<212> DNA<213> Homo sapien

ccctctagag gagcctgata tgcatttcga taaaccccga tcaacctcac cacctcttgc
60tcagcctata ttccgccatc ttcagcatc cctgatgaag gctacaaagt aagcgcaagt
120accacgtaa agacgttagg ttcagggtga tcctatgatg

160

<210> 3242<211> 379<212> DNA<213> Homo sapien

ggcacgagat cagccagccc ctgcagaaca gttcatcca cacagggcat ggcgacagtg
60acccccgcca ctgctggggc ttcccggaca ggattgacga actgtatctg ggaaacccca
120tggaaccccc cgacctctg agcgagaact actggtggcg tggccagaac acacggacgc
180tgtgtgtggg gcccttccct cgcaacgtgg tgacctcct ggccggcctg tcggcccagg
240acatcagcca gccctgccca cagaggggct gccctggcga tgggcccagag gcggggccgc
300cagcagacaa gatccagatg ctgcaggcca tgggtgatgg ggtgaccaca gaggagtgc
360aggcggccct gcagtgcct

379

<210> 3243<211> 462<212> DNA<213> Homo sapien

gcggtgctgt cgcttcaaga gcgttctgat gccccatgac ctcatcactc agctgtggcg
60ggggctggcc atcgagacca agcacgagaa ggcgatggcg cacgccgacc ccacggagct
120ggcgctgagc gggctggagg ccttctcttt cgactacatc ggcaagtggc ccctttcgct
180catcatcaac aggtgcgggt cggtgctcg ggcacctgcc agatcttcac tcaggtttgg
240cagaagcgag aactgtgcca cgcggtggcc acctcgtcgc acagaggacc caaggcggct
300ctccccagcc ttcagagtcc gggagattca cgggctgtcc gggggccacg gcgcggactg
360tgaggtacag acgccgtgta cacgacgccg tcggtcacgg agggccacct gaggtgccgc
420cacgtgtctg gcaggaaagc cctcactcgc taccagatgc tg

462

<210> 3244<211> 392<212> DNA<213> Homo sapien

cgctgctgtc gctatctctg tgcttcttct atctcctgca caaatggagg gagctcctaa
60gaactagtaa acgtctgagt gccagcacta tgctgaatgc ttacgtgtt tccatttaa
120ttatggcaaa cttgggagac aaggcaagtg ttctcacaga tgaaagacac tgatgtacaa
180agataagtaa cttaccaaac atcacagtca accaggattt gaaccagat agtccacttc
240tccccaaaatt tcattttctc accttggttc cgatactcaa aaagacgggg atcagcatga
300atgggaatga gccccagacg gtgagcaaga atctcatcct gaacaatgga tgtattattg
360tacaccagga ctttctccac agccatagtt gg

392

<210> 3245<211> 144<212> DNA<213> Homo sapien

atatgcannt cttctccacc taggaccgcc agcagagcgg ggggatctcc ctgccccac
60cccagttccc caaccactc cttccaaca acaaccagct ccaactgact ctggtcttgg
120aggtgaggct tccaaccac gga

144

<210> 3246<211> 433<212> DNA<213> Homo sapien

ggcacgagag cctcgataa gttttccact gaatacaca tgtagtctgg ctacagaat
60ctgcattttt acataaatga taggggagag gaagcaatca gatactcatt tgtctcaagt
120gaacctcaag ggatgacttt gaatagaatg agaggcagat tccccctaa cagttccag
180gttgactttt ccttttagct tagagatttt ggggtcccaa ttttgtttt catttcacac
240ccatcttctg caccctcatg actcacaaga gtctcacac ctggcctacg ttcaactctc
300cacggctctt gccagaaggc tgcacgtaca acacacacag aggcgggcat ttccctgacc
360actcctgtgt gccgaggggg aacggtagat ggccaaccc ccagtgggtc gaactttctg
420gccaacata ttg

433

<210> 3247<211> 232<212> DNA<213> Homo sapien

ctcccccta cttaccaac cacaggattc agtgtatgtc acatgctcag gcggagggtg
60ggaaacgtta cttccaactg ggaaactttt tgggggaaat taactggaca cctatctcg
120aggtttattt tcttgcaacc agtgaagtcg tctcctccc ttccctggat aactcttcag
180tttgactgtc actgttctgg tgtcaactcc agcgtcggca caggcagaag gg

232

<210> 3248<211> 427<212> DNA<213> Homo sapien

ggcacgaggg cggagccaag cgccgccatg tccgccgcc tgctgcggcg gggcctggag
60ctgctggcgg cgtccgaggc cccccgggac cctccaggtc aggccaagcc gagaggggt
120ccgggtgaaac ggccccgaa gacgaaggca attcaggccc agaaactgcg gaactcggc
180aaggggaaag tgccaagtc ggcactggac gagtaccgga agcgagagtg tcgagaccac
240ctcagagtaa acctgaagtt tctgaccagg acgagaagca ccgtggctga gtctgtgagc
300cagcagattt tgcgccagaa cgggggccgc aaggcctgtg accggcttgg gccaaaacca
360aaagaagaan gctgagggca cgtggtcacc gaggaagatt ccagaaggtc agcacgaata
420cttttgg

427

<210> 3249<211> 401<212> DNA<213> Homo sapien

ggcacgagct gcggcggggc ctggagctgc tggcggcgtc cgaggcccc cgggaccctc
60caggtcaggc caagccgaga ggggtcccg tgaacggcc ccggaagacg aaggcaattc
120aggcccagaa actgcggaac tcggccaagg gaaaggtgcc caagtcggca ctggacgagt
180accggaagcg agagtgtcga gaccacctca gagtaaacct gaagtttctg accaggacga
240gaagcaccgt ggctgagtct gtgagccagc agattttgcg ccagaaccgg ggccgcaagg

300cctgtgaccg gcctgtggcc aagaccaaga agaagaaggc tgagggcacc gtgttcaccg
360aggaagactt ccagaagttc cagcaggaat acttcggcag c

401

<210> 3250<211> 145<212> DNA<213> Homo sapien

atagcncatc catcctggag tacctcaccg cagaggtact tgaactggca ggaaatgcat
60caaaagactt aaaggtagag cgtattaccc ctctgtatctt gcaacttgct attcgtggag
120atgaagaatt ggattctctc atcag

145

<210> 3251<211> 388<212> DNA<213> Homo sapien

cgttgctgtc gggacagtgg ccgcaccaga caacctgccc aactacgaga acaccgtggt
60cttctctctg tccagcttcc agtacctcat cctggctgca gctgtgtcca agggggcgcc
120cttccgcccg ccgctctaca ccaatgtgcc ctctctggtg gccctggcgc tcttgagctc
180cgtcctggtg ggccttgtcc tggccccgg cctcctgcag gggccgctgg cgctgaggaa
240catcactgac accggcttca agctgctgct gctgggtctg gtcaccctca acttcgtggg
300ggccttcatg ctggagagcg tgctagacca gtgcctcccc gctgctgc gccgctccg
360gccccagcgg gcctccaaga agcgcttc

388

<210> 3252<211> 380<212> DNA<213> Homo sapien

tacggctgcg agaagacgac agaagggaca gtaagacatc agaaagtata tgtgagatca
60ataataattc cgaacatgga gccaaactaa ctacgcaaca agacattaga aaggacagta
120agacatcaga aagtatatgt gagatcaata ataattccaa acatggagcc aaaaacatgt
180ttgtctatct taaacaagga agtaatttgg tacaatcaaa gcatttgaat ccaggcagca
240tttcagtgcg gacatctttg acaaatagct cacaataga taagccaatg aagatggaga
300aaggggaaat gtatggaaat tctccaagat ttttaggtgc cacaatttgc actatgtatt
360ctaagatctc anactgtcag

380

<210> 3253<211> 154<212> DNA<213> Homo sapien

aatgttttcc aacatccang ctgtgtccct caagatccag aactcaagt ccaacaactc
60gatggcaca gcatgaagg gtgtcaccaa ggccatgggc accatgaaca gacagctgaa
120ggtgcccaga tccaaaagat catgatggag ttg

154

<210> 3254<211> 460<212> DNA<213> Homo sapien

cgttgctgtc gcttcaagat cgacctgatg ccccatgacc tcatcactca gctcttgccg
60gtcctggcca tcgagaccaa gcaggagaag gcgatggcgc acgccgaccc caccgagctg
120gcgctgagcg gcctggaggg cttctcttcc gactacatcg tcaagtggcc cctttcgctc
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240agaagcgaga actgtgccac gcggtggcca cctcgtccca cagaggaccc aaggcggctc
300tccccagcct tcagtgtccg ggagattcac gggctgtccg ggggccacgg tgcggactgt
360ggagtcaga cgccgtgtcc acgacgccgc cggtcacgga ggcccacctg aggtgccgc
420acgtctcttg caggaaagcc ctactcgtc accagatgct

460

<210> 3255<211> 382<212> DNA<213> Homo sapien

cgttgctgtc gaacagatcc attgtttcag gagtttcaat ttaaagttcg ggatgaaatg
60gtcatgtaa ctggacgct acttccagca cctatgctcc agtatggagg acggaatcgg
120acagtagcaa caccgagcca tggagtatgg gacatgcgag ggaaacaatt ccacacagga
180gttgaaatca aaatgtgggc tatcgttctg ttgcccacac agaggcagtg cagagaagaa
240atattgaagg gtttcacaga ccagctgcgt aagatttcta aggatgcagg gatgccatc
300caggggccagc catgcttctg caaatatgca cagggggcag acagcgtaga gccatgttc
360cggcatctca agaacacata tg

382

<210> 3256<211> 431<212> DNA<213> Homo sapien

ggcacgagat ggtgacaagg ctggagttgc tttgggaact gcactgacac ctacttgga
60gaattaagtg tctcaagctg tcttccctc cttaatttcc ctggaatttt gctgagcatt
120ttaccttctc attctttgta aatttctcat taaacattct aggaagagag atagctccct
180acctctggag gttggggtta cggggtatag taggggtct gttgggtttt tgcagataag
240tggttatttt tccttgggca ggtgccact atggctgtgg agaaggtcct ggtgtacaat

300aatacatcca ttgttcagga tgagattctt gtcaccgctc tggggctcat tcccattcat
360gctgatcccc gtctttttga gtatcggaac caaggtgaga aatgaaatt ttgggagaag
420tgactatct g

431

<210> 3257<211> 424<212> DNA<213> Homo sapien

ggcacgagat ggtgacaagg ctggagtgc tttgggaact gcactgacac ctacagttgga
60gaattaagtg tctcaagctg gccttccctc cttaattttc ctggaatttt gctgagcatt
120ttaccttctc attctttgta aatttctcat taaacattct aggaagagag atagctccct
180acctctggag gttgggggta cggggatagg tagggggctc gttgggtttt tgcagataag
240tggttatttt tccttgggca ggtgccaaact atggctgtgg agaaggtcct ggtgtacaat
300aatacatcca ttgttcagga tgagattctt gtcaccgctc tggggctcat tcccattcat
360gctgatcccc gtctttttga gtatcggaac caaggtgaga aatgaattt ttgtgagaag
420tggc

424

<210> 3258<211> 399<212> DNA<213> Homo sapien

cgttgctgtc ggattcaggc gtgtatacca gccggagcgg cgcggcagcg gcaggaccgc
60cgtgggcgct atagtagcga cccgggggga gcgcggggcg acgctggctg cagggaacccg
120gtgacagcgt gagaggtact aggttttgac aagcttgcac catgcgtgag tataagctag
180tcgttcttgg ctccaggagc gttggaaagt ctgctttgga gcaatttaca gcaatgaggg
240atttatacat gaaaaatgga caaggatttg cattagttaa ttccatcaca gcacagtcca
300catttatcga ttacgagac ctgagagaac agattcttcg agttaagac actgatgatg
360ttccactgat tcttggctgc aataagtgtg atttgtaag

399

<210> 3259<211> 344<212> DNA<213> Homo sapien

tacggctgct agaagacgac agaaggggtg tcagtattaa gatcactaaa gtggttctta
60gcaaagggtg gaggtgtctt gactgactg tgtgtgaggc ctgtgggaag gcaactgacc
120caggaagact cctgctgtgt gatgactgtg acataagtta tcacacctac tgcctagacc
180ctccattgca gacagttccc aaaggaggct ggaagtgcaa atggtgtgtt tgggtgcagac
240actgtggagc aacatctgca ggtctaagat gtgaatggca gaacaattac acacagtgcg
300ctccttgtgc aagcttatct tctgtccag tctgctatcg aan

344

<210> 3260<211> 423<212> DNA<213> Homo sapien

ggcacgaggg ggagtattcc aggaagaggc cactgcctat gtgatgacct caaggcactg
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120attactatgc taagcgaggt ctaataactg gaaacagttg tatgagctgc agacatgcag
180gcactgccgt gtacttttgt ccgcacatat atatctatgt gcctagctct tgttccctgac
240acacatgttt ctatatacac atacacatac atgcatatac caacagattt aatattatat
300tgcatttttc aacgatgcag aatgcagctg caattgtgtt ttaaggagaa gccacatggg
360gatgggtgtc cctgcaacat ggtgccactc ctggggccatg tgcagcctca gtggacactc
420ttg

423

<210> 3261<211> 382<212> DNA<213> Homo sapien

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60aaaaaaagga atggtccccccc cccacctccg gatttaaaaa aaaccctgg aatttttaat
120aaacattttt aaccacggg gattttttt ttaaccgggc ctttgggatt ccaaagttaa
180aaaggtaaaa agaaaaggct aacttttcct tttttttggg ggggggggccc cctgccaaaa
240atgtatttac tttggctcag gggctttatt ggagggccct ggccaccctt tggaatggct
300gccacagta aaactttccc agaaaaattt cgtaacgggc cccagccctt tcataacccc
360gggtttttttt gaccttgaaa aa

382

<210> 3262<211> 381<212> DNA<213> Homo sapien

cgttgctgtc ggcgaccgc cggggatgct ggggtgctcaa cgcgctgcc cctggggccc
60aacgcgttga cctcgcggtc aggttgcttc cgcggactac ggatctggct cgctagctct
120ggaaggagc accgggaggg aatggtggca actcccaagg aggggacca gggatccgag
180aaagggaagac ttgggactgt ggtacagacc tccatgagcc ggtcccaggt agccctgctg
240ggcctgagtc tgctgctcat gtcctactg tatgtggggc tgccaggccc ccctgagcag

300acttcctgcc tctggggaga .ccccaatgtc acagacctgg ctggactcac ccctggcgac
360tcgcccattct tttaccgcga n

381

<210> 3263<211> 336<212> DNA<213> Homo sapien

tacggctgcg agaagacgac agaagggaat gatgatgaac cacatacttc taaaagagat
60gaagttgatc gagctgtgat attgtttaaa ccaatgggtat cagagccaat tcatatacac
120aggaagtctc cacttccaag atctaggaag acggctacaa atgatgttg atctgaaaaat
180gctaattacc tgagaacacc aagaactctt gtggaacaga agcagaatcc tactgtaggc
240tttgaattgt attccatggg gccatctatt tgtcctctag aaactcttca taatgcccta
300tcttttaaagc aagtggatga atttcttgct tccatt

336

<210> 3264<211> 455<212> DNA<213> Homo sapien

tgcaggatcc cagcgactcg aattccgttg ctgtcgaggg gctcccagtc ctttcttctg
60ggaggccaag gcggcttcgc gttctgagaa tagacagaac ctctgttact ctgtgaccgg
120caggcaccgg gagatccgta gtcagacgc caggacatcc cggaagctgg gaaatggtga
180atgtgccagg gactgttgac attcagggtat gtggccatag aattctctcg gggggagtgg
240gaacacctgg actcacatca aaagctttta tatggggatg tgatgttaga gaactacgga
300aacctggtct ctctgggtct cgctgtctct aagccggacc tgatcacctt tttggagcaa
360aggaaagagc cctggaatgt gaagagtgc gagacagtag ccattccagcc agctcctgaa
420gagcaccatt ctgcctaata tttctatgag tttag

455

<210> 3265<211> 165<212> DNA<213> Homo sapien

tggtgcagga tgcacagcag gaggatttcg gaatcttcca ggcctgggcc gaggccactg
60gtgcatatgt tcccgggagg gataagccag acctgccaac ctggaagagg aatttccgct
120ctgccctcaa ccgcaaagaa ggggtgctgt tagcaaagga ccggt

165

<210> 3266<211> 148<212> DNA<213> Homo sapien

aggcacgctt tcaggttttt attatggcag ccactaacag gccagatata attgarcctg
60caatcctgcg cccggggcgc ctggacaaaa cactgtttgt gggtttaccg cccctgcag
120atgccttgc catcttaaaa actatcan

148

<210> 3267<211> 386<212> DNA<213> Homo sapien

cgttgctgtc gggccaccct gaagacctat ggacgacatc gagactgtcc ttcagctctt
60ccggcttggc aacatcaatg ccaaagccag ccaggcagga cagacggccc tgatgctggc
120cgtcagccac gggcgggtgg acgttgtcaa agccctgctg gcctgtgagg cagatgtcaa
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240gatcgcgggg ctgctgctgg ccgtgccag ctgtgacatc tcaactcacag atcgcgatgg
300gagcacagct ctgatggtgg ccttgagcgc agggcagagt gagattgcgt ccattgctga
360ttcccgcatt aacatcaagt gctcgt

386

<210> 3268<211> 424<212> DNA<213> Homo sapien

ggcacgaggc agaccctcca cctcctggt tacatcccag agtccgggca gaatcagctg
60ttacagcccc ttaagccatc tccctccagt gacaacctct attcagcctt caccagtgat
120gggtgccattt cagtaccaag cttttctgct ccagggtcaag gaaccagcag cacaacact
180gttggggcaa cagtgaacag ccaagccgcc caagctcagc ctctgcccatt gacgtccagc
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300atgaatctct caggcaggag aggaagcaaa gggcacatga attatgaggg ccctggaatg
360gcaaggaagt tctctgcacc tgggcaactg tgcattctca tgacctcgaa cctgggtggc
420tctg

424

<210> 3269<211> 410<212> DNA<213> Homo sapien

cgttgctgtc gcacagatgc ccgcttacca ggagctggtg gaggaggcga ttgcctatgg
60ccggaagctg ggcgggtcac aagaggacca gattaaaaat gctattgata aactttttgt
120gttgtttgga gcagaaatac taaagaagat tccggggcca gtatccacag aagtagacgc
180aaggctctcc tttgataaag atgcgatggg ggccagagcc aggcggctca tgcagctcta
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300aattcaggct ggaaaggagc tgcaggagca gcacggcatc cactgcaaca tgacgttact
360cttctccttc gcccaggctg tggcctgtgc cgaggcgggt gtgaccctca

410

<210> 3270<211> 389<212> DNA<213> Homo sapien

cggtgctgtc ggagaaccct gttataatgg gactgtcag cctaaatggt caggtgacaa
60ggcctgtgaa acccactggt ggccctggag gagggggcgc acaaacacag cctcagaaga
120gccagctgat taacaccaac acaatcgcta atggcactca gcagcacgca cagagtatga
180ccaccactat taagtatgtg gtagagtaaa ttatgtatta tacacttgcg gggaaccaag
240atatgggata ctttgaggtt gactattaat acttatgcct taagttaacc attttgattg
300caaatagagg acagatgact ttgttttatg gccagtatgt atttgcaata caataatata
360tatctgccat aatttgtgca gcatgtagg

389

<210> 3271<211> 374<212> DNA<213> Homo sapien

cggtgctgtc ggggcctccg gggaagcgtc cccgctaggg gtgggggtctt gggactccct
60ggggcctccg gagctgaccc gtgggggggtc tgctgccctc agttcctgct gaccaaagtc
120ctgccggatc tggcgcctac gaggacgtgg cgggtggagc tcagaccggt gggctaggtt
180tcaacctgcg cattgggagg ccgaagggtc cccgggaccc gcctgctgag tggaccggg
240tgtctctgga cctctgactg aactgtgcc tgcccaggtc cctgtatgca ctgccacagt
300gccctgggccc ccatgtccac ccctgtcctg cccttctctg ggataggggt ggccttcctc
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374

<210> 3272<211> 381<212> DNA<213> Homo sapien

cggtgctgtc ggggcctccg gggaagcgtc cccgctaggg gtgggggtctt gggactccct
60ggggcctccg gagctgaccc gcgggggggtc tgctgccctc agttcctgct gaccaaagtc
120ctgccggatc tggcgcctac gaggacgtgg cgggtggagc tcagaccggt gggctaggtt
180tcaacctgcg cattgggagg ccgaagggtc cccgggaccc gcctgctgag tggaccggg
240tgtctctgga cctctgactg aactgtgcc tgcccaggtc cctgtatgca ctgccacagt
300gccctgggccc ccatgtccac ccctgtcctg cccttctctg ggataggggt ggccttcctc
360tgccctctgcc tggctgcata n

381

<210> 3273<211> 290<212> DNA<213> Homo sapien

agcgaggctca gaggccatga gggaaaggca gactcgggag gagagtggag tacttccaca
60tctgggcggc tgtgggggga acaactgtgt gtgtgcttta catccatccc ctgaaccttc
120agagctgact atcccagcct cggctaagtgt attctacgcc atggatggag cttcacacga
180tttctcctctg cggcagcggc gaaggctctc tactgtaca cctggcgta ccagtggccc
240gtctgcctca ggaactcctc cgagtgaggg aggagggggc tcctttccct

290

<210> 3274<211> 382<212> DNA<213> Homo sapien

ggcacgagct cgaatctcca gaaaagcagc taacactaaa tgagatctat aactggttca
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120atcttagtct tcacaagtgt tttgtgcgag tagaaaacgt taaaggggca gtatggacag
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240ttaaaaaacat gcagagcagc cacgcctact gcacacctct caatgcagct ttacaggctt
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382

<210> 3275<211> 403<212> DNA<213> Homo sapien

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120agagagggga gaagaggcag gagctggaaa ggagagaggg aggaggggga ggagatgcgt
180gatggagacc tggagttagg tggcttggga gagcttaatg aatagagaac ggagaggagg
240tgtggggttag gaaccaagag gtagccctgg tggcagcaga aggctgagag gtagtaggaag
300atcaggagct agagggagac tggatgggtc cgggaaatga gcagaggaaa gaggaaagac
360acagagagac gggagagaga agaatagtgg ttttgtatgg cgg

403

<210> 3276<211> 405<212> DNA<213> Homo sapien

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120ctccacacgc accgagccat gaggagctgc gcctctgaga gcctcttccct gccctactac
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240gatgccacac agatggctct cgtgctggct cactgaagag ctgagcctga ggctggcctc
300acaatcaagc tgggtgcagt ggctcacacc tgtaatccca gcattttggg aggctgagtg
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405

<210> 3277<211> 377<212> DNA<213> Homo sapien

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120aggctggtct cgaactcctg acctcaggtg atctgcccac cttggcctcc caaagtgtg
180ggattacagg catgagccac tgtgctggc cccttctgt aaaattttta aatggagaat
240tgggtgcgag atgtggtttc cagcctggtg cctggggtgc tgagctagtg agtgggtgcag
300tccaggacac ctttgcctta tgtcattac acggtcacct ggagccggct caagtggcta
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377

<210> 3278<211> 384<212> DNA<213> Homo sapien

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60tataagaact ctgaaggagg aatagatttg actgtattaa atgttggcga gagactctct
120ttgatacatt aaaaaaactg ttgcagaag cagttctatg gaagagactg gaataattat
180ggccgtgtaa cgtgtaccgc cttaatggg aaatattctt gatcttcaac attgttcttt
240ggttcttttt tcttttttta ggaaaaacaa aacaacagac ttcattcctta gggtttctca
300agatttaagc gaacacattt acacatatca atttcttaaa gaacacagaa tgtttcctcc
360ctagcttaac tatttaagag ccag

384

<210> 3279<211> 181<212> DNA<213> Homo sapien

acccnnnn nctgcctcac ctctctgggc cagtttcccc atagtacagt ggtgctgac
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120gaggccccgt gatgcatcag ggtcagctg aggtctgag ctaactggga aacacagtgg
180c

181

<210> 3280<211> 152<212> DNA<213> Homo sapien

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120tgtgcacatt gatagagctt ggagttgagg ct

152

<210> 3281<211> 189<212> DNA<213> Homo sapien

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120accttccact tccaagagtt agacaataaa agcctcatca agaaccatc ggagcgagct
180gacctgaag

189

<210> 3282<211> 392<212> DNA<213> Homo sapien

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120acagaagaga aagaagctgg gggctcagat gaggagcagg agaagggcag cagcagtgag
180aaggagggca gtgaagatga gctcgggc agcgagagt aacgggagga aggtgacagg
240acgagggcca gtgacaagag tggcagtggg gaggacgaga gcagcgagga tgaggccgg
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360tctgatgatg aggacagagg acaggcccaa gg

392

<210> 3283<211> 170<212> DNA<213> Homo sapien

gaatttnncc ncnncacctg ccaactactac nccaacaagt acagcttctg gctgaccacc
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120ccgcacacat caaccgctgc caggtgtgca tgaagaacct gtgagccgga

170

<210> 3284<211> 158<212> DNA<213> Homo sapien

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60ggctctagaa gacctggctg gcttttaaaga gctcttccag acacgaggtc aactgagga
120tcaatgacta acgataatac tgccaaagta gcctgcaa
158

<210> 3285<211> 153<212> DNA<213> Homo sapien

ccaanaacag attgctgaat tcaaggaagc cttctcccta ttgataaag atggcgatgg
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120agctgaattg caggatatga tcaatgaagt gga
153

<210> 3286<211> 350<212> DNA<213> Homo sapien

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120agccgcgaca atccagggag caacacctat agccttcatt acatcgttca acttcacttt
180gaggtatgct acgtagaaat agatcatgga gccaaagtga gtgcactttg tcaaagttaa
240gggtctgctt tggtcttgtt gcttttctgt ttttaacct tttgttccgc catttaaaaa
300aagaaaaaaa aaaagttatg tttcttgtca aatgcagaaa tgttctctcc
350

<210> 3287<211> 162<212> DNA<213> Homo sapien

agctcggctt ttatcttctt ccgtaccact tgacaacat ggggccctgg tcttctgtac
60tcaggggctg gtctcccaga gatgggcaaa agccagcttg cccgtttct ttatgcttca
120agagaaaacc ctcttcttgg gtccagactc tgggtggagt gt
162

<210> 3288<211> 184<212> DNA<213> Homo sapien

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60gagacatgac tattgggcag ctacaagtga tagtcaatga tctccattcc cagatagaag
120cttgaatgaa gagttggtcc agctgcttct catccgagat gagctgcaca cagagcanga
180tgcn
184

<210> 3289<211> 188<212> DNA<213> Homo sapien

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60agaacagtga tgtgacttct tggtcagaag aaaaacgtga agagaaaatg ctctttaccg
120gttatcttga ggacagaaaag ttaaaaaaga acaagaagaa ttcccatgaa ggagtttctt
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188

<210> 3290<211> 383<212> DNA<213> Homo sapien

cggtgctgtc gcacacacct gtaatcccag ctaccgggga ggctgaggca ggagaatcgc
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120gtgacagagc gagactccat gtcaaaaaaa aaaaaagggt gggaactcaa attttctttt
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240aaaagcagct atgggtaaat ttctgaaata tagcaggaga ccaaaacatg tttggaaaga
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383

<210> 3291<211> 158<212> DNA<213> Homo sapien

ctttcaagac agcctccctt tattgaattg gcattaggga ataaacaagc ctttaaactg
60gataaaagat caaaaacctg gttagacatg ccagcctttg caaggcaggt tatgtacaa
120agactaacct ccaagtggct ttatggacgc tgcatatg
158

<210> 3292<211> 378<212> DNA<213> Homo sapien

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60caggaccttc gctggccaca gcaagtggat cacaggcctg agctgggagc cctccatgc
120gaaccctgag tgccgctatg tggccagcag ctccaaggat ggcagtgtgc ggaatctggg
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240ccgggtgggga ggggacgggc ttctctactc tgctcccag gaccgcacca tcaaagtctg

300gagagctcat gacggtgtgc tgtgccggac tctgcaaggc cacggccact ggggtgaacac
360catggccctc agcactga

378

<210> 3293<211> 342<212> DNA<213> Homo sapien

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60tgagaatcgg aaaaaagcag aagaagctca taaaattttt gaaggctttg gccc aaaagt
120tgaactgcca ctgtataacc agccatcaga taccaagggtg taccatgaga acatcaagac
180tgaggtacct gcaaggcgca tgatgaaaaa ccagggtgatg aggaaaaaac tcattttatt
240tttttaaaaga agaaatcatg catgaaaaca aagggaacaa aaaatctgcc agcgttatga
300tcagctcatg gaggcatggg agaaaaaagt ggacagaata gn

342

<210> 3294<211> 396<212> DNA<213> Homo sapien

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120gagaaaaata ctgcaaacc caaatgaca taacaagtac catcaatggg tccagccatt
180gccttttgaa actatagacc tgggaattcaa agtggaggaa ccattgaaca aaaggctatt
240aagcggctac caggcctgaa ttttgatgat .aatggaaaaa ggaacaacaa atttttgagg
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360caagctctac cgataaatac agacatgccca ccaaat

396

<210> 3295<211> 187<212> DNA<213> Homo sapien

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60atcgggtgctc aaccgcgtgc cgcagcccga ataccggcag ctgctggagg aagccatcat
120ggagctgacg ctgctctcgg acacggagat gaccagcatc gggggcatca tccacgtgga
180ccagatc

187

<210> 3296<211> 163<212> DNA<213> Homo sapien

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60attcacaacc aagatctacc accccaacgt ggacgagaac ggacagattt gctgcccac
120atcagcagtg agaactggaa gccttgcacc aagacttgcc aag

163

<210> 3297<211> 156<212> DNA<213> Homo sapien

cattgccatc caccgtggga tgccccaaga ggagaggctt tctcgggtatc agcagtttaa
60agattttcaa cgacgaattc ttgtggctac caacctatct ggccgaggca tggacatcga
120gcgggtgaac attgctttta attatgacat gcctga

156

<210> 3298<211> 345<212> DNA<213> Homo sapien

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60ctggagcagc aagaccgtgc actggagaag gcgaggtcaa gtgcccact gcagaccaac
120taccctctct cagacaacag cctctacacc aacgccaagg gcagcaccat ctctgcttcc
180gatgggggag gtgtgggagg ttttttatcc tttctccgta tgacttcaca ccagatgcta
240tctgcctctg gtacgaatt tctcatttcc tgacaatccg aaaatactat tagtttacc
300ccgtcagcta atcctttctt catcgagtgc cataccccca ctacg

345

<210> 3299<211> 422<212> DNA<213> Homo sapien

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60tgagcgggag tggcacaat tctgtctgga gtacattgcg cccatgacag agaagctcta
120ccccggctac tacaccaggg cccagggtga cctggccttt gtcgtccgct acaagcctga
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300gtctttggag ccaccaatca aagagattca aagagattcc tgcaggccag aggcggaaca
360cacctttatg gctggagctc tccgtggtga tctggaccca gcctctggag acaccattca
420ct

422

<210> 3300<211> 182<212> DNA<213> Homo sapien

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60cacacatgag ctctaggaga gaaaactgag atcactgggg caatgacat gacttctgtg
120gtcatcagtc catgaccctt ggagagaaag ccctgacccc tgtgggtatc aatctgtgac
180ca

182

<210> 3301<211> 391<212> DNA<213> Homo sapien

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60caattgccaa aagtgttagg tggcgacagt gctatgaggg ccttccagaa cacggcaact
120gcatgtgcac cagtatcaca ttatcgagct gttgaaagtg tggattcaag tgaagaaagt
180ttttctgatt cagatgatga tagctgtctt tggaaacgca aacgacagaa atgttttaac
240cctcctccca aaccagagcc ttttcagttt ggccagagca gtcagaaacc acctgttgct
300ggaggaaaga agattaacaa catatggggt gctgtgctgc aggaacagaa tcaagatgca
360gtggccactg aacttggtat cttgggaatg g

391

<210> 3302<211> 380<212> DNA<213> Homo sapien

ccattcactc gttcagcaga cacgcatggt actgatgctt tgagttttct tctgtgggga
60tttctttct ctggactctg tgcagccctt gccctccctc ggggtgctgct ggctcaaaag
120gaggaaactg tggcgaggag tgtggaatta ttcacctaag cctgaccttt tgttagttg
180acagcattcg tttctgtgtt gccaatcttg gctcatagca gatgcatagg aatgagctcg
240agccttctc cttttgcttc cgatatatt tttcctcttg ggaacatgag tccacttcga
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380

<210> 3303<211> 175<212> DNA<213> Homo sapien

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120gttttgggcc gggggtcgcc tttcgcgcgc ccagcattca cgggggctcc ggcgg

175

<210> 3304<211> 356<212> DNA<213> Homo sapien

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120tagaagcagc cagtcacaga ccattctat gcaatggaca tttatttgaa aaaaattctc
180aaaagttttt tttttttttt tggggggggg gggtttttaa gctgttttta cctccgagac
240tccactttta agggacccag ggaattaagg catataaaat ttaccccccc aagattaaaa
300gccaggaag aggttcaacc catgtgagaa ctgccctcct aggaaaggg ttaagg

356

<210> 3305<211> 170<212> DNA<213> Homo sapien

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60ccatctatga atttactgct gcgcagaaca tttgaccttt actcgaatgt ccgacctgt
120gtttctatcg aaggctatcc aacccttac accgatgtaa atattgtgag

170

<210> 3306<211> 413<212> DNA<213> Homo sapien

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120tcagacatca gagaattcat agtggggagg aaccttatca gtgtaatgaa tgtggcaaaa
180ctttcaaaaag gagctcagcc cttgttcagc atcagagaat tcattctggg gatgaagctt
240atatatgtaa tgaatgtggg aaggctttca ggcacagatc ggtccttatg cgccatcaaa
300gagtccacac tataaagtaa tttgtgaata ctgtgaatag tgtaaatact tcagtcagat
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413

<210> 3307<211> 402<212> DNA<213> Homo sapien

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120ggacagtcac tcattccaag gagcttatgg gctggccctc aagggtggcca caccgccacc
180cagtgccag ccctggaaag gggaccccggt ggaacagctg gtccgccatt tctcatcga
240gactgggccc aaaggggtga agatcaaggg ctgccccagt gagccctact ttggcagcct
300gtccgccttg gtctccagc actccatctc ccccatctcc ctgcctgct gctgctgcat

360tcccagcaaa gatcctctgg aagagacccc agaggctcca gt
402

<210> 3308<211> 388<212> DNA<213> Homo sapien

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60agctgtaccg tgggtgcgatg actagtagca tggagcgaga ttttgacgt ggtgatattg
120gaataaatcg aggcttttga gattcctttg gtagacttgg tgggtggaatg ggtagcatga
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240tgggaccagg tataggagct atactggaaa ggagcatcga tatggatcga ggatttttat
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388

<210> 3309<211> 387<212> DNA<213> Homo sapien

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60agttgaggag gaggagcgc ttgaggggga ctggcctggc gtgcactccg cacctcgggg
120acattattgc gcgtggaacg gctgcttttg gaagactatt gccagaaga aaagatgttt
180ggttttcaca agccaaagat gtaccgaagt atagagggct gctgtatttg cagagctaag
240tctccagtt ctgcattcac tgacagtaaa cgctatgaaa aggacttcca gagctgtttt
300ggattgcatg agactcgttc aggagacatc tgcaatgcct gtgtcctgct tgtgaaaaga
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387

<210> 3310<211> 422<212> DNA<213> Homo sapien

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120acctggaaaa caaagtgaag aagatgggct taggtcacga gcaaggattt ggagcccctt
180gttttaaatg caaagaaaaa tgtgaaggat tcgaactgca cttctggaga aaaatatgtc
240gtaactgcaa gtgtggccaa gaagagcatg atgtcctctt gagcaatgaa gaggatcgaa
300aagtgggaaa actttttgaa gacaccaagt ataccactct gattgcaaaa ctaaagtcag
360atggaattcc catgtataaa cgcaatgtta tgatattgac gaatccagtt gctgccaaga
420an

422

<210> 3311<211> 441<212> DNA<213> Homo sapien

aagctactgg ggnnttggca ggatcccac gattcgctac accttcccgg ccagcggtag
60caactgcaga actgcaggag actatctttc tagacaaggc agttgaggag gagggagcgc
120ttgaggggga ctggcctggc gtgcactccg cacctcgggg acattattgc gcgtggaacg
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300tgacagtaaa cgctatgaaa aggacttcca gagctgtttt ggattgcatg agactcgttc
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420atcaaaaaaa aactggaatc a

441

<210> 3312<211> 382<212> DNA<213> Homo sapien

ggcacgagat acatttatga tggagaactg ttatcaaaga atggattttt tcagggatat
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120aataacagct acttttttgt atggttatga tcccaaacct gcaggaaatc ccactaaagc
180atagttgtat actatcttta actggttttt cactaggaat ctgcacatta
240atcttgcaca gaggacttct acagagtctg agaagatata atcatgctga atctgatcat
300actgtttttt aaaagttaa ggataagaca tgtgtatatg taacaaaaca cattgcatct
360agaaatcaaa acttgaaagt ag

382

<210> 3313<211> 385<212> DNA<213> Homo sapien

ggcacgagtg cttttctatg acctgacac cagcatcatt tacttatgtg gaaagggtag
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120attcagcagc aaggagcctc agagagggat gggttacatg cccaagaggg gacttgatgt
180taacaaatgt gagattgcca gattcttcaa acttcatgag agaaagtgtg aacctattat
240tatgactgtt ccaggaagt ctgacctttt ccaagatgac ctgtatcctg acacagcggg
300gccagaggcc gcgctggagg cagaagagtg gttcgaaggc aagaatgcag acccaatcct

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385

<210> 3314<211> 456<212> DNA<213> Homo sapien

ncaggtaaac tagnnctntg cgnncngnca nnnngncaaaa ngcaggagcc catttattct
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120agaagaggtg aagatatttg ttggattaaa accaataaaa acaatcctgg gaagactaag
180actttagatc caaaggctgt ctttcagaga acaaaggaac actgcctcat ggggatcaaa
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300attatcacag aagaacctga aattggcaat atagaaaaac ctgtagaaat ttttcatata
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456

<210> 3315<211> 329<212> DNA<213> Homo sapien

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180gccggatgat ttgtaggcag ggacgtttta gtgtcggttt tacgagattc cttgatatat
240tacagaatta gagtccagat ttacacaaa aaggaccccc ttttccctct ccggaccacg
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329

<210> 3316<211> 414<212> DNA<213> Homo sapien

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120cggagaacca ggccctgcag cagcagcttc accaggagca agagcagctc tacctgaggt
180caggtgtggt gtccctctgcc accttcgagc agccgagtcg ccaggtgaag ctgtgggtga
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300agatgacagg catggccggg gtcagctctt tcagccgcgc ttcagcgatg actccagtct
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414

<210> 3317<211> 380<212> DNA<213> Homo sapien

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120agctgtgctt tgggaagcag ctcttcctgg aggtgtgga acggagccag gcgctgcca
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240accgcggccat cgaggaccag ggtggggagt acgtgcagcc catgctgagc aagtacgcgg
300ctgtgtgcgt gcgctgccct ggctacggca ccagaaccaa cactatcatc ctggtagatg
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380

<210> 3318<211> 427<212> DNA<213> Homo sapien

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360tctaacttgg ttatgagact aacaccattc ctactgctc taacatgctg aagaaatcat
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427

<210> 3319<211> 408<212> DNA<213> Homo sapien

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240cggtgttatt attcattatg gtagaatcat ttttaattca cgtgctttgt gttcagtttt
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408

<210> 3320<211> 393<212> DNA<213> Homo sapien

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240aagcaaatca ggccccgaaa tctaagtctg gctcccgtcc ccgcaagcca ccaccccgga
300agcacactcg ttcctgggct gtgctgaagc tgctgctgct gctgctgcta tttgggtgtg
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393

<210> 3321<211> 423<212> DNA<213> Homo sapien

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120gttcaacctc agcaagggtta tattcctcca atggcacagc caggactgcc accagtacca
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240ccaggaatgc caccagttat gccaggcatg ccacctggat tgcacatca gagaaaatac
300acccagtcac tttgcgggtga aaacataatg atgccaatgg gtggaatgat gccacctgga
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420cct

423

<210> 3322<211> 397<212> DNA<213> Homo sapien

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120agattgcat cgtgacggag aaccaggccc tgcagcagca gcttcaccag gagcaagagc
180agctctacct gaggtcaggt gtggtgtcct ctgccacctt cgagcagccg agtcgccagg
240tgaagctgtg ggtgaagatg gtgactccac tgatcaagaa cttcttctga ggacagacag
300gaatggcctt gatgaagatg acaggcatgg ccggggtcag ctctttcagc cgcgcttcag
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397

<210> 3323<211> 398<212> DNA<213> Homo sapien

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180ttcctcacia cagggacgca gaacaaaaag aggaggatct agagaaaaag gagctgaact
240ccttatatat atacagtttt ataaaagaag ccaatacact gaacctggct ccctatgatg
300cctgctggaa tgcctgtcga ggagacaggt gggaagactt gtccagatca catgtgcgct
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398

<210> 3324<211> 399<212> DNA<213> Homo sapien

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240tcgctacagg cccgggaccg tggcgcttcg agagattcgt cgttatcaga agtcgaccga
300gctgctcatc cggaagctgc ccttccagag gttggtgagg gagatcgcgc aagatttcaa
360aaccgacctg aggtttcaga gcgcagccat cgggtgcgct

399

<210> 3325<211> 439<212> DNA<213> Homo sapien

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360agggcgtact gcgggttggtg acgggggtcc cctcagtcac actcactttt tttccttgg
420atgttattga ggatattct

439

<210> 3326<211> 429<212> DNA<213> Homo sapien

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360gccactaag ggaagccaat gaggaggttg cacttcgtgt accacaactt gtggcccaag
420aattggccc

429

<210> 3327<211> 449<212> DNA<213> Homo sapien

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60cttcaaaactg aaggcagcca gtgtgctaaa acatttataa atctgatgac tcatactgc
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360aattggataa aaactcagct gagttcacag aaactggcgt gtancgggtg tgctgttgaa
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449

<210> 3328<211> 398<212> DNA<213> Homo sapien

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240actccacct cctgagaaag tactatcagc tgtggtccag accctttagt ctaaagaaaa
300agcactgagg cctgtggacc agaatactca gtcaaaaaat agagctgctt tgggtgatgga
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398

<210> 3329<211> 426<212> DNA<213> Homo sapien

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360cccacttngg gaagcgaatg aggaggttgc actccgcgta ccacagctgg tgggcccagg
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426

<210> 3330<211> 399<212> DNA<213> Homo sapien

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240ttctcctgtt cctatgttaa gggatctgac acagaactc gtagtcagta ttaattttaa
300agaccacag tttgctgaag attacatttt taaagctgta atgcttccag gagcaagaaa
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399

<210> 3331<211> 402<212> DNA<213> Homo sapien

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240cgctacctgt acatcatgga cttgcggaca gagagcctga ttagtcgctg gcctctgcca
300gagtacagga aatcaaagag aggctcaagc ttcctggcag gcgaagcatc ctggctgaat

360ggactggatg ggcacaatga cacgggcttg gtctttgcc a cc
402

<210> 3332<211> 372<212> DNA<213> Homo sapien

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300caggaggacc aatgattagc atttatgatg cagagacaga gcaacttcgt ataggaccgt
360actcctggac cg
372

<210> 3333<211> 436<212> DNA<213> Homo sapien

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240actgtgaaca tgggtcagaa acaggaaatt ctggatctct tttcttcagt actctatgaa
300tgtgttacc aggagacccc agagatgttg cctgcataca tagcaatgga tcaggctata
360agaagacttg ggagaagaga aatgtctgag acttctgaac ttggcagat acagatgggtg
420tttagtttt tcagct
436

<210> 3334<211> 377<212> DNA<213> Homo sapien

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300caggaggacc aatgattagc atttatgatg cagagacaga gcaacttcgt ataggaccgt
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377

<210> 3335<211> 408<212> DNA<213> Homo sapien

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240caaatgatgt agttattact gtcccgtttg attttgagaa aaagcaaaaa aatgctcttg
300gagaagcagc tagagctgct ggatttaatg ttttgcgatt aattcacgaa ccgtctgacg
360ctcttcttgc ttatggaatt ggacaagact cccctactgg aaaaagct
408

<210> 3336<211> 421<212> DNA<213> Homo sapien

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420t
421

<210> 3337<211> 455<212> DNA<213> Homo sapien

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360cattggagcg aaaataccag ccttaactat gcagctcatg ctgcgaaatc caggggtccag
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455

<210> 3338<211> 417<212> DNA<213> Homo sapien

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417

<210> 3339<211> 414<212> DNA<213> Homo sapien

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414

<210> 3340<211> 387<212> DNA<213> Homo sapien

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387

<210> 3341<211> 415<212> DNA<213> Homo sapien

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240accaacagag actgcgccga gtgtgaagtg ggtgggtgc tggacgaggg cgctgtgtg
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415

<210> 3342<211> 398<212> DNA<213> Homo sapien

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240agtcaagcgg ccagggagag atgacatgct ggacgtggag accgatgcct acatccactg
300cgtcagtgcc ttcgtcaagc tggcgcagag cgagtaccag ctgctggccg acatcatccc
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398

<210> 3343<211> 374<212> DNA<213> Homo sapien

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374

<210> 3344<211> 405<212> DNA<213> Homo sapien

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405

<210> 3345<211> 425<212> DNA<213> Homo sapien

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410

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461

<210> 3351<211> 419<212> DNA<213> Homo sapien

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419

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WO 01/02568 A3

(54) Title: HUMAN GENES AND GENE EXPRESSION PRODUCTS

(57) Abstract: The invention provides novel polynucleotides. The invention further provides novel members of protein families, and polynucleotides that are differentially expressed in cancer cells relative to normal cells, and in metastatic cancer cells relative to normal cells or non-metastatic cancer cells.

INTERNATIONAL SEARCH REPORT

International Application No
PCT/US 00/18374

A. CLASSIFICATION OF SUBJECT MATTER

IPC 7 C12N15/12 C12N15/55 C12N15/54 C12N15/61 C07K14/47
C12N9/64 C12N9/12 C12N9/90 C12Q1/68 C12N15/11
C07K16/18 C07K16/40 G01N33/56 A61K38/00

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 7 C12N C07K C12Q G01N

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

STRAND, EMBL, EPO-Internal, PAJ, WPI Data, BIOSIS

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
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A	<p>DATABASE EMBL [Online] ACCESSION NUMBER : AC004067, 31 January 1998 (1998-01-31) N.E. STONE ET AL.: "Homo sapiens chromosome 4 clone B366024 map 4q25, complete sequence" XP002155218 Sequence data</p>	1-3,9-13
A	<p>--- DATABASE EMBL [Online] ACCESSION NUMBER : R09152, 20 April 1995 (1995-04-20) L. HILLIER ET AL.: "yf25h12.r1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone." XP002155219 Sequence data</p> <p>---</p>	1-3,9-13

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☒ Further documents are listed in the continuation of box C.

☒ Patent family members are listed in annex.

* Special categories of cited documents :

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier document but published on or after the international filing date

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"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

"&" document member of the same patent family

Date of the actual completion of the international search

18 December 2000

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Hix, R

INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 00/18374

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	<p>WO 97 40151 A (GENETICS INST) 30 October 1997 (1997-10-30) the whole document</p> <p>-----</p>	

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US 00/18374

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☐ Claims Nos.:
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Claims 1 to 3, 9 to 13 partially

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application. as follow :

Invention 1: Claims 1 to 3, 9 to 13
{partially}

A polynucleotide library comprising the sequence SEQ ID NO: 1, an isolated polynucleotide comprising the nucleotide sequence having at least 90% sequence identity to SEQ ID NO: 1, a recombinant host cell containing said polynucleotide, isolated polypeptide encoded by said polynucleotide, antibody that binds specifically to said polypeptide and vector comprising said polynucleotide.

Invention 2: Claims 1-15 (partially and as far as applicable)

Idem invention 1 but limited to a polynucleotide library comprising the sequence SEQ ID NO: 2.

Inventions 3-3351 : Claims 1-15 (partially and as far as applicable)

Idem invention 1 but each invention limited to a polynucleotide library comprising a sequence SEQ ID NO: 3-3351.

INTERNATIONAL SEARCH REPORT

information on patent family members

International Application No

PCT/US 00/18374

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
WO 9740151 A	30-10-1997	AU 2459397 A	12-11-1997
		AU 2728697 A	12-11-1997
		CA 2251934 A	30-10-1997
		EP 0939807 A	08-09-1999
		EP 0954577 A	10-11-1999
		JP 2000508908 T	18-07-2000
		JP 2000508909 T	18-07-2000
		WO 9740069 A	30-10-1997
		US 5958726 A	28-09-1999
